? ds

Set	Items	Description
S1	1305	TAU AND PHOSPHORYL? AND (MONOCLONAL OR MAB)
S2	599	RD S1 (unique items)
S3	304	S2 AND PY<1996
S4	111	S3 AND PY<1993
S5	234	E3-E9
S6	805	E1-E11
S7	148	E3-E11
S8	1128	S5 OR S6 OR S7
S9	77	S8 AND TAU AND (MONOCLONAL OR MAB)
S10	33	RD S9 (unique items)

? logoff y

20may02 08:29:42 User226352 Session D629.3

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Search Results -

Terms	Documents
tau and phosphorylat? and (monoclonal or mab) and Alzheimer?	7

Database: US Patents Full-Text Database
US Pre-Grant Publication Full-Text Database
JPO Abstracts Database
EPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search: L3

Refine Search

Recall Text | Clear

Search History

DATE: Monday, May 20, 2002 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT; PLUR=YES; OP=AND		
L3	tau and phosphorylat? and (monoclonal or mab) and Alzheimer?	7	L3
L2	tau and phosphoryl? and (monoclonal ro mab) and Alzheimer?	0	L2
L1	tau and phosphory? and (monoclonal or mab)	8	L1

STIC-Biotech/ChemLib

66969

From: Duffy, Patricia
Sent: Monday, May 20, 2002 9:47 AM
To: STIC-Biotech/ChemLib
Subject: Sequence Search 09/734,281

Importance: High

In re: 09/734,281

Please search SEQ ID NOs:1 and 2.
Please include an interference search.
Please print out top 40 hits in each category.

Thank you.

Patricia A. Duffy
Art Unit 1645
Office CM-1, 8D05
Mailbox CM-1, 8E12
Phone 703-305-7555

Mary Hale – Supervisor, Info. Branch
STIC – Biotech/Chem. Library
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Searcher: Mary
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Date Completed: 5/21
Searcher Prep/Review: _____
Clerical: _____
Online time: 10

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 2
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 21, 2002, 11:10:10 ; Search time 51.55 Seconds
(without alignments)
19.392 Million cell updates/sec

Title: US-09-734-281-1
Perfect score: 50
Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : A_Geneseq_032802:*
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
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19: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
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21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	9	14	AAR36557	Peptide sequence f
2	50	100.0	12	14	AAR38235	Alzheimer paired h
3	50	100.0	12	14	AAR37554	Phosphorylated tau
4	50	100.0	12	18	AAW34857	Human tau protein
5	50	100.0	12	21	AAY81390	Human phosphorylat
6	50	100.0	14	21	AAB21959	Phosphorylated tau
7	50	100.0	34	15	AAR61330	Peptide phosphoryl
8	50	100.0	34	18	AAW34875	Human tau protein
9	50	100.0	67	15	AAR59837	Sequence of human
10	50	100.0	78	22	AAB85640	Tau peptide region
11	50	100.0	106	17	AAR92516	Microtubule-associ
12	50	100.0	112	16	AAR76937	PHF-tau (143-254)
13	50	100.0	351	21	AAY15200	Human Tau protein.
14	50	100.0	352	10	AAP91294	Paired helical fil
15	50	100.0	352	14	AAR32708	Human tau-protein.
16	50	100.0	352	19	AAY20248	Human microtubule
17	50	100.0	390	17	AAW05283	Truncated human ta
18	50	100.0	441	15	AAR58810	Human tau protein.
19	50	100.0	441	17	AAW05282	Human tau protein.
20	50	100.0	441	18	AAW34856	Human tau protein.
21	50	100.0	441	21	AAY81386	Human paired helic
22	43	86.0	13	13	AAR28237	Phosphopeptide as
23	43	86.0	13	18	AAW34860	Human tau protein
24	43	86.0	13	18	AAW34858	Human tau protein
25	40	80.0	263	18	AAW29455	Oerskovia xanthine
26	40	80.0	435	18	AAW29456	Oerskovia xanthine
27	39	78.0	7	14	AAR38233	Alzheimer paired h
28	39	78.0	7	14	AAR37552	Phosphorylated tau
29	39	78.0	263	22	AAU17141	Novel signal trans
30	39	78.0	376	22	AAM80057	Human protein SEQ
31	39	78.0	424	21	AAB41838	Human ORFX ORF1602
32	39	78.0	424	22	AAM79073	Human protein SEQ
33	39	78.0	424	22	AAB27227	Human EXMAD-5 SEQ
34	38	76.0	98	22	AAO05662	Human polypeptide
35	37	74.0	284	22	ABG27348	Novel human diagno
36	37	74.0	335	13	AAR25063	Soluble human IL-5
37	37	74.0	335	14	AAR33699	shIL-5R-alpha. Sy
38	37	74.0	350	22	AAM93217	Human polypeptide,
39	37	74.0	351	22	AAM52310	Chicken zyxine fra
40	37	74.0	353	13	AAR28314	AHSV protein. Afr
41	37	74.0	395	22	AAM39380	Human polypeptide
42	37	74.0	396	13	AAR22216	Sequence of human
43	37	74.0	396	13	AAR22220	Sequence of secret
44	37	74.0	418	17	AAR98562	Human neurotensin
45	37	74.0	418	22	ABB56371	Non-endogenous hum
46	37	74.0	420	13	AAR22215	Sequence of human
47	37	74.0	420	13	AAR22219	Sequence of secret
48	37	74.0	420	19	AAW82842	Human interleukin-
49	37	74.0	421	13	AAR25064	Human IL-5 recepto
50	37	74.0	464	22	AAM93631	Human polypeptide,
51	37	74.0	494	22	AAM41166	Human polypeptide
52	37	74.0	539	21	AAY87747	Human brain proteo
53	37	74.0	542	22	ABG12316	Novel human diagno
54	37	74.0	542	22	AAM52304	Chicken zyxine. G
55	37	74.0	545	18	AAW28867	Human brain Neurog

ALIGNMENTS

RESULT 1
AAR36557
ID AAR36557 standard; peptide; 9 AA.
XX
AC AAR36557;
XX
DT 10-AUG-1993 (first entry)
XX
DE Peptide sequence for abnormally phosphorylated tau protein.
XX
KW Alzheimer's disease; Down's syndrome; Pick's disease; monoclonal;
KW antibody; detection; SSPE; antigen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 3
FT /note= "may be phoshorylated"
FT Misc-difference 6
FT /note= "may be phosphorylated"
XX
PN WO9308302-A.
XX
PD 29-APR-1993.

XX
PF 17-OCT-1992; 92WO-EP02392.
XX
PR 25-OCT-1991; 91EP-0402871.
XX
PA (INNO-) INNOGENETICS NV SA.
XX
PI Mandelkow E, Mercken M, Van DE VOORDE A, Vandermeeren M;
PI Vanmechelen E;
XX
DR WPI; 1993-152493/18.
XX
PT Monoclonal antibodies binding abnormal micro-tubule-associated
PT tau-protein - for diagnosing neurological disorders e.g.
PT Alzheimer's disease, Downs syndrome, Picks disease, etc.
XX
PS Claim 8; Page 36; 47pp; English.
XX
CC The peptide is able to form an immunogenic complex with a
CC monoclonal antibody contg. a phosphorylated epitope of an antigen
CC belonging to human abnormally phosphorylated tau protein which can be
CC obtd. from a brain homogenate isolated from the cerebral cortex of a
CC patient having Alzheimer's disease. The monoclonal antibody is able
CC to specifically detect only abnormally phosphorylated tau protein and
CC not react with normal tau protein, and thus may be used in the detection
CC or diagnosis of neurological diseases, e.g. Alzheimer's disease, Down's
CC syndrome, Pick's disease or SSPE.
CC See also AAR36556.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||||||||| |
Db 1 ysspgspgt 9

RESULT 2
AAR38235
ID AAR38235 standard; peptide; 12 AA.
XX
AC AAR38235;
XX
DT 08-OCT-1993 (first entry)
XX
DE Alzheimer paired helical filament tau protein epitope 197-208.
XX
KW Alzheimer tau protein; phosphorylation-dependent; PHF;
KW neuronal microtubule; mitogen activated protein kinase; MAP kinase.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 3..4
FT /label= Phosphorylation_motif
FT Modified-site 6..7
FT /label= Phosphorylation_motif
FT Modified-site 9..10
FT /label= Phosphorylation_motif
XX
PN WO9311231-A.
XX
PD 10-JUN-1993.
XX
PF 07-DEC-1992; 92WO-EP02829.
XX
PR 06-DEC-1991; 91EP-0120974.
PR 16-NOV-1992; 92EP-0119551.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow E;
PI Steiner B;
XX
DR WPI; 1993-197050/24.
XX
PT Tau protein epitope(s), specific antibodies and protein kinase(s)
PT - used in the prevention, diagnosis and treatment of Alzheimer's
PT disease
XX
PS Claim 5; Page 89; 148pp; English.
XX
CC This is one of 26 preferred epitopes which occur in a phosphorylated
CC state in tau protein from Alzheimer paired helical filaments. The
CC epitopes all include phosphorylatable serine residues in Ser-Pro
CC motifs, Ile-Gly-Ser motifs or Cys-Gly-Ser motifs and/or
CC phosphorylatable threonine residues in Thr-Pro motifs. The pattern
CC of tau protein phosphorylation differs between Alzheimer's and
CC non-Alzheimer's individuals. Knowledge of the phosphorylated
CC epitopes and antibodies which recognise them may be useful in
CC diagnosis, treatment and prevention of Alzheimer's Disease. The
CC protein kinases present in mammalian brain which phosphorylate the
CC different epitopes are also claimed but no sequences are given.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 50; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||||||||| |
Db 1 ysspgspgt 9

RESULT 3
AAR37554
ID AAR37554 standard; peptide; 12 AA.
XX
AC AAR37554;
XX
DT 07-OCT-1993 (first entry)
XX
DE Phosphorylated tau protein epitope.
XX
KW Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
KW treatment; formation; inhibition; inhibitor.
XX
OS Homo sapiens.
XX
PN EP544942-A.
XX
PD 09-JUN-1993.
XX
PF 06-DEC-1991; 91EP-0120974.
XX
PR 06-DEC-1991; 91EP-0120974.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow EM, Steiner B;
XX
DR WPI; 1993-183841/23.
XX
PT Phosphorylated tau protein epitope associated with Alzheimer's
PT disease - is used as protein kinase inhibitor for treatment and
PT diagnosis
XX
PS Claim 4; Page 16; 34pp; English.
XX
CC The sequence is that of an epitope of tau protein which specifically

CC occurs in a phosphorylated state in tau protein from Alzheimer's
CC paired helical fragments. It may be used as part of a method for the
CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may
CC also be used in an in vitro model for the study of the generation of
CC the Alzheimer state of proteins and the testing of substances which
CC prevent the conversion of normal to Alzheimer tau protein. The
CC epitope occurs at residues 197-208 of human tau protein.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 50; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 1 yssgpgspgt 9

RESULT 4
AAW34857
ID AAW34857 standard; peptide; 12 AA.
XX
AC AAW34857;
XX
DT 27-MAR-1998 (first entry)
XX
DE Human tau protein fragment.
XX
KW Antibody; phosphorylated tau protein; paired helical filament;
KW detection; Alzheimer's disease; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 6
FT /note= "phosphoserine"
XX
PN WO9734145-A1.
XX
PD 18-SEP-1997.
XX
PF 13-MAR-1997; 97WO-JP00804.
XX
PR 13-MAR-1996; 96JP-0056090.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
PI Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
XX
DR WPI; 1997-470978/43.
XX
PT Antibody prepared using a partial peptide containing part of
PT phosphorylated tau protein - used for detecting Alzheimer's disease
XX
PS Example; Page 28; 48pp; Japanese.
XX
CC An antibody, prepared using a partial peptide containing the
CC phosphorylated residue of the phosphorylated tau protein, e.g. the
CC present sequence, in a paired helical filament, can be used to
CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC protein in brain extracts or tissue fragments.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 50; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 4 yssgpgspgt 12

RESULT 5
AAY81390
ID AAY81390 standard; protein; 12 AA.
XX
AC AAY81390;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human phosphorylated tau protein derived peptide fragment, PS199.
XX
KW Phosphorylated tau protein; human; paired helical filament; fragment;
KW polyclonal antibody; Alzheimer's disease; cerebrospinal fluid; CSF;
KW diagnosis; detection.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6
FT /note= "Phosphorylated"
XX
PN JP2000034300-A.
XX
PD 02-FEB-2000.
XX
PF 17-JUL-1998; 98JP-0204040.
XX
PR 17-JUL-1998; 98JP-0204040.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
DR WPI; 2000-285529/25.
XX
PT Anti-phosphated tau protein antibody - for the detection of Alzheimer
PT disease
XX
PS Claim 4; Page 4; 12pp; Japanese.
XX
CC The invention relates to an antibody against a phosphorylated tau
CC protein (AAY81386), which is a component of the paired helical filament
CC found in the plaques associated with Alzheimer's disease. A
CC phosphorylated tau protein fragment selected from peptides
CC AAY81387-Y81390 is conjugated to keyhole limpet haemocyanin (KLH), and
CC used to raise polyclonal antibodies in a rabbit. The antibodies of the
CC invention are specific for phosphorylated tau protein and may be used to
CC detect phosphorylated tau protein in the cerebrospinal fluid (CSF) of a
CC patient suspected of having Alzheimer's disease. Use of the antibodies of
CC the invention provides specific diagnosis of Alzheimer's disease.
CC Sequences AAY81387-Y81390 represent phosphorylated peptides derived from
CC tau protein used to raise anti-phosphorylated tau antibodies. The
CC N-terminal residue is not part of the full-length tau protein, but
CC facilitates KLH conjugation.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 50; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 4 yssgpgspgt 12

RESULT 6
AAB21959
ID AAB21959 standard; Peptide; 14 AA.
XX
AC AAB21959;

```
XX
DT   02-JAN-2001  (first entry)
XX
DE   Phosphorylated tau peptide #3.
XX
KW   WW-domain; protein-protein interaction; cell growth regulation;
KW   protein degradation regulation; Alzheimer's; Dementia pugilistica;
KW   Down's syndrome; Parkinson's disease; Pick's; neurodegenerative;
KW   microtubule assembly; hyperplasia; neoplasia; malignancy;
KW   psoriasis; retinosis; atherosclerosis; leukaemia; lymphoma; papiloma;
KW   pulmonary fibrosis; rhematoid arthritis; multiple sclerosis;
KW   muscular dystrophy; tau.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                   /note= "Phosphorylated residue"
XX
PN   WO200048621-A2.
XX
PD   24-AUG-2000.
XX
PF   18-FEB-2000; 2000WO-US04278.
XX
PR   18-FEB-1999;   99US-0252404.
XX
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI   Lu KP,  Zhou XZ;
XX
DR   WPI; 2000-594014/56.
XX
PT   Mediating protein-protein interactions, useful for regulating cell
PT   growth and for treating neurodegenerative disorders, comprises
PT   modulating binding of WW domain containing polypeptide with
PT   phosphorylated ligand -
XX
PS   Example 10; Page 45; 82pp; English.
XX
CC   The present invention relates to a method for mediating protein-protein
CC   interaction, which comprises modulating the binding of a WW-domain
CC   containing peptide with a phosphorylated ligand. WW-domains are highly
CC   conserved regions of approximately 40 amino acid residues with two
CC   invariant tryptophans (W) in a triple stranded beta-sheet. When a
CC   WW-domain containing peptide is phosphorylated at serine or threonine
CC   residues, dephosphorylation of ligands bound to the peptide is inhibited.
CC   WW-domain peptides may be useful for mediating protein-protein
CC   interaction, regulating cell growth, regulating protein degradation,
CC   restoring the function of tau to bind microtubules and promote or restore
CC   microtubule assembly in neurodegenerative diseases e.g. Alzheimer's,
CC   Dementia pugilistica, Down's syndrome, Parkinson's disease, Pick's
CC   disease, multiple sclerosis, muscular dystrophy, Corticobasal
CC   degeneration, Frontotemporal dementias, Myotonic dystrophy, Niemann-Pick
CC   disease, prion disease with tangles, progressive supranuclear palsy and
CC   subacute sclerosing panencephalistis. In addition, inhibitors or
CC   stimulators of interactions between WW-domains and ligands of the present
CC   invention can be used to treat hyperplastic and neoplastic disorders e.g.
CC   all forms of malignancies, psoriasis, retinosis, atherosclerosis
CC   resulting from plaque formation, leukaemias, benign tumour growth,
CC   lymphomas, papilomas, pulmonary fibrosis and rhematoid arthritis. The
CC   present sequence is a phosphorylated tau peptide. Tau is a WW-domain
CC   containing peptide ligand. This peptide was used to investigate the
CC   interactions between Tau and the WW-domain of Pin1 peptide. It was found
CC   that the Pin1 WW-domain mediates specific interactions between Pin1 and
CC   tau.
XX
SQ   Sequence   14 AA;

  Query Match             100.0%;  Score 50;  DB 21;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db       2 ysspgspgt 10


RESULT   7
AAR61330
ID   AAR61330 standard; Protein; 34 AA.
XX
AC   AAR61330;
XX
DT   24-APR-1995  (first entry)
XX
DE   Peptide phosphorylated by human tau-protein kinase.
XX
KW   Tau-protein kinase I enzyme; TPK-I; Phosphorylated peptide.
XX
OS   Synthetic.
XX
PN   EP616032-A.
XX
PD   21-SEP-1994.
XX
PF   01-MAR-1994;   94EP-0103057.
XX
PR   02-MAR-1993;   93JP-0041160.
PR   22-MAR-1993;   93JP-0085143.
PR   02-AUG-1993;   93JP-0191246.
XX
PA   (TAKA/) TAKASHIMA A.
PA   (MITU ) MITSUBISHI KASEI CORP.
XX
PI   Hoshino T,  Imahori K,  Saito K,  Sato S,  Shiratsuchi A;
PI   Takashima A;
XX
DR   WPI; 1994-287181/36.
XX
PT   Newly isolated tau-protein kinase I enzyme - with specificity for
PT   tau-protein providing means for prevention and treatment of
PT   Alzheimer's disease
XX
PS   Example 4; Page 25; 30pp; English.
XX
CC   AAR61330 is a peptide which has been phosphorylated by human
CC   tau-protein kinase (AAR61326).
XX
SQ   Sequence   34 AA;

  Query Match             100.0%;  Score 50;  DB 15;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db       7 ysspgspgt 15


RESULT   8
AAW34875
ID   AAW34875 standard; peptide; 34 AA.
XX
AC   AAW34875;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Human tau protein fragment.
XX
KW   Antibody; phosphorylated tau protein; paired helical filament;
KW   detection; Alzheimer's disease; human.
XX
OS   Homo sapiens.
```

XX
PN WO9734145-A1.
XX
PD 18-SEP-1997.
XX
PF 13-MAR-1997; 97WO-JP00804.
XX
PR 13-MAR-1996; 96JP-0056090.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
PI Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
XX
DR WPI; 1997-470978/43.
XX
PT Antibody prepared using a partial peptide containing part of
PT phosphorylated tau protein - used for detecting Alzheimer's disease
XX
PS Example; Pages 36-37; 48pp; Japanese.
XX
CC An antibody, prepared using a partial peptide containing the
CC phosphorylated residue of the phosphorylated tau protein, e.g. the
CC present sequence, in a paired helical filament, can be used to
CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC protein in brain extracts or tissue fragments.
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 50; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 7 yssPgspgt 15

RESULT 9
AAR59837
ID AAR59837 standard; peptide; 67 AA.
XX
AC AAR59837;
XX
DT 04-MAR-1995 (first entry)
XX
DE Sequence of human microtubule-associated protein tau.
XX
KW Tau protein; brain; cerebral cortex; hybridoma ECACC 92100853;
KW Alzheimer's disease; monoclonal antibody; paried helical filament.
XX
OS Homo sapiens.
XX
PN WO9413795-A.
XX
PD 23-JUN-1994.
XX
PF 10-DEC-1993; 93WO-EP03499.
XX
PR 14-DEC-1992; 92EP-0403403.
XX
PA (INNO-) INNOGENETICS NV SA.
XX
PI Mercken M, Van De Voorde A, Vandermeeren M, Vanmechelen E;
XX
DR WPI; 1994-234211/28.
XX
PT Monoclonal antibody reactive with tau protein - used to develop
PT prods. for detection of brain diseases involving tau or paired
PT helical filaments esp. Alzheimer's disease
XX
PS Claim 6; Page 38; 52pp; English.
XX
CC Paired helical filament (PHF) tau was partially purified from
CC postmortem tissue, consisting mostly of grey matter from the frontal
CC and temporal cortex obtd. from Anzheimer patients. The tissue (5-10g)
CC was homogenised with 10 vols of cold buffer (10mM Tris, 1mM EGTA,
CC 0.8M NaCl, 10% sucrose, pH 7.4). After centrifugation for 20 mins at
CC 4 degrees C, the supernatant was adjusted to 1% (wt/vol) N-
CC laurosylsarcosine and 1% (vol/vol) 2-mercaptoethanol and incubated
CC while rotating on a mixer for 2.5 hrs at 37 degrees C. The mixt. was
CC centrifuged at 108,000 g for 35 mins at 20 degrees C. The PHF-tau
CC contg. pellet was washed with PBS and resuspended in 1ml of the same
CC buffer. Hybridomas which produced MAbs reactive with tau protein
CC were obtd. from the spleen cells of Balb/C mice primed s.c. with
CC partially purified PHF. A MAb which forms an immunological complex
CC with a human tau protein of sequence in AAR59837 is secreted by the
CC hybridoma deposited at ECACC on Oct. 8 1992 under No. 92100853.
XX
SQ Sequence 67 AA;

Query Match 100.0%; Score 50; DB 15; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 43 yssPgspgt 51

RESULT 10
AAB85640
ID AAB85640 standard; peptide; 78 AA.
XX
AC AAB85640;
XX
DT 29-OCT-2001 (first entry)
XX
DE Tau peptide region (residues 155-232).
XX
KW Tauopathy; phospho-tau (181); neurological marker; monoclonal antibody;
KW HT7; AT270; nootropic; neuroprotective; cerobroprotective; epitope.
XX
OS Homo sapiens.
XX
PN WO200155725-A2.
XX
PD 02-AUG-2001.
XX
PF 18-JAN-2001; 2001WO-EP00560.
XX
PR 24-JAN-2000; 2000EP-0870008.
PR 27-JAN-2000; 2000US-0178391.
PR 22-NOV-2000; 2000EP-0870280.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Vanmechelen E, Vanderstichele H;
XX
DR WPI; 2001-476242/51.
XX
PT Determining the ratio of phospho-tau / total tau is useful for
PT diagnosing a tauopathy i.e. Alzheimer's disease or Pick's disease,
PT versus a non tauopathy -
XX
PS Example 1; Fig 1; 71pp; English.
XX
CC The invention provides a method of diagnosis of tauopathies in an
CC individual that comprises determining the ratio of phospho-tau (181)/
CC total tau. Tau and phospho tau are useful as neurological markers for the
CC manufacture of a diagnostic kit for the diagnosis of a tauopathy and/or
CC the differential diagnosis of a tauopathy versus a non tauopathy. A
CC phospho-peptide liable to form an immunological complex with monoclonal
CC antibody HT7 and MAb AT270 comprising at least the minimal epitope of HT7
CC or AT270 is useful to measure phospho-tau levels and diagnose a tauopathy

```
CC   and/or for the differential diagnosis of a tauopathy versus a non
CC   tauopathy. The kit is useful for the diagnosis of Alzheimer's disease,
CC   Pick's disease, sporadic Frontotemporal dementia and/or Frontotemporal
CC   dementia with Parkinsonism linked to chromosome 17, Creutzfeldt Jacob
CC   disease, stroke and/or neurotoxicity in patients with leukemia. The
CC   phosphopeptide kits and methods are useful for therapeutic monitoring and
CC   for determining the effectiveness of a treatment. The present sequence
CC   represents a tau peptide fragment.
XX
SQ   Sequence   78 AA;

  Query Match             100.0%;  Score 50;  DB 22;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db      43 ysspgspgt 51


RESULT  11
AAR92516
ID   AAR92516 standard; peptide; 106 AA.
XX
AC   AAR92516;
XX
DT   20-SEP-1996  (first entry)
XX
DE   Microtubule-associated tau protein epitope corresp. to pos. 146-251.
XX
KW   Epitope; microtubule-associated protein; tau; phosphorylation; subclass;
KW   paired helical fibre; neurofibrillary tangle; dementia; neurological;
KW   Alzheimer's disease; monoclonal antibody; brain; pathology.
XX
OS   Synthetic.
XX
PN   WO9604309-A1.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;   95WO-EP03032.
XX
PR   29-JUL-1994;   94EP-0870131.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Van DE VOORDE A,  Vanmechelen E;
XX
DR   WPI; 1996-129338/13.
XX
PT   Monoclonal antibodies specific for phosphorylated tau - for improved
PT   detection and diagnosis of e.g. Alzheimer's Disease
XX
PS   Claim 2; Page 32; 42pp; English.
XX
CC   This is the amino acid of an epitope derived from the microtubule-
CC   associated tau protein.  The phosphorylated subclass of tau protein
CC   from which this epitope originates, forms a major part of the paired
CC   helical fibres which make up neurofibrillary tangles seen in patients
CC   suffering from dementia e.g. Alzheimer's disease.  The epitope is esp.
CC   isolated from patients who have recently died from Alzheimer's disease.
CC   It is used to generate monoclonal antibodies for the in vitro detection
CC   or diagnosis of brain/neurological diseases such a Alzheimer's disease
CC   or other diseases where neurofibrillary tangles are a pathological
CC   symptom.
XX
SQ   Sequence   106 AA;

  Query Match             100.0%;  Score 50;  DB 17;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db      52 ysspgspgt 60


RESULT  12
AAR76937
ID   AAR76937 standard; Peptide; 112 AA.
XX
AC   AAR76937;
XX
DT   04-DEC-1995  (first entry)
XX
DE   PHF-tau (143-254) peptide.
XX
KW   PHF-tau; paried helical filament tau protein; monoclonal antibody;
KW   MAb; phosphorylation; neurological disease; Alzheimer disease;
KW   cerebrospinal fluid.
XX
OS   Homo sapiens.
XX
PN   WO9517429-A.
XX
PD   29-JUN-1995.
XX
PF   14-DEC-1994;   94WO-EP04146.
XX
PR   21-DEC-1993;   93EP-0403133.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Van De Voorde A,  Vandermeeren M,  Vanmechelen E;
XX
DR   WPI; 1995-240616/31.
XX
PT   Novel monoclonal antibodies specific for abnormally phosphorylated
PT   paired helical filament tau protein (PHF-Tau) - useful for post
PT   mortem or in vitro detection of neurological diseases eg. Alzheimer's
PT   disease
XX
PS   Claim 1; Page 44; 57pp; English.
XX
CC   Novel MAbs AT180 and AT270 (ECACC 92122204, 93070774) form
CC   immunological complexes with a phosphorylated epitope, given in
CC   AAR76937, of abnormally phosphorylated tau protein (PHF-tau).  The
CC   MAbs are used to specifically detect PHF-tau in cerebrospinal fluid.
XX
SQ   Sequence   112 AA;

  Query Match             100.0%;  Score 50;  DB 16;  Length 112;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db      55 ysspgspgt 63


RESULT  13
AAY15200
ID   AAY15200 standard; Protein; 351 AA.
XX
AC   AAY15200;
XX
DT   28-FEB-2000  (first entry)
XX
DE   Human Tau protein.
XX
KW   Human Tau gene; neurofibrillary tangle formation; abnormal tau filament;
KW   brain; mutation; phosphorylation; isoform ratio; diagnosis; tauopathy;
KW   treatment; neurodegenerative disorder; Fronto-Temporal Dementia;
```

KW Familial Multiple System Tauopathy with presenile Dementia; MSTD;
KW Pick's Disease; Progressive Supranuclear Palsy; PSP; Alzheimer's Disease;
KW Corticobasal Degeneration; CD; Prion Protein Cerebral Amyloid Angiopathy;
KW cognitive disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1..351
FT /label= Tau_protein
FT /note= "Microtubule related protein"
XX
PN WO9962548-A1.
XX
PD 09-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US12036.
XX
PR 01-JUN-1998; 98US-0087557.
XX
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
PI Ghetti B, Spillantini MG, Murrell JR, Goedert M, Farlow MR;
PI Klug A;
XX
DR WPI; 2000-086858/07.
DR N-PSDB; AAZ29262.
XX
PT Diagnosing a tauopathy, especially a Fronto-Temporal Dementia -
XX
PS Disclosure; Page 85; 90pp; English.
XX
CC The present amino acid sequence is a form of human Tau protein.
CC There are six tau isoforms, expressed in the normal adult brain with a
CC slight preponderance of those with 3 repeats over those with 4 repeats.
CC Mutations in the tau gene affects phosphorylation and leads to formation
CC of neurofibrillary tangles and alters the tau isoform ratio. The
CC increased ratio of 4:3 repeat and abnormal tau filaments is closely
CC related to neurodegenerative disorders. This sequence can be used for
CC diagnosis and treatment of tauopathies, like Fronto-Temporal Dementia,
CC Familial Multiple System Tauopathy with presenile Dementia (MSTD),
CC Pick's Disease, Progressive Supranuclear Palsy (PSP), Corticobasal
CC Degeneration (CD) or Alzheimer's Disease. A composition that decreases
CC the ratio of 4:3 repeat tau isomers, along with an agent for treatment
CC of a cognitive disorder, is useful for treating a tauopathy. It may also
CC be useful in diagnosis of Prion Protein Cerebral Amyloid Angiopathy and
CC other prion protein associated disease characterized by abnormal tau
CC filament formation.
XX
SQ Sequence 351 AA;

Query Match 100.0%; Score 50; DB 21; Length 351;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 139 ysspgspgt 147

RESULT 14
AAP91294
ID AAP91294 standard; protein; 352 AA.
XX
AC AAP91294;
XX
DT 18-DEC-1989 (first entry)
XX
DE Paired helical filament (PHF) core protein.
XX
KW Paired helical filament (PHF) core protein; Alzheimer's disease;
KW neurofibrillary tangles.
XX
OS Homo sapiens.
XX
PN WO8903993-A.
XX
PD 05-MAY-1989.
XX
PF 19-OCT-1988; 88WO-GB00867.
XX
PR 19-OCT-1987; 87GB-0024412.
XX
PA (MEDI) MEDICAL RESEARCH COUNCIL.
XX
PI Wischik CM, Milstein C, Klug A;
XX
DR WPI; 1989-150854/20.
XX
PT Paired helical filament core protein - used for providing reagents
PT sensitive to neurofibrillary tangles used for diagnosing Alzheimer's
PT disease.
XX
PS Disclosure; fig 1; 29pp; English.
XX
CC Paired helical filament core protein was sequenced from DNA obtained
CC from brain tissue contg. Alzheimer neurofibrillary tangles. The protein
CC can be used to make MAb's to the PHF core or nucleotide probes, used to
CC diagnose Alzheimer's disease. The protein sequence QIVYKP (AAs 218-223)
CC was used to design the probes.
CC See also AAN91707.
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 50; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 139 ysspgspgt 147

RESULT 15
AAR32708
ID AAR32708 standard; Protein; 352 AA.
XX
AC AAR32708;
XX
DT 15-JUN-1993 (first entry)
XX
DE Human tau-protein.
XX
KW Alzheimer's disease; diagnosis; subtyping; monitoring; assay.
XX
OS Homo sapiens.
XX
PN WO9303369-A.
XX
PD 18-FEB-1993.
XX
PF 03-AUG-1992; 92WO-US06382.
XX
PR 01-AUG-1991; 91US-0738778.
XX
PA (VOOR/) VOORHEIS P H.
XX
PI Voorheis PH;
XX
DR WPI; 1993-076670/09.
DR N-PSDB; AAQ37305.
XX
PT Method for diagnosing, subtyping and monitoring Alzheimer's
PT disease - by assaying a sample of body fluid for the presence of a

PT tau-peptide using an anti-tau antibody
XX
PS Disclosure; Fig 1; 43pp; English.
XX
CC The sequence is that one form of human tau protein (from Goedert
CC et al., PNAS USA 85: 4051-4055) which was used for the prodn.
CC of anti-tau peptide antibodies. These are used as part of a method
CC for diagnosing, subtyping or monitoring Alzheimer's disease by
CC assaying a sample of body fluid for the presence of a tau-peptide
CC using an anti-tau antibody or the presence of an anti-tau-peptide
CC autoantibody. The methods can be used for confirming a clinical
CC diagnosis of Alzheimer's disease and in following the course of the
CC disease and treatment.
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 50; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 139 yspgspgt 147

RESULT 16
AAY20248
ID AAY20248 standard; Protein; 352 AA.
XX
AC AAY20248;
XX
DT 22-JUL-1999 (first entry)
XX
DE Human microtubule associated protein Tau wild type fragment.
XX
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.
XX
OS Homo sapiens.
XX
PN WO9845322-A2.
XX
PD 15-OCT-1998.
XX
PF 02-APR-1998; 98WO-IB00705.
XX
PR 10-APR-1997; 97US-0043163.
XX
PA (UYUT-) RIJKSUNIV UTRECHT.
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
XX
DR WPI; 1998-609901/51.
DR N-PSDB; AAX75754.
XX
PT Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also
PT for treatment and prevention with specific ribozymes or wild-type
PT RNA
XX
PS Disclosure; Figure 3; 258pp; English.
XX
CC This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC and many others listed) or susceptibility to these disorders. The method
CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the
CC used of neuronal system RNA molecules, specifically proteins including
CC beta-amyloid precursor protein (beta-APP), the microtubule associated
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC protein-C (HMGP-C) and neuroendocrine specific protein A.
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 50; DB 19; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 139 yspgspgt 147

RESULT 17
AAW05283
ID AAW05283 standard; Protein; 390 AA.
XX
AC AAW05283;
XX
DT 20-DEC-1996 (first entry)
XX
DE Truncated human tau protein.
XX
KW Tau protein; inhibition; modulation; prophylaxis; treatment;
KW Alzheimer's disease; motor neurone disease; Lewy body disease;
KW progressive supranuclear palsy; Pick's disease.
XX
OS Homo sapiens.
XX
PN WO9630766-A1.
XX
PD 03-OCT-1996.
XX
PF 25-MAR-1996; 96WO-EP01307.
XX
PR 27-MAR-1995; 95GB-0006197.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
XX
DR WPI; 1996-455570/45.
XX
PT Assay for inhibitors of tau-tau interaction - used for identifying
PT cpds., partic. phenothiazine cpds., for treating pathological
PT tau-tau or neuro:filament aggregation
XX
PS Claim 11; ; 97pp; English.
XX
CC Detecting an agent which modulates or inhibits tau-tau protein
CC association comprises contacting two tau proteins, distinct from
CC each other yet capable of binding to the other and where one of the
CC tau proteins is labelled, in the presence of the agent suspected of
CC being capable of modulating or inhibiting tau-tau interaction.

```
CC   Agents identified as being modulators or inhibitors of tau-tau
CC   interaction may be used for the prophylaxis and treatment of
CC   Alzheimer's disease, motor neurone disease, Lewy body disease,
CC   Pick's disease or progressive supranuclear palsy. This sequence of
CC   the human tau protein is truncated at amino acid residue 390.  The
CC   full length protein is given in AAW05282.
XX
SQ   Sequence   390 AA;


  Query Match             100.0%;  Score 50;  DB 17;  Length 390;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     197 yssgpgspgt 205


RESULT  18
AAR58810
ID   AAR58810 standard; protein; 441 AA.
XX
AC   AAR58810;
XX
DT   27-MAR-1995  (first entry)
XX
DE   Human tau protein.
XX
KW   Tau; cerebrospinal fluid; immunoassay; antibody; detection;
KW   diagnosis; central nervous system; CNS; cytopathies; cytopathy;
KW   Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO9418560-A.
XX
PD   18-AUG-1994.
XX
PF   10-FEB-1994;   94WO-JP00196.
XX
PR   12-FEB-1993;   93JP-0046133.
XX
PA   (TEIJ ) TEIJIN LTD.
XX
PI   Eguchi H,  Hosoda K,  Kobayashi S,  Kubota T,  Mori H;
PI   Nakamoto T;
XX
DR   WPI; 1994-279910/34.
XX
PT   Sandwich immunoassay of tau protein in cerebrospinal fluid - for
PT   diagnosis of Alzheimer's disease and other CNS cytopathies
XX
PS   Claim 1; Page 16-18; 36pp; Japanese.
XX
CC   Detection of the human tau protein (or fragments of it) in samples
CC   of cerebrospinal fluid enables the diagnosis of central nervous
CC   system cytopathies such as Alzheimer's disease.  Detection is
CC   performed using labelled antibodies which recognise sites within the
CC   region defined by the amino acid residues 251-441.  The antibodies
CC   are preferably polyclonal.
XX
SQ   Sequence   441 AA;


  Query Match             100.0%;  Score 50;  DB 15;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     197 yssgpgspgt 205


RESULT  19
AAW05282
ID   AAW05282 standard; Protein; 441 AA.
XX
AC   AAW05282;
XX
DT   20-DEC-1996  (first entry)
XX
DE   Human tau protein.
XX
KW   Tau protein; inhibition; modulation; prophylaxis; treatment;
KW   Alzheimer's disease; motor neurone disease; Lewy body disease;
KW   progressive supranuclear palsy; Pick's disease.
XX
OS   Homo sapiens.
XX
PN   WO9630766-A1.
XX
PD   03-OCT-1996.
XX
PF   25-MAR-1996;   96WO-EP01307.
XX
PR   27-MAR-1995;   95GB-0006197.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Edwards PC,  Harrington CR,  Klug A,  Roth M,  Wischik CM;
XX
DR   WPI; 1996-455570/45.
DR   N-PSDB; AAT39591.
XX
PT   Assay for inhibitors of tau-tau interaction - used for identifying
PT   cpds., partic. phenothiazine cpds., for treating pathological
PT   tau-tau or neuro:filament aggregation
XX
PS   Example 2; Page 53-54; 97pp; English.
XX
CC   Detecting an agent which modulates or inhibits tau-tau protein
CC   association comprises contacting two tau proteins, distinct from
CC   each other yet capable of binding to the other and where one of the
CC   tau proteins is labelled, in the presence of the agent suspected of
CC   being capable of modulating or inhibiting tau-tau interaction.
CC   Agents identified as being modulators or inhibitors of tau-tau
CC   interaction may be used for the prophylaxis and treatment of
CC   Alzheimer's disease, motor neurone disease, Lewy body disease,
CC   Pick's disease or progressive supranuclear palsy.
XX
SQ   Sequence   441 AA;


  Query Match             100.0%;  Score 50;  DB 17;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     197 yssgpgspgt 205


RESULT  20
AAW34856
ID   AAW34856 standard; protein; 441 AA.
XX
AC   AAW34856;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Human tau protein.
XX
KW   Antibody; phosphorylated tau protein; paired helical filament;
KW   detection; Alzheimer's disease; human.
XX
```

```
OS   Homo sapiens.
XX
PN   WO9734145-A1.
XX
PD   18-SEP-1997.
XX
PF   13-MAR-1997;   97WO-JP00804.
XX
PR   13-MAR-1996;   96JP-0056090.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
PI   Imahori K,  Ishiguro K,  Park J,  Sato K,  Uchida T;
XX
DR   WPI; 1997-470978/43.
XX
PT   Antibody prepared using a partial peptide containing part of
PT   phosphorylated tau protein - used for detecting Alzheimer's disease
XX
PS   Claim 2; Pages 25-27; 48pp; Japanese.
XX
CC   An antibody, prepared using a partial peptide containing the
CC   phosphorylated residue of the phosphorylated tau protein, e.g. the
CC   present sequence, in a paired helical filament, can be used to
CC   detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC   protein in brain extracts or tissue fragments.
XX
SQ   Sequence   441 AA;

  Query Match             100.0%;  Score 50;  DB 18;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     197 ysspgspgt 205


RESULT  21
AAY81386
ID   AAY81386 standard; protein; 441 AA.
XX
AC   AAY81386;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Human paired helical filament phosphorylated tau protein.
XX
KW   Phosphorylated tau protein; human; paired helical filament;
KW   polyclonal antibody; Alzheimer's disease; cerebrospinal fluid; CSF;
KW   diagnosis; detection.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   199
FT                   /note= "Phosphorylated"
FT   Modified-site   231
FT                   /note= "Phosphorylated"
FT   Modified-site   235
FT                   /note= "Phosphorylated"
FT
XX
PN   JP2000034300-A.
XX
PD   02-FEB-2000.
XX
PF   17-JUL-1998;   98JP-0204040.
XX
PR   17-JUL-1998;   98JP-0204040.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
DR   WPI; 2000-285529/25.
XX
PT   Anti-phosphated tau protein antibody - for the detection of Alzheimer
PT   disease
XX
PS   Claim 1; Page 8-9; 12pp; Japanese.
XX
CC   The invention relates to an antibody against a phosphorylated tau
CC   protein (AAY81386), which is a component of the paired helical filament
CC   found in the plaques associated with Alzheimer's disease. A
CC   phosphorylated tau protein fragment selected from peptides
CC   AAY81387-Y81390 is conjugated to keyhole limpet haemocyanin (KLH), and
CC   used to raise polyclonal antibodies in a rabbit. The antibodies of the
CC   invention are specific for phosphorylated tau protein and may be used to
CC   detect phosphorylated tau protein in the cerebrospinal fluid (CSF) of a
CC   patient suspected of having Alzheimer's disease. Use of the antibodies of
CC   the invention provides specific diagnosis of Alzheimer's disease. The
CC   present sequence represents phosphorylated tau protein.
XX
SQ   Sequence   441 AA;

  Query Match             100.0%;  Score 50;  DB 21;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     197 ysspgspgt 205


RESULT  22
AAR28237
ID   AAR28237 standard; peptide; 13 AA.
XX
AC   AAR28237;
XX
DT   18-MAR-1993  (first entry)
XX
DE   Phosphopeptide as Alzheimers's disease detection antigen.
XX
KW   AD; antigen; antibody; paired helical filament; PHF; brain.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   6
FT                   /note= "at least one of Ser6 and Thr9 is modified
FT                   by PO(OH)"
FT   Modified-site   9
FT                   /note= "at least one of Ser6 and Thr9 is modified
FT                   by PO(OH)"
FT   Modified-site   13
FT                   /note= "the C-terminal is amidated"
FT
XX
PN   JP04270299-A.
XX
PD   25-SEP-1992.
XX
PF   25-FEB-1991;   91JP-0146476.
XX
PR   25-FEB-1991;   91JP-0146476.
XX
PA   (MITU ) MITSUBISHI KASEI CORP.
XX
DR   WPI; 1992-369427/45.
XX
PT   New phospho:peptide(s) - useful as antigen for detection of
PT   Alzheimer's disease
XX
PS   Claim 1; Page 2; 4pp; Japanese.
XX
CC   The C-terminal of the peptide is amidated.
```

```
CC   The phosphopeptide is useful as antigen for preparing antibody
CC   against paired helical filaments (PHF) present in brain of patients
CC   with Alzheimer's disease.
XX
SQ   Sequence   13 AA;


  Query Match             86.0%;  Score 43;  DB 13;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||||||
Db       2 sspgspgt 9


RESULT  23
AAW34860
ID   AAW34860 standard; peptide; 13 AA.
XX
AC   AAW34860;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Human tau protein fragment.
XX
KW   Antibody; phosphorylated tau protein; paired helical filament;
KW   detection; Alzheimer's disease; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   3
FT                   /note= "phosphoserine"
FT   Modified-site   6
FT                   /note= "phosphoserine"
XX
PN   WO9734145-A1.
XX
PD   18-SEP-1997.
XX
PF   13-MAR-1997;   97WO-JP00804.
XX
PR   13-MAR-1996;   96JP-0056090.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
PI   Imahori K,  Ishiguro K,  Park J,  Sato K,  Uchida T;
XX
DR   WPI; 1997-470978/43.
XX
PT   Antibody prepared using a partial peptide containing part of
PT   phosphorylated tau protein - used for detecting Alzheimer's disease
XX
PS   Example; Page 29; 48pp; Japanese.
XX
CC   An antibody, prepared using a partial peptide containing the
CC   phosphorylated residue of the phosphorylated tau protein, e.g. the
CC   present sequence, in a paired helical filament, can be used to
CC   detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC   protein in brain extracts or tissue fragments.
XX
SQ   Sequence   13 AA;


  Query Match             86.0%;  Score 43;  DB 18;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||||||
Db       2 sspgspgt 9


RESULT  24
AAW34858
ID   AAW34858 standard; peptide; 13 AA.
XX
AC   AAW34858;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Human tau protein fragment.
XX
KW   Antibody; phosphorylated tau protein; paired helical filament;
KW   detection; Alzheimer's disease; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   6
FT                   /note= "phosphoserine"
XX
PN   WO9734145-A1.
XX
PD   18-SEP-1997.
XX
PF   13-MAR-1997;   97WO-JP00804.
XX
PR   13-MAR-1996;   96JP-0056090.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
PI   Imahori K,  Ishiguro K,  Park J,  Sato K,  Uchida T;
XX
DR   WPI; 1997-470978/43.
XX
PT   Antibody prepared using a partial peptide containing part of
PT   phosphorylated tau protein - used for detecting Alzheimer's disease
XX
PS   Example; Page 28; 48pp; Japanese.
XX
CC   An antibody, prepared using a partial peptide containing the
CC   phosphorylated residue of the phosphorylated tau protein, e.g. the
CC   present sequence, in a paired helical filament, can be used to
CC   detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC   protein in brain extracts or tissue fragments.
XX
SQ   Sequence   13 AA;


  Query Match             86.0%;  Score 43;  DB 18;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||||||
Db       2 sspgspgt 9


RESULT  25
AAW29455
ID   AAW29455 standard; Protein; 263 AA.
XX
AC   AAW29455;
XX
DT   14-APR-1998  (first entry)
XX
DE   Oerskovia xanthineolytica mature beta-1,3-glucanase.
XX
KW   Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation;
KW   fungal cell wall; intracellular product; purification; protoplast.
XX
OS   Oerskovia xanthineolytica LLG109 (DSM 10297).
XX
FH   Key             Location/Qualifiers
```

```
FT   CDS             23..955
FT                   /*tag=  a
FT   sig_peptide     23..120
FT                   /*tag=  b
FT   mat_peptide     164..952
FT                   /*tag=  c
FT
XX
PN   WO9739114-A1.
XX
PD   23-OCT-1997.
XX
PF   14-APR-1997;   97WO-DK00160.
XX
PR   23-AUG-1996;   96DK-0000885.
PR   12-APR-1996;   96DK-0000427.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Diers I,  Ferrer P,  Halkier T,  Hedegaard L;
XX
DR   WPI; 1997-526451/48.
DR   N-PSDB; AAT89155.
XX
PT   New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia
PT   xanthineolytica, used particularly for the lysis of microbial cells
PT   for obtaining desirable products
XX
PS   Example 2; Page 35-36; 64pp; English.
XX
CC   This polypeptide comprises a novel Oerskovia xanthineolytica (OX)
CC   enzyme that exhibits beta-1,3-glucanase (BG) activity.  Its amino
CC   acid sequence was deduced from an isolated genomic DNA sequence
CC   (see AAT89155).  Claimed DNA constructs that encode the novel BG (see
CC   also AAW29456 for corrected sequence), a mannose binding domain (see
CC   AAW29458) or a full-length enzyme, i.e. BG with mannose binding
CC   domain (see AAW29456), can be used to produce recombinant BG
CC   polypeptides, with or without a mannose binding domain, in fungal
CC   or bacterial host cells.  BG polypeptides are used for the
CC   degradation or modification of beta-glucan containing material,
CC   especially for the gentle lysis of microbial cell walls, thereby
CC   enabling recovery of desirable intracellular products with a
CC   reduced amount of contaminants.  They can also be used for the
CC   production of e.g. pigments, colourants, flavourants, yeast
CC   extracts, pharmaceuticals, food or feed compositions, and to
CC   prepare protoplasts for use in fusion, transformation and cloning
CC   studies.
XX
SQ   Sequence   263 AA;

  Query Match             80.0%;  Score 40;  DB 18;  Length 263;
  Best Local Similarity   87.5%;  Pred. No. 1e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||:|||
Db     244 sspgnpgt 251


RESULT  26
AAW29456
ID   AAW29456 standard; Protein; 435 AA.
XX
AC   AAW29456;
XX
DT   14-APR-1998  (first entry)
XX
DE   Oerskovia xanthineolytica beta-1,3-glucanase.
XX
KW   Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation;
KW   fungal cell wall; intracellular product; purification; protoplast.
XX
OS   Oerskovia xanthineolytica LLG109 (DSM 10297).
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..52
FT                   /label= Sig_peptide
FT   Protein         53..435
FT                   /label= Mat_protein
FT   Domain          304..435
FT                   /label= Mannose-binding_domain
FT
XX
PN   WO9739114-A1.
XX
PD   23-OCT-1997.
XX
PF   14-APR-1997;   97WO-DK00160.
XX
PR   23-AUG-1996;   96DK-0000885.
PR   12-APR-1996;   96DK-0000427.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Diers I,  Ferrer P,  Halkier T,  Hedegaard L;
XX
DR   WPI; 1997-526451/48.
DR   N-PSDB; AAT89156.
XX
PT   New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia
PT   xanthineolytica, used particularly for the lysis of microbial cells
PT   for obtaining desirable products
XX
PS   Example 2; Page 39-40; 64pp; English.
XX
CC   This sequence comprises the polypeptide precursor of a novel
CC   Oerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase
CC   (BG) activity and which includes a mannose binding domain (MBD).
CC   Its amino acid sequence was deduced from an isolated genomic DNA
CC   sequence (see AAT89156).  Claimed DNA constructs that encode the
CC   novel BG lacking a MBD (see AAW29455 and AAW29457), a MDB (see
CC   AAW29458), or the full-length enzyme can be used to produce recombinant
CC   BG polypeptides, with or without a mannose binding domain, in fungal
CC   or bacterial host cells.  BG polypeptides are used for the
CC   degradation or modification of beta-glucan containing material,
CC   especially for the gentle lysis of microbial cell walls, thereby
CC   enabling recovery of desirable intracellular products with a
CC   reduced amount of contaminants.  They can also be used for the
CC   production of e.g. pigments, colourants, flavourants, yeast
CC   extracts, pharmaceuticals, food or feed compositions, and to
CC   prepare protoplasts for use in fusion, transformation and cloning
CC   studies.
XX
SQ   Sequence   435 AA;

  Query Match             80.0%;  Score 40;  DB 18;  Length 435;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||:|||
Db     297 sspgnpgt 304


RESULT  27
AAR38233
ID   AAR38233 standard; peptide; 7 AA.
XX
AC   AAR38233;
XX
DT   08-OCT-1993  (first entry)
XX
DE   Alzheimer paired helical filament tau protein epitope 197-203.
XX
KW   Alzheimer tau protein; phosphorylation-dependent; PHF;
KW   neuronal microtubule; mitogen activated protein kinase; MAP kinase.
```

XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 3..4
FT /label= Phosphorylation_motif
FT Modified-site 6..7
FT /label= Phosphorylation_motif
XX
PN WO9311231-A.
XX
PD 10-JUN-1993.
XX
PF 07-DEC-1992; 92WO-EP02829.
XX
PR 06-DEC-1991; 91EP-0120974.
PR 16-NOV-1992; 92EP-0119551.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow E;
PI Steiner B;
XX
DR WPI; 1993-197050/24.
XX
PT Tau protein epitope(s), specific antibodies and protein kinase(s)
PT - used in the prevention, diagnosis and treatment of Alzheimer's
PT disease
XX
PS Claim 5; Page 89; 148pp; English.
XX
CC This is one of 26 preferred epitopes which occur in a phosphorylated
CC state in tau protein from Alzheimer paired helical filaments. The
CC epitopes all include phosphorylatable serine residues in Ser-Pro
CC motifs, Ile-Gly-Ser motifs or Cys-Gly-Ser motifs and/or
CC phosphorylatable threonine residues in Thr-Pro motifs. The pattern
CC of tau protein phosphorylation differs between Alzheimer's and
CC non-Alzheimer's individuals. Knowledge of the phosphorylated
CC epitopes and antibodies which recognise them may be useful in
CC diagnosis, treatment and prevention of Alzheimer's Disease. The
CC protein kinases present in mammalian brain which phosphorylate the
CC different epitopes are also claimed but no sequences are given.
XX
SQ Sequence 7 AA;

Query Match 78.0%; Score 39; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSP 7
|||||||
Db 1 ysspgsp 7

RESULT 28
AAR37552
ID AAR37552 standard; peptide; 7 AA.
XX
AC AAR37552;
XX
DT 07-OCT-1993 (first entry)
XX
DE Phosphorylated tau protein epitope.
XX
KW Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
KW treatment; formation; inhibition; inhibitor.
XX
OS Homo sapiens.
XX
PN EP544942-A.
XX
PD 09-JUN-1993.
XX
PF 06-DEC-1991; 91EP-0120974.
XX
PR 06-DEC-1991; 91EP-0120974.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow EM, Steiner B;
XX
DR WPI; 1993-183841/23.
XX
PT Phosphorylated tau protein epitope associated with Alzheimer's
PT disease - is used as protein kinase inhibitor for treatment and
PT diagnosis
XX
PS Claim 4; Page 16; 34pp; English.
XX
CC The sequence is that of an epitope of tau protein which specifically
CC occurs in a phosphorylated state in tau protein from Alzheimer's
CC paired helical fragments. It may be used as part of a method for the
CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may
CC also be used in an in vitro model for the study of the generation of
CC the Alzheimer state of proteins and the testing of substances which
CC prevent the conversion of normal to Alzheimer tau protein. The
CC epitope occurs at residues 197-203 of human tau protein.
XX
SQ Sequence 7 AA;

Query Match 78.0%; Score 39; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSP 7
|||||||
Db 1 ysspgsp 7

RESULT 29
AAU17141
ID AAU17141 standard; Protein; 263 AA.
XX
AC AAU17141;
XX
DT 07-NOV-2001 (first entry)
XX
DE Novel signal transduction pathway protein, Seq ID 706.
XX
KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
KW immune system disorder; rheumatoid arthritis; inflammatory condition;
KW organ transplant rejection; infection; hepatitis C; blood disorder;
KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW reproductive system; gastrointestinal; liver disorder; AIDS;
KW acquired immune deficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200154733-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01312.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465460/50.
DR N-PSDB; AAS27058.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders -
XX
PS Claim 1; SEQ ID No 706; 880pp; English.
XX
CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for

```
CC   diagnosing, preventing and treating diseases including immune system
CC   disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC   disorders (e.g rheumatoid arthritis), inflammatory conditions, organ
CC   transplant rejections and graft versus host disease, infectious diseases
CC   (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC   other blood-related disorders (sickle cell anaemia), myeloproliferative
CC   disorders, primary haematopoietic disorders, hyperproliferative
CC   disorders (e.g. Gaucher's disease and cancer), neurodegenerative
CC   disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
CC   abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
CC   disorders (e.g. glomerulonephritis), cardiovascular disorders
CC   (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
CC   wound healing, epithelial cell proliferation, endocrine disorders (e.g.
CC   Addison's disease), reproductive system disorders, gastrointestinal
CC   disorder (inflammatory disorders), liver disorders (cirrhosis),
CC   as stimulators of B-cell responsiveness to pathogens, activators of
CC   T-cells, to induce higher affinity antibodies, and as a means to induce
CC   tumour proliferation in pathologies e.g. acquired immune deficiency
CC   syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction
CC   pathway protein, amino acid sequences of the invention.
XX

  Query Match             78.0%;  Score 39;  DB 22;  Length 263;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db     180 spgspgt 186


RESULT  30
AAM80057
ID   AAM80057 standard; Protein; 376 AA.
XX
AC   AAM80057;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human protein SEQ ID NO 3703.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US04098.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
PR   20-JUN-2000; 2000US-0598075.
PR   19-JUL-2000; 2000US-0620325.
PR   01-SEP-2000; 2000US-0654936.
PR   15-SEP-2000; 2000US-0663561.
PR   20-OCT-2000; 2000US-0693325.
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   N-PSDB; AAK53190.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 20; Page 415; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence   376 AA;

  Query Match             78.0%;  Score 39;  DB 22;  Length 376;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db     358 spgspgt 364


RESULT  31
AAB41838
ID   AAB41838 standard; Protein; 424 AA.
XX
AC   AAB41838;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human ORFX ORF1602 polypeptide sequence SEQ ID NO:3204.
XX
KW   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW   vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW   anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW   immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW   hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW   antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW   antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW   neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW   cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW   cholesterol ester storage; systemic lupus erythematosus; infection;
KW   severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW   allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW   bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW   thrombosis; contraceptive.
XX
OS   Homo sapiens.
XX
PN   WO200058473-A2.
XX
PD   05-OCT-2000.
XX
PF   31-MAR-2000; 2000WO-US08621.
XX
PR   31-MAR-1999;   99US-0127607.
PR   02-APR-1999;   99US-0127636.
PR   05-APR-1999;   99US-0127728.
PR   30-MAR-2000;  2000US-0540763.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
```

DR WPI; 2000-602362/57.
DR N-PSDB; AAC76047.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
PS Claim 11; Page 2417-2418; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ Sequence 424 AA;

Query Match 78.0%; Score 39; DB 21; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SPGSPGT 9
|||||||
Db 341 spgspgt 347

RESULT 32
AAM79073
ID AAM79073 standard; Protein; 424 AA.
XX
AC AAM79073;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1735.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK52206.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 4070-4071; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 424 AA;

Query Match 78.0%; Score 39; DB 22; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SPGSPGT 9
|||||||
Db 341 spgspgt 347

RESULT 33
AAB27227
ID AAB27227 standard; Protein; 424 AA.
XX
AC AAB27227;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human EXMAD-5 SEQ ID NO: 5.
XX
KW Extracellular matrix and adhesion-associated protein; EXMAD; cancer;
KW inflammation; reproductive disorder; cardiovascular disorder;
KW immune disorder; musculoskeletal disorder; developmental disorder;
KW gastrointestinal disorder; cell proliferation disorder.
XX
OS Homo sapiens.
XX
PN WO200068380-A2.
XX
PD 16-NOV-2000.
XX
PF 10-MAY-2000; 2000WO-US12811.
XX
PR 11-MAY-1999; 99US-0133643.
PR 23-AUG-1999; 99US-0150409.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Hillman JL, Tang YT, Lal P, Yue H, Baughn MR, Lu DAM;
PI Azimzai Y;

XX
DR WPI; 2001-007395/01.
DR N-PSDB; AAC66894.
XX
PT Isolated polynucleotide encoding extracellular matrix or
PT adhesion-associated protein (EXMAD) useful for diagnosing, treating, or
PT preventing disorders associated with expression of EXMAD such as
PT proliferative, immune and genetic disorders -
XX
PS Claim 1; Page 92-93; 129pp; English.
XX
CC The present invention provides the protein and coding sequences for 25
CC novel extracellular matrix and adhesion-associated proteins (EXMADs).
CC These are designated EXMAD-1, EXMAD-2, EXMAD-3, EXMAD-4, EXMAD-5,
CC EXMAD-6, EXMAD-7, EXMAD-8, EXMAD-9, EXMAD-10, EXMAD-11, EXMAD-12,
CC EXMAD-13, EXMAD-14, EXMAD-15, EXMAD-16, EXMAD-17, EXMAD-18, EXMAD-19,
CC EXMAD-20, EXMAD-21, EXMAD-22, EXMAD-23, EXMAD-24 and EXMAD-25. They are
CC useful in the prevention and treatment of cancers, cell proliferation,
CC cardiovascular, reproductive, immune, musculoskeletal, developmental and
CC gastrointestinal disorders and inflammation.
XX
SQ Sequence 424 AA;

Query Match 78.0%; Score 39; DB 22; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SPGSPGT 9
|||||||
Db 341 spgspgt 347

RESULT 34
AAO05662
ID AAO05662 standard; Protein; 98 AA.
XX
AC AAO05662;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 19554.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI85593.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 19554; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 98 AA;

Query Match 76.0%; Score 38; DB 22; Length 98;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPG 8
|||||||
Db 79 sspgspg 85

RESULT 35
ABG27348
ID ABG27348 standard; Protein; 284 AA.
XX
AC ABG27348;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #27339.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS91535.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 57707; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as

```
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   284 AA;

  Query Match             74.0%;  Score 37;  DB 22;  Length 284;
  Best Local Similarity   75.0%;  Pred. No. 3.2e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           : ||||||
Db      56 fgspgspg 63


RESULT  36
AAR25063
ID   AAR25063 standard; Protein; 335 AA.
XX
AC   AAR25063;
XX
DT   10-DEC-1992  (first entry)
XX
DE   Soluble human IL-5 receptor alpha chain.
XX
KW   Soluble interleukin-5; chronic asthma; eosinophilia;
KW   screening antagonists; ss.
XX
OS   Homo sapiens.
XX
PN   EP492214-A.
XX
PD   01-JUL-1992.
XX
PF   06-DEC-1991;   91EP-0120951.
XX
PR   27-DEC-1990;   90EP-0811030.
PR   30-APR-1991;   91EP-0810327.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Devos R,  Fiers W,  Plaetinck G,  Tavernier J,  Van Der Hayden J;
XX
DR   WPI; 1992-218502/27.
DR   N-PSDB; AAQ25789.
XX
PT   Recombinant alpha chain of human interleukin-5 receptor - and DNA
PT   encoding it, for treatment of interleukin-5 mediated disorders
PT   such as chronic asthma
XX
PS   Claim 7; Fig 1; 15pp; English.
XX
CC   This amino acid sequence was deduced from the nucleotide sequence,
CC   isolated as detailed in AAQ25789. Recombinant IL-5 alpha chain can be
CC   used as an IL-5 antagonist in chronic asthma or other disease
CC   states with demonstrated esosinophilia. It may also be used either
CC   alone or with the beta chain of the whole IL-5 receptor as a tool
CC   for screening for IL-5 antagonists. See also AAQ25790-2, AAQ30767,8
CC   AAR25064.
XX
SQ   Sequence   335 AA;

  Query Match             74.0%;  Score 37;  DB 13;  Length 335;
  Best Local Similarity   66.7%;  Pred. No. 3.7e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 happgspgt 127


RESULT  37
AAR33699
ID   AAR33699 standard; Protein; 335 AA.
XX
AC   AAR33699;
XX
DT   09-JUL-1993  (first entry)
XX
DE   shIL-5R-alpha.
XX
KW   Probe; murine; interleukin-5; IL-5; receptor; IL-5R; IL-5R-alpha; IgG;
KW   chain; human; hIL-5R; constant domain; heavy; light; immunoglobulin;
KW   IgA; IgM; IgE; chimeric protein; antagonist; asthma; half-life.
XX
OS   Synthetic.
XX
PN   EP533006-A.
XX
PD   24-MAR-1993.
XX
PF   05-SEP-1992;   92EP-0115246.
XX
PR   18-SEP-1991;   91EP-0810738.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Devos R,  Fiers W,  Tavernier J;
XX
DR   WPI; 1993-095341/12.
DR   N-PSDB; AAQ38440.
XX
PT   Deoxyribonucleic acid sequence for chimeric polypeptide prodn. -
PT   comprises parts coding fragment of alpha and/or beta chain of
PT   human interleukin-5 receptor and heavy or light chain of
PT   immunoglobulin, for chronic asthma treatment
XX
PS   Disclosure; Fig 1; 17pp; English.
XX
CC   The sequence given reppresents soluble human interleukin-5 (IL-5)
CC   receptor (IL-5R)-alpha chain.  This sequence was used in the
CC   construction of a chimeric human IL-5R-alpha-IgG1 molecule.  Chimeric
CC   proteins such as this can be used as IL-5 antagonists in the treatment
CC   of diseases, esp. chronic asthma.  The chimeric proteins have an
CC   increased half-life in vivo compared to hIL-5R.  See also AAQ38433-40.
XX
SQ   Sequence   335 AA;

  Query Match             74.0%;  Score 37;  DB 14;  Length 335;
  Best Local Similarity   66.7%;  Pred. No. 3.7e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 happgspgt 127


RESULT  38
AAM93217
ID   AAM93217 standard; Protein; 350 AA.
XX
AC   AAM93217;
XX
DT   06-NOV-2001  (first entry)
```

XX
DE Human polypeptide, SEQ ID NO: 2622.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
DR N-PSDB; AAK94126.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Claim 8; SEQ ID NO 2622; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a polypeptide
CC encoded by a full length human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 350 AA;

Query Match 74.0%; Score 37; DB 22; Length 350;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
::||| |||
Db 249 ftspgypgt 257

RESULT 39
AAM52310
ID AAM52310 standard; Protein; 351 AA.
XX
AC AAM52310;
XX
DT 18-JAN-2002 (first entry)
XX
DE Chicken zyxine fragment.
XX
KW Actin polymerisation; Ena/VASP; vasodilator-stimulated phosphoprotein;
KW metastatic cancer; parasitic infection; cytotoxic; Chicken; zyxine.
XX
OS Gallus gallus.
XX
PN WO200171356-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-FR00843.
XX
PR 22-MAR-2000; 2000FR-0003637.
XX
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
XX
PI Fradelizi J, Friederich E, Golsteyn RM, Louvard D, Noireaux V;
PI Sykes C;
XX
DR WPI; 2001-639148/73.
DR N-PSDB; AAI71780.
XX
PT Identifying modulators of actin polymerization, potentially useful for
PT treating tumor metastasis and parasitic infection, using proteins that
PT contain Ena/VASp binding sites -
XX
PS Claim 16; Pages 77-78; 109pp; French.
XX
CC The present invention relates to a method for identifying modulators of
CC actin polymerisation. The method involves using proteins that contain at
CC least one binding motif for proteins of the Ena/VASP
CC (vasodilator-stimulated phosphoprotein) family in the preparation of
CC reagents for identification/screening of molecules that modulate
CC formation of the actin cytoskeleton. The proteins used in the method
CC (i.e. the proteins with binding motif(s) for Ena/VASP proteins) do not
CC bind to the Arp2/3 protein complex. The modulators identified by the
CC method are potentially useful for treating disorders of actin
CC polymerisation, e.g. metastatic cancer or parasitic infection; and as
CC cytotoxic agents. The present sequence one such protein with binding
CC motif(s) for Ena/VASP proteins, which was used in the method of the
CC present invention.
XX
SQ Sequence 351 AA;

Query Match 74.0%; Score 37; DB 22; Length 351;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
:|||:|||
Db 2 aspgtpgt 9

RESULT 40
AAR28314
ID AAR28314 standard; Protein; 353 AA.
XX
AC AAR28314;
XX
DT 24-MAR-1993 (first entry)
XX
DE AHSV protein.
XX
KW African horse sickness virus; diagnosis; S7.
XX
OS African horse sickness virus serotype 7.
XX
PN EP515235-A.
XX
PD 25-NOV-1992.
XX
PF 26-MAY-1992; 92EP-0304734.
XX
PR 23-MAY-1991; 91GB-0011111.
PR 14-JUN-1991; 91GB-0012875.
XX
PA (NAIN-) INST NACIONAL INVESTIGACIONS AGRARIAS.
PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.
XX
PI Roy P, Sanchez-Vizcaino Rodrique, JM;

XX
DR WPI; 1992-391791/48.
DR N-PSDB; AAQ30130.
XX
PT DNA coding for African horse sickness virus protein - used for
PT diagnosis, and producing polypeptide(s) for use in diagnosis and
PT vaccines
XX
PS Claim 9; Fig 1; 29pp; English.
XX
CC African horse sickness virus serotype 7 clones were identified by
CC colony hybridisation and Northern blot analysis. A full length clone
CC contained fragments at the 5' and 3' ends of the sequence which are
CC characteristic of orbivirus RNA segments. The DNA fragment may be
CC inserted into an expression system and used in assays for detecting
CC AHSV RNA and as primers in amplification processes.
XX
SQ Sequence 353 AA;

Query Match 74.0%; Score 37; DB 13; Length 353;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
|:||:|||
Db 204 sapgapgt 211

Search completed: May 21, 2002, 11:18:07
Job time: 477 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 21, 2002, 11:15:45 ; Search time 26.77 Seconds
(without alignments)
32.305 Million cell updates/sec

Title: US-09-734-281-1
Perfect score: 50
Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	316	1	QRHUT2	microtubule-associ
2	50	100.0	341	2	B28820	microtubule-associ
3	50	100.0	364	2	A28820	microtubule-associ
4	50	100.0	374	2	S46264	microtubule-associ
5	50	100.0	402	1	QRBOT2	microtubule-associ
6	50	100.0	432	2	JS0306	microtubule-associ
7	50	100.0	441	1	QRHUT1	microtubule-associ
8	50	100.0	448	1	QRBOT1	microtubule-associ
9	50	100.0	686	2	A38235	microtubule-associ
10	50	100.0	733	2	A45301	microtubule-associ
11	39	78.0	150	2	T35638	microtubule-associ
12	39	78.0	272	2	T36770	hypothetical prote
13	39	78.0	2232	2	T34434	probable expressio
14	38	76.0	710	2	S72497	hypothetical prote
15	38	76.0	756	1	A55943	oligopeptide trans
16	38	76.0	1345	2	T29090	1-phosphatidylinos
17	38	76.0	3122	2	T17202	surface layer-asso
18	37	74.0	168	2	B88066	DNA-directed DNA p
19	37	74.0	302	2	T40490	protein R52.4 [imp
20	37	74.0	335	2	A40267	probable 26s prote
21	37	74.0	353	1	JQ1946	interleukin-5 rece
22	37	74.0	372	2	AE3191	core protein VP7 -
23	37	74.0	393	2	S16844	conserved hypothet
24	37	74.0	415	1	W2WLEP	titin - rabbit (fr
25	37	74.0	418	2	S29506	E2 protein - Europ
26	37	74.0	420	2	S21052	neurotensin recept
27	37	74.0	515	2	H75589	interleukin-5 rece
28	37	74.0	542	2	A44358	aldehyde dehydroge
29	37	74.0	847	1	A53800	zyxin - chicken
30	37	74.0	963	2	T19140	mixed-lineage prot
31	37	74.0	1387	2	JC5502	hypothetical prote
32	37	74.0	1986	2	S28353	G-protein signalin
33	37	74.0	3623	2	T09456	probable polyketid
34	37	74.0	6805	2	S20901	intrinsic factor-B
35	37	74.0	26926	1	I38344	titin - rabbit (fr
36	36	72.0	119	2	T17003	titin, cardiac mus
37	36	72.0	305	2	S41860	dormancy-associate
38	36	72.0	323	2	A55983	gene Nkx-1.1 prote
39	36	72.0	329	2	T32783	microtubule-associ
40	36	72.0	351	2	A75621	hypothetical prote
41	36	72.0	381	2	S51375	TorS-related prote
42	36	72.0	425	2	F97437	microtubule-associ
43	36	72.0	425	2	AI2655	phosphoribosylamin
44	36	72.0	438	2	C86271	phosphoribosylamin
45	36	72.0	472	2	I67793	F21F23.21 protein
46	36	72.0	501	2	D64453	microtubule-associ
47	36	72.0	506	2	H83396	biotin carboxylase
48	36	72.0	511	2	S10527	probable aldehyde
49	36	72.0	603	2	S51461	endoglucanase B pr
50	36	72.0	680	2	S31216	BUD8 protein - yea
51	36	72.0	729	2	E70803	collagen alpha 1(X
52	36	72.0	914	2	S18942	hypothetical prote
53	36	72.0	1321	2	T00382	hypothetical prote
54	36	72.0	1824	1	QRHUMT	hypothetical prote
55	36	72.0	1825	2	S13507	microtubule-associ

ALIGNMENTS

RESULT 1
QRHUT2
microtubule-associated protein tau, fetal (clone p18) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 02-Sep-1997
C;Accession: PN0001
R;Lee, G.; Neve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A;Title: The microtubule binding domain of tau protein.
A;Reference number: JN0009; MUID:90180482
A;Accession: PN0001
A;Molecule type: mRNA
A;Residues: 1-316 <LEE>
A;Note: this sequence differs from a previously reported fetal tau protein sequence
C;Genetics:
A;Gene: GDB:MAPT; MTBT1
A;Cross-references: GDB:119434; OMIM:157140
A;Map position: 17q21-17q21
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule bind
F;158-188/Domain: MAP2/tau repeat homology <MT1>
F;189-219/Domain: MAP2/tau repeat homology <MT2>
F;220-251/Domain: MAP2/tau repeat homology <MT3>

Query Match 100.0%; Score 50; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 YSSPGSPGT 9
           |||||||||
Db     103 YSSPGSPGT 111
```

RESULT 2
B28820
microtubule-associated protein tau type 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: B28820
R;Lee, G.; Cowan, N.; Kirschner, M.
Science 239, 285-288, 1988

```
A;Title: The primary structure and heterogeneity of tau protein from mouse brain.
A;Reference number: A94298; MUID:88099510
A;Accession: B28820
A;Molecule type: mRNA
A;Residues: 1-341 <LEE>
A;Cross-references: GB:M18775; NID:g201114; PIDN:AAA40165.1; PID:g201115
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; tandem repeat
F;183-213/Domain: MAP2/tau repeat homology <MT1>
F;214-244/Domain: MAP2/tau repeat homology <MT2>
F;245-276/Domain: MAP2/tau repeat homology <MT3>


  Query Match             100.0%;  Score 50;  DB 2;  Length 341;
  Best Local Similarity   100.0%;  Pred. No. 0.64;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     128 YSSPGSPGT 136


RESULT   3
A28820
microtubule-associated protein tau type 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: A28820
R;Lee, G.; Cowan, N.; Kirschner, M.
Science 239, 285-288, 1988
A;Title: The primary structure and heterogeneity of tau protein from mouse brain.
A;Reference number: A94298; MUID:88099510
A;Accession: A28820
A;Molecule type: mRNA
A;Residues: 1-364 <LEE>
A;Cross-references: GB:M18776; NID:g201116; PIDN:AAA40166.1; PID:g201117
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; tandem repeat
F;183-213/Domain: MAP2/tau repeat homology <MT1>
F;214-244/Domain: MAP2/tau repeat homology <MT2>
F;245-276/Domain: MAP2/tau repeat homology <MT3>


  Query Match             100.0%;  Score 50;  DB 2;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 0.68;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     128 YSSPGSPGT 136


RESULT   4
S46264
microtubule-associated protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 13-Aug-1999
C;Accession: S46264
R;Sadot, E.; Marx, R.; Barg, J.; Behar, L.; Ginzburg, I.
J. Mol. Biol. 241, 325-331, 1994
A;Title: Complete sequence of 3'-untranslated region of tau from rat central nervous sys
A;Reference number: S46264; MUID:94334997
A;Accession: S46264
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <SAD>
A;Cross-references: EMBL:X79321; NID:g517393; PIDN:CAA55889.1; PID:g517394
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
F;185-215/Domain: MAP2/tau repeat homology <MT1>
F;216-246/Domain: MAP2/tau repeat homology <MT2>
F;247-277/Domain: MAP2/tau repeat homology <MT3>
F;278-309/Domain: MAP2/tau repeat homology <MT4>


  Query Match             100.0%;  Score 50;  DB 2;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 0.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     130 YSSPGSPGT 138


RESULT   5
QRBOT2
microtubule-associated protein tau, form 3 - bovine
N;Contains: microtubule-associated protein tau, form 4; microtubule-associated prot
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 31-Mar-1996
C;Accession: B31939; A48885; A28173
R;Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.
Mol. Cell. Biol. 9, 1381-1388, 1989
A;Title: Tau consists of a set of proteins with repeated C-terminal microtubule-bi
A;Reference number: A31939; MUID:89261765
A;Accession: B31939
A;Molecule type: mRNA
A;Residues: 1-402 <HIM>
A;Cross-references: GB:M26157; GB:M26158
R;Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.
J. Biol. Chem. 268, 23512-23518, 1993
A;Title: Brain proline-directed protein kinase phosphorylates tau on sites that ar
A;Reference number: A48885; MUID:94043150
A;Accession: A48885
A;Molecule type: protein
A;Residues: 'X',157-162,'X',164-165,'X',167-170;192-195,'X',197-201,'X';358-364,'X
A;Experimental source: brain
A;Note: sequence modified after extraction from NCBI backbone
R;Aizawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
J. Biol. Chem. 263, 7703-7707, 1988
A;Title: Microtubule-binding domain of Tau proteins.
A;Reference number: A28173; MUID:88227970
A;Accession: A28173
A;Molecule type: protein
A;Residues: 159-172,'X',174-177 <AIZ>
A;Experimental source: brain
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repe
F;1-402/Product: microtubule-associated protein tau, form 3 #status predicted <BT4
F;1-234,297-402/Product: microtubule-associated protein tau, form 5 #status predic
F;101-402/Product: microtubule-associated protein tau, form 4 #status predicted <B
F;159-177/Region: microtubule binding #status experimental
F;213-243/Domain: MAP2/tau repeat homology <MT1>
F;244-274/Domain: MAP2/tau repeat homology <MT2>
F;275-305/Domain: MAP2/tau repeat homology <MT3>
F;306-337/Domain: MAP2/tau repeat homology <MT4>
F;156,163,196,202,365/Binding site: phosphate (Ser) (covalent) (by proline-directe
F;166/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #statu


  Query Match             100.0%;  Score 50;  DB 1;  Length 402;
  Best Local Similarity   100.0%;  Pred. No. 0.75;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     158 YSSPGSPGT 166


RESULT   6
JS0306
microtubule-associated protein tau - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Dec-1993
C;Accession: JS0306; A33574
R;Kosik, K.S.; Orecchio, L.D.; Bakalis, S.; Neve, R.L.
Neuron 2, 1389-1397, 1989
```

A;Title: Developmentally regulated expression of specific tau sequences.
A;Reference number: JS0306; MUID:90180457
A;Accession: JS0306
A;Molecule type: mRNA
A;Residues: 1-432 <KOS>
A;Note: the sequence shown is from adult rat brain
A;Note: the partial sequence from fetal rat brain is lacking residues 266-296; the fetal
A;Note: both fetal and adult forms were found in the paired helical filaments characteri
R;Kanai, Y.; Takemura, R.; Oshima, T.; Mori, H.; Ihara, Y.; Yanagisawa, M.; Masaki, T.;
J. Cell Biol. 109, 1173-1184, 1989
A;Title: Expression of multiple tau isoforms and microtubule bundle formation in fibrobl
A;Reference number: A33574; MUID:89359509
A;Accession: A33574
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-432 <KAN>
A;Note: a variant lacking residues 63-91 was also found
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; Alzheimer's disease; calmodulin binding; microtubule b
F;243-273/Domain: MAP2/tau repeat homology <MT1>
F;274-304/Domain: MAP2/tau repeat homology <MT2>
F;305-335/Domain: MAP2/tau repeat homology <MT3>
F;336-367/Domain: MAP2/tau repeat homology <MT4>
F;282-313/Disulfide bonds: #status experimental
F;347/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 100.0%; Score 50; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 188 YSSPGSPGT 196

RESULT 7
QRHUT1
microtubule-associated protein tau, long splice form - human
N;Alternate names: microtubule-binding protein tau; neurofibrillary tangle protein paire
N;Contains: microtubule-associated protein tau type II; microtubule-associated protein t
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 03-May-1996 #text_change 22-Jun-1999
C;Accession: JS0370; A30217; JN0009; S03796; S26665; S26666; S26662; S17302; A43444; A27
R;Goedert, M.; Spillantini, M.G.; Jakes, R.; Rutherford, D.; Crowther, R.A.
Neuron 3, 519-526, 1989
A;Title: Multiple isoforms of human microtubule-associated protein tau: sequences and lo
A;Reference number: JS0370; MUID:90380393
A;Accession: JS0370
A;Molecule type: mRNA
A;Residues: 1-441 <GOE>
A;Note: six isoforms are found; the clone htau40 sequence is shown. Residues 45-73, 74-1
the clone htau24 sequence lacks inserts 1 and 2; the clone htau37 sequence lacks insert
R;Goedert, M.; Wischik, C.M.; Crowther, R.A.; Walker, J.E.; Klug, A.
Proc. Natl. Acad. Sci. U.S.A. 85, 4051-4055, 1988
A;Title: Cloning and sequencing of the cDNA encoding a core protein of the paired helica
A;Reference number: A30217; MUID:88234557
A;Accession: A30217
A;Molecule type: mRNA
A;Residues: 1-44,103-274,306-441 <GO2>
A;Cross-references: GB:J03778; NID:g338684; PIDN:AAA60615.1; PID:g338685
R;Lee, G.; Neve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A;Title: The microtubule binding domain of tau protein.
A;Reference number: JN0009; MUID:90180482
A;Accession: JN0009
A;Molecule type: mRNA
A;Residues: 1-44,103-274,306-441 <LEE>
R;Goedert, M.; Spillantini, M.G.; Potier, M.C.; Ulrich, J.; Crowther, R.A.
EMBO J. 8, 393-399, 1989
A;Title: Cloning and sequencing of the cDNA encoding an isoform of microtubule-associate
A;Reference number: S03796; MUID:89251564
A;Accession: S03796
A;Molecule type: mRNA
A;Residues: 1-44,103-441 <GO3>
A;Cross-references: EMBL:X14474; NID:g36724; PIDN:CAA32636.1; PID:g36725
R;Andreadis, A.; Brown, W.M.; Kosik, K.S.
Biochemistry 31, 10626-10633, 1992
A;Title: Structure and novel exons of the human tau gene.
A;Reference number: S26662; MUID:93041757
A;Accession: S26665
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 144-185 <AND>
A;Cross-references: EMBL:X61372; NID:g36718; PID:g36719
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
A;Accession: S26666
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 187-274 <AN2>
A;Cross-references: EMBL:X61374; NID:g36722; PID:g36723
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
A;Accession: S26662
A;Molecule type: DNA
A;Residues: 371-441 <ANW>
A;Cross-references: EMBL:X61373
R;Jakes, R.; Novak, M.; Davison, M.; Wischik, C.M.
EMBO J. 10, 2725-2729, 1991
A;Title: Identification of 3- and 4-repeat tau isoforms within the PHF in Alzheimer's
A;Reference number: S17302; MUID:92007714
A;Accession: S17302
A;Status: preliminary
A;Molecule type: protein
A;Residues: 268-274,306-395 <JAK>
R;Hasegawa, M.; Morishima-Kawashima, M.; Takio, K.; Suzuki, M.; Titani, K.; Ihara, Y
J. Biol. Chem. 267, 17047-17054, 1992
A;Title: Protein sequence and mass spectrometric analyses of tau in the Alzheimer's
A;Reference number: A43444; MUID:92381012
A;Accession: A43444
A;Molecule type: protein
A;Residues: 2-73;103-130;151-180;191-254;260-269;275-290;299-317;322-340;344-347;354
A;Experimental source: Alzheimer's disease brain
A;Note: sequence extracted from NCBI backbone (NCBIP:112039)
C;Comment: This heterogeneous protein, which is found predominantly in cells of the
o the core protein of the paired helical filament of Alzheimer's disease.
C;Genetics:
A;Gene: GDB:MAPT
A;Cross-references: GDB:119434; OMIM:157140
A;Map position: 17q21-17q21
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule bindi
F;1-441/Product: microtubule-associated protein tau, long splice form #status predict
F;1-274,306-441/Product: microtubule-associated protein tau (clone htau39) #status pr
F;1-73,103-441/Product: microtubule-associated protein tau (clone htau34) #status pre
F;1-73,103-274,306-441/Product: microtubule-associated protein tau (clone htau37) #st
F;1-44,103-274,306-441/Product: microtubule-associated protein tau, fetal #status pre
F;1-44,103-441/Product: microtubule-associated protein tau type II #status predicted
F;252-282/Domain: MAP2/tau repeat homology <MT1>
F;283-313/Domain: MAP2/tau repeat homology <MT2>
F;314-344/Domain: MAP2/tau repeat homology <MT3>
F;345-376/Domain: MAP2/tau repeat homology <MT4>

Query Match 100.0%; Score 50; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 197 YSSPGSPGT 205

RESULT 8
QRBOT1
microtubule-associated protein tau, form 1 - bovine
N;Contains: microtubule-associated protein tau, form 2

```
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: A31939; A33914; S04005; A48885; A28173; B33734
R;Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.
Mol. Cell. Biol. 9, 1381-1388, 1989
A;Title: Tau consists of a set of proteins with repeated C-terminal microtubule-binding
A;Reference number: A31939; MUID:89261765
A;Accession: A31939
A;Molecule type: mRNA
A;Residues: 1-448 <HIM>
A;Cross-references: GB:M26157; NID:g514913; PIDN:AAA30770.1; PID:g514914
R;Iqbal, K.; Grundke-Iqbal, I.; Smith, A.J.; George, L.; Tung, Y.C.; Zaidi, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 5646-5650, 1989
A;Title: Identification and localization of a tau-peptide to paired helical filaments of
A;Reference number: A33914; MUID:89315854
A;Accession: A33914
A;Molecule type: protein
A;Residues: 28,'A',30-38,'IG',41,'AP',44,'LK' <IQB>
A;Experimental source: brain
A;Note: 40-Pro was also found
R;Iqbal, K.; Smith, A.J.; Zaidi, T.; Grundke-Iqbal, I.
FEBS Lett. 248, 87-91, 1989
A;Title: Microtubule-associated protein tau. Identification of a novel peptide from bovi
A;Reference number: S04005; MUID:89252057
A;Accession: S04005
A;Molecule type: protein
A;Residues: 28,'A',30-38,'IG',41,'AP',44,'LK' <IQ2>
A;Experimental source: brain
A;Note: 40-Pro was also found
R;Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.
J. Biol. Chem. 268, 23512-23518, 1993
A;Title: Brain proline-directed protein kinase phosphorylates tau on sites that are abnc
A;Reference number: A48885; MUID:94043150
A;Accession: A48885
A;Molecule type: protein
A;Residues: 'X',203-208,'X',210-211,'X',213-216;238-241,'X',243-247,'X';404-410,'X',412-
A;Experimental source: brain
A;Note: sequence modified after extraction from NCBI backbone
R;Aizawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
J. Biol. Chem. 263, 7703-7707, 1988
A;Title: Microtubule-binding domain of Tau proteins.
A;Reference number: A28173; MUID:88227970
A;Accession: A28173
A;Molecule type: protein
A;Residues: 205-218,'X',220-223 <AIZ>
A;Experimental source: brain
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
F;1-448/Product: microtubule-associated protein tau, form 1 #status predicted <BT43>
F;1-174,193-448/Product: microtubule-associated protein tau, form 2 #status predicted <E
F;205-223/Region: microtubule binding #status experimental
F;259-289/Domain: MAP2/tau repeat homology <MT1>
F;290-320/Domain: MAP2/tau repeat homology <MT2>
F;321-351/Domain: MAP2/tau repeat homology <MT3>
F;352-383/Domain: MAP2/tau repeat homology <MT4>
F;202,209,242,248,411/Binding site: phosphate (Ser) (covalent) (by proline-directed kina
F;212/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status expe


  Query Match             100.0%;  Score 50;  DB 1;  Length 448;
  Best Local Similarity   100.0%;  Pred. No. 0.84;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            |||||||||
Db     204 YSSPGSPGT 212


RESULT   9
A38235
microtubule-associated protein, 110K tau - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Aug-1999
C;Accession: A38235
R;Goedert, M.; Spillantini, M.G.; Crowther, R.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 1983-1987, 1992
A;Title: Cloning of a big tau microtubule-associated protein characteristic of the
A;Reference number: A38235; MUID:92179305
A;Accession: A38235
A;Molecule type: mRNA
A;Residues: 1-686 <GOE>
A;Cross-references: GB:M84156; NID:g207157; PIDN:AAA42204.1; PID:g207158
A;Note: sequence extracted from NCBI backbone (NCBIN:87358, NCBIP:87359)
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; tandem repeat
F;497-527/Domain: MAP2/tau repeat homology <MT1>
F;528-558/Domain: MAP2/tau repeat homology <MT2>
F;559-589/Domain: MAP2/tau repeat homology <MT3>
F;590-621/Domain: MAP2/tau repeat homology <MT4>


  Query Match             100.0%;  Score 50;  DB 2;  Length 686;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            |||||||||
Db     442 YSSPGSPGT 450


RESULT  10
A45301
microtubule-associated protein tau - mouse
N;Alternate names: microtubule binding protein tau
C;Species: Mus musculus (house mouse)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 13-Aug-1999
C;Accession: A45301; S31658
R;Couchie, D.; Mavilia, C.; Georgieff, I.S.; Liem, R.K.; Shelanski, M.L.; Nunez, J
Proc. Natl. Acad. Sci. U.S.A. 89, 4378-4381, 1992
A;Title: Primary structure of high molecular weight tau present in the peripheral n
A;Reference number: A45301; MUID:92262443
A;Accession: A45301
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-733 <COU>
A;Note: this sequence is inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:102045, NCBIP:102046)
R;Kenner, L.; Forstner, M.; Hutter, H.; Hoefler, G.; Kurzbauer, R.; Zatloukal, K.;
submitted to the EMBL Data Library, May 1992
A;Description: First observation of mRNA for a tau-protein from murine liver and k
A;Reference number: S31658
A;Accession: S31658
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'T',529-651 <KEN>
A;Cross-references: EMBL:Z12133; NID:g54263; PIDN:CAA78121.1; PID:g388534
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: microtubule binding; tandem repeat
F;544-574/Domain: MAP2/tau repeat homology <MT1>
F;575-605/Domain: MAP2/tau repeat homology <MT2>
F;606-636/Domain: MAP2/tau repeat homology <MT3>
F;637-668/Domain: MAP2/tau repeat homology <MT4>


  Query Match             100.0%;  Score 50;  DB 2;  Length 733;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            |||||||||
Db     489 YSSPGSPGT 497


RESULT  11
T35638
hypothetical protein SC6G9.42c - Streptomyces coelicolor
```

```
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35638
R;Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21584
A;Accession: T35638
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-150 <SEE>
A;Cross-references: EMBL:AL079356; PIDN:CAB45633.1; GSPDB:GN00070; SCOEDB:SC6G9.42c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC6G9.42c


  Query Match             78.0%;  Score 39;  DB 2;  Length 150;
  Best Local Similarity   87.5%;  Pred. No. 18;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            |||| |||
Db       3 SSPGKPGT 10


RESULT  12
T36770
probable expression regulator - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36770
R;Saunders, D.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21613
A;Accession: T36770
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-272 <SAU>
A;Cross-references: EMBL:AL096849; PIDN:CAB50963.1; GSPDB:GN00070; SCOEDB:SCI11.37c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCI11.37c


  Query Match             78.0%;  Score 39;  DB 2;  Length 272;
  Best Local Similarity   66.7%;  Pred. No. 32;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            |: ||:|||
Db     170 YAPPGAPGT 178


RESULT  13
T34434
hypothetical protein K06A9.1a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T34434
R;Geisel, C.; Gattung, S.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid K06A9.
A;Reference number: Z21525
A;Accession: T34434
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2232 <GEI>
A;Cross-references: EMBL:U80846; PIDN:AAC70890.1; GSPDB:GN00028; CESP:K06A9.1a
A;Experimental source: strain Bristol N2; clone K06A9
C;Genetics:
A;Gene: CESP:K06A9.1a
A;Map position: X
A;Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 2075/

  Query Match             78.0%;  Score 39;  DB 2;  Length 2232;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
            |||||||
Db     886 SPGSPGT 892


RESULT  14
S72497
oligopeptide transport protein PepT1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C;Accession: S72497; S68161
R;Miyamoto, K.I.
submitted to the EMBL Data Library, June 1995
A;Reference number: S72497
A;Accession: S72497
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-710 <MIY>
A;Cross-references: EMBL:D50664; NID:g1384098; PIDN:BAA09318.1; PID:g1212746
R;Miyamoto, K.; Shiraga, T.; Morita, K.; Yamamoto, H.; Haga, H.; Taketani, Y.; Tamai
Biochim. Biophys. Acta 1305, 34-38, 1996
A;Title: Sequence, tissue distribution and developmental changes in rat intestinal c
A;Reference number: S68161; MUID:96180982
A;Accession: S68161
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-258,'E',260-278,'MV',281-710 <MI2>
A;Cross-references: GB:D50664
C;Genetics:
A;Gene: PepT1
C;Superfamily: peptide transport protein PEPT1
C;Keywords: oligopeptide transport; transmembrane protein; transport protein


  Query Match             76.0%;  Score 38;  DB 2;  Length 710;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
            |||||||
Db     441 SSPGSPG 447


RESULT  15
A55943
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-1 [val
N;Alternate names: phosphoinositidase C; phospholipase C-delta-1; triphosphoinositide
C;Species: Homo sapiens (man)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: A55943
R;Cheng, H.F.; Jiang, M.J.; Chen, C.L.; Liu, S.M.; Wong, L.P.; Lomasney, J.W.; King,
J. Biol. Chem. 270, 5495-5505, 1995
A;Title: Cloning and identification of amino acid residues of human phospholipase Cde
A;Reference number: A55943; MUID:95197554
A;Accession: A55943
A;Molecule type: mRNA
A;Residues: 1-756 <CHE>
A;Cross-references: GB:U09117; NID:g483919; PIDN:AAA73567.1; PID:g483920
A;Experimental source: aortic smooth muscle
C;Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-tripho
C;Genetics:
A;Gene: GDB:PLCD1
A;Cross-references: GDB:6075994
C;Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-p
phosphodiesterase domain Y homology; calmodulin repeat homology; pleckstrin repeat ho
C;Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; si
F;19-128/Domain: pleckstrin repeat homology <PLK>
```

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F;140-172/Domain: calmodulin repeat homology <EF1>
F;176-208/Domain: calmodulin repeat homology <EF2>
F;298-440/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
F;491-612/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
F;614-724/Domain: protein kinase C C2 region homology <KC2>


  Query Match             76.0%;  Score 38;  DB 1;  Length 756;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
            :||||:||
Db     507 FSSPGTPG 514


RESULT  16
T29090
surface layer-associated STABLE proteinase - Staphylothermus marinus
N;Alternate names: hyperthermostable proteinase
C;Species: Staphylothermus marinus
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T29090
R;Mayr, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J.
Curr. Biol. 6, 739-749, 1996
A;Title: A hyperthermostable protease of the subtilisin family bound to the surface laye
A;Reference number: Z20559; MUID:96385442
A;Accession: T29090
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1345 <MAY>
A;Cross-references: EMBL:U57968; NID:g1374755; PID:g1374756; PIDN:AAB02323.1
A;Experimental source: strain F1
C;Function:
A;Description: probably serves an exodigestive function related to the organism's energy
A;Note: stoichiometric S-layer component


  Query Match             76.0%;  Score 38;  DB 2;  Length 1345;
  Best Local Similarity   77.8%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            ||| |:|||
Db     596 YSSNGAPGT 604


RESULT  17
T17202
DNA-directed DNA polymerase (EC 2.7.7.7) zeta chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17202
R;Van Sloun, P.P.H.; Romeijn, R.J.; Eeken, J.C.J.
Mutat. Res. 433, 109-116, 1999
A;Title: Molecular cloning, expression and chromosomal localisation of the mouse Rev31 g
A;Reference number: Z18720; MUID:99202265
A;Accession: T17202
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3122 <VAN>
A;Cross-references: EMBL:AF083464; NID:g4079830; PID:g4079831; PIDN:AAC98785.1
A;Experimental source: strain 129/Ola; testis
C;Genetics:
A;Map position: 10
C;Keywords: nucleotidyltransferase


  Query Match             76.0%;  Score 38;  DB 2;  Length 3122;
  Best Local Similarity   87.5%;  Pred. No. 5.4e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
            |||| |||
Db    2108 YSSPDSPG 2115


RESULT  18
B88066
protein R52.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: B88066
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating b
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 199
A;Accession: B88066
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-168 <STO>
A;Cross-references: GB:chr_II; PIDN:AB71062.1; PID:g2429536; GSPDB:GN00020; CESP:R
C;Genetics:
A;Gene: R52.4
A;Map position: 2


  Query Match             74.0%;  Score 37;  DB 2;  Length 168;
  Best Local Similarity   75.0%;  Pred. No. 43;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            ::||||||
Db      40 TTPGSPGT 47


RESULT  19
T40490
probable 26s proteasome regulatory subunit - fission yeast (Schizosaccharomyces po
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: T40490
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft
submitted to the EMBL Data Library, February 1998
A;Reference number: Z21910
A;Accession: T40490
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-302 <WOO>
A;Cross-references: EMBL:AL021730; PIDN:CAA16829.1; GSPDB:GN00067; SPDB:SPBC4C3.07
A;Experimental source: strain 972h-; cosmid c4C3
C;Genetics:
A;Gene: SPDB:SPBC4C3.07
A;Map position: 2
C;Superfamily: mov-34 protein


  Query Match             74.0%;  Score 37;  DB 2;  Length 302;
  Best Local Similarity   66.7%;  Pred. No. 77;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            |:||  |||
Db     123 YASPAEPGT 131


RESULT  20
A40267
interleukin-5 receptor alpha chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
C;Accession: A40267
R;Tavernier, J.; Devos, R.; Cornelis, S.; Tuypens, T.; Van der Heyden, J.; Fiers,
Cell 66, 1175-1184, 1991
```

A;Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-speci
A;Reference number: A40267; MUID:92005669
A;Accession: A40267
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-335 <TAV>
A;Cross-references: GB:M75914; NID:g186387; PIDN:AAA36110.1; PID:g186388
C;Keywords: cytokine receptor; transmembrane protein

Query Match 74.0%; Score 37; DB 2; Length 335;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
:: ||||||
Db 119 HAPPGSPGT 127

RESULT 21
JQ1946
core protein VP7 - African horse sickness virus (serotype 4, strain Spane)
C;Species: African horse sickness virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jun-2000
C;Accession: JQ1946
R;Roy, P.; Hirasawa, T.; Fernandez, M.; Blinov, V.M.; Sanchez-Vixcain Rodrique, J.M.
J. Gen. Virol. 72, 1237-1241, 1991
A;Title: The complete sequence of the group-specific antigen, VP7, of African horsesickn
A;Reference number: JQ1946; MUID:91259049
A;Accession: JQ1946
A;Molecule type: genomic RNA
A;Residues: 1-353 <ROY>
A;Cross-references: GB:D12533; NID:g221010; PIDN:BAA02096.1; PID:g221011
C;Genetics:
A;Map position: segment 7
C;Superfamily: bluetongue virus core protein VP7
C;Keywords: core protein

Query Match 74.0%; Score 37; DB 1; Length 353;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
|:||:|||
Db 204 SAPGAPGT 211

RESULT 22
AE3191
conserved hypothetical protein Atu5258 [imported] - Agrobacterium tumefaciens (strain C5
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AE3191
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AE3191
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-372 <KUR>
A;Cross-references: GB:AE008687; PIDN:AAL45947.1; PID:g17743697; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu5258
A;Genome: plasmid

Query Match 74.0%; Score 37; DB 2; Length 372;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
| |||||:
Db 146 YHQPGSPGS 154

RESULT 23
S16844
titin - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Jun-1999
C;Accession: S16844
R;Fritz, J.D.; Greaser, M.L.; Wolff, J.A.
Nucleic Acids Res. 19, 3747, 1991
A;Title: A novel 3' extension technique using random primers in RNA-PCR.
A;Reference number: S16844; MUID:91305130
A;Accession: S16844
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-393 <FRI>
A;Cross-references: EMBL:X59596; NID:g1722; PIDN:CAA42165.1; PID:g1723
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1991
C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology;

Query Match 74.0%; Score 37; DB 2; Length 393;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
| || |||
Db 55 YKEPGPPGT 63

RESULT 24
W2WLEP
E2 protein - European elk papillomavirus
C;Species: European elk papillomavirus
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-May-2000
C;Accession: D29499; D94457; D94506
R;Ahola, H.; Bergman, P.; Stroem, A.C.; Moreno-Lopez, J.; Pettersson, U.
Gene 50, 195-205, 1986
A;Title: Organization and expression of the transforming region from the European el
A;Reference number: A91567; MUID:87219878
A;Accession: D29499
A;Molecule type: DNA
A;Residues: 1-415 <AHO>
A;Cross-references: GB:M15953; NID:g333025; PIDN:AAA66854.1; PID:g484020
R;Eriksson, A.
unpublished results 1987, cited by GenBank
A;Reference number: A94457
A;Accession: D94457
A;Molecule type: DNA
A;Residues: 1-415 <ERI>
A;Cross-references: GB:M15953; NID:g333025; PIDN:AAA66854.1; PID:g484020
R;Pettersson, U.
submitted to GenBank, August 1987
A;Reference number: A94506
A;Accession: D94506
A;Molecule type: DNA
A;Residues: 1-415 <PET>
A;Cross-references: GB:M15953; NID:g333025; PIDN:AAA66854.1; PID:g484020
C;Superfamily: papillomavirus E2 protein
C;Keywords: early protein

Query Match 74.0%; Score 37; DB 1; Length 415;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 YSSPGSPGT 9
             ||:| |||:
Db     268 YSAPSSPGS 276


RESULT  25
S29506
neurotensin receptor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000
C;Accession: S29506
R;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Dumont, X.; Kaghad, M.; Gully, D.; le F
FEBS Lett. 317, 139-142, 1993
A;Title: Cloning and expression of a complementary DNA encoding a high affinity human ne
A;Reference number: S29506; MUID:93154505
A;Accession: S29506
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-418 <VIT>
A;Cross-references: EMBL:X70070; NID:g35020; PIDN:CAA49675.1; PID:g35021
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein


  Query Match             74.0%;  Score 37;  DB 2;  Length 418;
  Best Local Similarity   75.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           |:||:|||
Db       6 SAPGTPGT 13


RESULT  26
S21052
interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored is
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C;Accession: S21052; S21050; S21053; A46175; S78106; S78107
R;Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression of the human interleukin 5 receptor.
A;Reference number: S21050; MUID:92121815
A;Accession: S21052
A;Molecule type: DNA
A;Residues: 1-420 <MUR>
A;Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844
A;Experimental source: clone lambda h5R.12
A;Accession: S21050
A;Molecule type: DNA
A;Residues: 1-395,'I' <MU2>
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
A;Experimental source: clone lambda h5R.27
A;Accession: S21053
A;Molecule type: mRNA
A;Residues: 1-332,'K' <MU3>
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
A;Experimental source: clone lambda h5R.25
R;Tavernier, J.; Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A;Title: Molecular basis of the membrane-anchored and two soluble isoforms of the human
A;Reference number: A46175; MUID:92357767
A;Accession: A46175
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 333-420 <TAV>
A;Experimental source: HL-60 cells and eosinophils
A;Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
R;Murata, Y.
submitted to the EMBL Data Library, July 1991
A;Reference number: S78106
A;Accession: S78106
A;Molecule type: DNA
A;Residues: 1-128,'I',130-395,'I' <MUW>
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
R;Murata, Y.
submitted to the EMBL Data Library, September 1991
A;Reference number: S78107
A;Accession: S78107
A;Molecule type: mRNA
A;Residues: 1-128,'I',130-332,'K' <MU4>
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane pr
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>
F;345-365/Domain: transmembrane #status predicted <TMM>
F;35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predic


  Query Match             74.0%;  Score 37;  DB 2;  Length 420;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
             :: ||||||
Db     119 HAPPGSPGT 127


RESULT  27
H75589
aldehyde dehydrogenase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: H75589
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson,
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R
A;Reference number: A75250; MUID:20036896
A;Accession: H75589
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-515 <WHI>
A;Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12436.1; PID:g
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRA0348
A;Map position: 2
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology


  Query Match             74.0%;  Score 37;  DB 2;  Length 515;
  Best Local Similarity   55.6%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
             |::||:||:
Db      13 YANPGTPGS 21


RESULT  28
A44358
zyxin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Jun-1993 #sequence_revision 06-Feb-1995 #text_change 21-Jul-2000
C;Accession: A44358; S30506
R;Sadler, I.; Crawford, A.W.; Michelsen, J.W.; Beckerle, M.C.
J. Cell Biol. 119, 1573-1587, 1992
A;Title: Zyxin and cCRP: two interactive LIM domain proteins associated with the
A;Reference number: A44358; MUID:93107157
A;Accession: A44358
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-542 <SAD>
A;Cross-references: EMBL:X69190; NID:g63897; PIDN:CAA48936.1; PID:g63898
```

A;Note: sequence extracted from NCBI backbone (NCBIN:121172, NCBIP:121174)
A;Note: this sequence may be one segment of several
C;Superfamily: LIM metal-binding repeat homology
F;352-404/Domain: LIM metal-binding repeat homology <LIM1>
F;412-463/Domain: LIM metal-binding repeat homology <LIM2>
F;472-533/Domain: LIM metal-binding repeat homology <LIM3>

Query Match 74.0%; Score 37; DB 2; Length 542;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
:|||:|||
Db 2 ASPGTPGT 9

RESULT 29
A53800
mixed-lineage protein kinase (EC 2.7.1.-) 3 - human
N;Alternate names: protein kinase PTK1; protein kinase SPRK
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A53800; I58395
R;Gallo, K.A.; Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J.
J. Biol. Chem. 269, 15092-15100, 1994
A;Title: Identification and characterization of SPRK, a novel src-homology 3 domain-cont
A;Reference number: A53800; MUID:94253068
A;Accession: A53800
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-847 <GAL>
A;Cross-references: GB:U07747; NID:g464027; PIDN:AAA19647.1; PID:g464028
R;Ing, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassam, N.J.
Oncogene 9, 1745-1750, 1994
A;Title: MLK-3: identification of a widely-expressed protein kinase bearing an SH3 domai
A;Reference number: I58395; MUID:94239754
A;Accession: I58395
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-847 <RES>
A;Cross-references: GB:L32976; NID:g488295; PIDN:AAA59859.1; PID:g488296
C;Genetics:
A;Gene: GDB:MLK3; PTK1; SPRK
A;Cross-references: GDB:134755; OMIM:600050
A;Map position: 11q13.1-11q13.3
C;Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
C;Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein k
F;48-100/Domain: SH3 homology <SH32>
F;115-383/Domain: protein kinase homology <KIN>
F;123-131/Region: protein kinase ATP-binding motif
F;403-424/Region: leucine zipper motif
F;438-459/Region: leucine zipper motif
F;468-482/Region: basic

Query Match 74.0%; Score 37; DB 1; Length 847;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
|:||:|||
Db 748 SAPGTPGT 755

RESULT 30
T19140
hypothetical protein C09G5.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19140
R;Palmer, S.
submitted to the EMBL Data Library, November 1994
A;Reference number: Z19080
A;Accession: T19140
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-963 <WIL>
A;Cross-references: EMBL:Z46791; PIDN:CAA86755.1; GSPDB:GN00020; CESP:C09G5.6
A;Experimental source: clone C09G5
C;Genetics:
A;Gene: CESP:C09G5.6
A;Map position: 2
A;Introns: 48/3; 862/3; 898/1

Query Match 74.0%; Score 37; DB 2; Length 963;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
|:||:|||
Db 559 SAPGAPGT 566

RESULT 31
JC5502
G-protein signaling regulator 12 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C;Accession: JC5502
R;Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, D.P.
Biochem. Biophys. Res. Commun. 233, 770-777, 1997
A;Title: Molecular cloning and expression analysis of rat Rgs12 and Rgs14.
A;Reference number: JC5502; MUID:97312490
A;Accession: JC5502
A;Molecule type: mRNA
A;Residues: 1-1387 <SNO>
A;Cross-references: GB:U92280; NID:g2088557; PIDN:AAC53176.1; PID:g2088558
C;Comment: This protein funcitons as GTPase activating protein. It interacts with re
F;18-80/Domain: rhophilin-like #status predicted <RHO>
F;712-761/Domain: GH1 #status predicted <GH1>
F;765-800/Domain: GH2 #status predicted <GH2>
F;804-828/Domain: GH3 #status predicted <GH3>
F;1204-1220/Region: conserved #status predicted
F;1266-1295/Region: coiled heptad repeat (S-P-X-S-A)

Query Match 74.0%; Score 37; DB 2; Length 1387;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
:|:|| |||
Db 1296 HSTPGPPGT 1304

RESULT 32
S28353
probable polyketide synthase - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-May-2000
C;Accession: S28353
R;Mayorga, M.E.; Timberlake, W.E.
Mol. Gen. Genet. 235, 205-212, 1992
A;Title: The developmentally regulated Aspergillus nidulans wA gene encodes a polype
A;Reference number: S28353; MUID:93101122
A;Accession: S28353
A;Molecule type: DNA
A;Residues: 1-1986 <MAY>
A;Cross-references: EMBL:X65866; NID:g5508; PID:g5509
C;Genetics:
A;Gene: wA
A;Introns: 96/2; 193/3; 1336/3; 1588/3
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acyl carrier pro
C;Keywords: carrier protein

F;397-805/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F;911-1199/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1648-1718/Domain: acyl carrier protein homology <ACP>
F;1766-1840/Domain: acyl carrier protein homology <ACP1>

Query Match 74.0%; Score 37; DB 2; Length 1986;
Best Local Similarity 87.5%; Pred. No. 5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
|||| ||||
Db 1749 SSPASPGT 1756

RESULT 33
T09456
intrinsic factor-B12 receptor Cubilin precursor - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09456
R;Kozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
ion.
A;Reference number: Z16677; MUID:98241400
A;Accession: T09456
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3623 <KOZ>
A;Cross-references: EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3929529
C;Genetics:
A;Map position: 10p12
C;Superfamily: unassigned EGF-related proteins; EGF homology
C;Keywords: receptor; vitamin B12 uptake
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F;436-467/Domain: EGF homology <EGF>

Query Match 74.0%; Score 37; DB 2; Length 3623;
Best Local Similarity 66.7%; Pred. No. 9.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
::||| |||
Db 3522 FTSPGYPGT 3530

RESULT 34
S20901
titin - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C;Accession: S20901; I46520
R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.
EMBO J. 11, 1711-1716, 1992
A;Title: Towards a molecular understanding of titin.
A;Reference number: S20897; MUID:92258380
A;Accession: S20901
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-6805 <LAB>
A;Cross-references: EMBL:X64696
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R;Labeit, S.; Barlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Hsieh, C.L.; Francke, U.;
Nature 345, 273-276, 1990
A;Title: A regular pattern of two types of 100-residue motif in the sequence of titin.
A;Reference number: I46520; MUID:90238553
A;Accession: I46520
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 4235-5250 <LA2>
A;Cross-references: EMBL:X17329; NID:g1756; PIDN:CAA35207.1; PID:g930251
C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology
C;Keywords: muscle

Query Match 74.0%; Score 37; DB 2; Length 6805;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
| || |||
Db 5282 YKEPGPPGT 5290

RESULT 35
I38344
titin, cardiac muscle [validated] - human
N;Alternate names: connectin
N;Contains: serine/threonine-specific protein kinase (EC 2.7.1.-)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Sep-2000
C;Accession: I38344; I38345; S20898; S20897; S20899; S63665; S37393
R;Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Reference number: A57430; MUID:96026330
A;Accession: I38344
A;Status: nucleic acid sequence not shown; translation not shown; translated from
A;Molecule type: mRNA
A;Residues: 1-26926 <LAB1>
A;Cross-references: EMBL:X90568; NID:g1017424; PID:g1017425
R;Musco, G.; Tziatzios, C.; Schuck, P.; Pastore, A.
Biochemistry 34, 553-561, 1995
A;Title: Dissecting titin into its structural motifs: identification of an alpha-h
A;Reference number: I38345; MUID:95119041
A;Accession: I38345
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1977-2014 <MUS>
A;Cross-references: EMBL:X83270; NID:g602579; PIDN:CAA58243.1; PID:g602580
A;Note: conformation and properties are reported for a synthetic peptide correspon
R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.
EMBO J. 11, 1711-1716, 1992
A;Title: Towards a molecular understanding of titin.
A;Reference number: S20897; MUID:92258380
A;Accession: S20898
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 13597-14200,'I',14202-14696 <LAB2>
A;Cross-references: EMBL:X64698; NID:g37192; PIDN:CAA45939.1; PID:g37193
A;Accession: S20897
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 16330-16382,'S',16384-16756,'F',16758-16860 <LAB3>
A;Cross-references: EMBL:X64699; NID:g37190; PIDN:CAA45940.1; PID:g37191
A;Accession: S20899
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 'P',22278-22431,'R',22433-22448,'G',22450-22453,'Q',22455-22480,'TR',
A;Cross-references: EMBL:X64697; NID:g37190; PIDN:CAA45938.1; PID:g37195
R;Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labeit, S.
J. Mol. Biol. 256, 556-563, 1996
A;Title: Genomic organization of M line titin and its tissue-specific expression
A;Reference number: S63665; MUID:96177761
A;Accession: S63665
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 26729-26825 <KOL>
A;Cross-references: EMBL:X92412; NID:g1236761
R;Gautel, M.; Leonard, K.; Labeit, S.
EMBO J. 12, 3827-3834, 1993
A;Title: Phosphorylation of KSP motifs in the C-terminal region of titin in diffe
A;Reference number: S37393; MUID:94008990

```
A;Accession: S37393
A;Molecule type: mRNA
A;Residues: 26831-26926 <GAU>
R;Improta, S.; Politou, A.S.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, February 1996
A;Reference number: A66736; PDB:1TIT
A;Contents: annotation; conformation by (1)H-NMR, residues 5253-5341
R;Pfuhl, M.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A66201; PDB:1NCT
A;Contents: annotation; conformation by (1)H-NMR, residues 'S',26059-26155
C;Genetics:
A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q32
C;Function:
A;Description: structural protein forming filaments in striated muscle
C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; prc
C;Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; glycc
structural protein
F;24752-25008/Domain: protein kinase homology <KIN>
F;84,177,905,2276,2378,2459,2481,2563,2669,2763,2896,3088,3179,3384,3432,3628,3772,4068,
98,11066,11488,11515,11635,11949,12170,12478,12526,12645,12875,13001,13036,13295,13540,1
tatus predicted
F;16780,16976,17579,17602,17667,17681,17845,17899,18121,18188,18209,18336,18670,18680,18
,21900,21935,22295,22495,22627,22897,23024,23318,23883,24012,24177,24290,24447,24642,248
F;26171,26178,26184,26190/Binding site: phosphate (Ser) (covalent) #status experimental


  Query Match             74.0%;  Score 37;  DB 1;  Length 26926;
  Best Local Similarity   66.7%;  Pred. No. 6.7e+03;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |  || |||
Db   16923 YKEPGPPGT 16931


RESULT  36
T17003
dormancy-associated protein [similarity] - apple tree
C;Species: Malus domestica (apple tree)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T17003
R;Lee, S.A.; Gardner, R.C.; Lay-Yee, M.
Plant Physiol. 103, 1017, 1993
A;Title: An apple gene highly expressed in fruit.
A;Reference number: Z18646; MUID:94294548
A;Accession: T17003
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-119 <LEE>
A;Cross-references: EMBL:L15194; NID:g439878; PIDN:AAA71994.1; PID:g439879
A;Experimental source: cultivar Golden delicious; fruit cortical


  Query Match             72.0%;  Score 36;  DB 2;  Length 119;
  Best Local Similarity   85.7%;  Pred. No. 44;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||:|||
Db      51 SPGTPGT 57


RESULT  37
S41860
gene Nkx-1.1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C;Accession: S41860
R;Schubert, F.R.; Gruss, P.
submitted to the EMBL Data Library, October 1993
A;Description: Expression of the novel Murine homeobox gene Nkx-1.1 in the developi
A;Reference number: S41860
A;Accession: S41860
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <SCH>
A;Cross-references: EMBL:X75384; NID:g453171; PIDN:CAA53153.1; PID:g453172
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;157-213/Domain: homeobox homology <HOX>


  Query Match             72.0%;  Score 36;  DB 2;  Length 305;
  Best Local Similarity   75.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           :||||||:
Db     134 ASPGSPGS 141


RESULT  38
A55983
microtubule-associated protein MAP2 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 23-Aug-1997
C;Accession: A55983; A41011; A33734
R;Coffey, R.L.; Joly, J.C.; Cain, B.D.; Purich, D.L.
Biochemistry 33, 13199-13207, 1994
A;Title: Exploring the microtubule-binding region of bovine microtubule-associated p
A;Reference number: A55983; MUID:95034751
A;Accession: A55983
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-323 <COF>
A;Cross-references: GB:S74025
R;Dingus, J.; Obar, R.A.; Hyams, J.S.; Goedert, M.; Vallee, R.B.
J. Biol. Chem. 266, 18854-18860, 1991
A;Title: Use of a heat-stable microtubule-associated protein class-specific antibody
A;Reference number: A41011; MUID:92011652
A;Accession: A41011
A;Molecule type: protein
A;Residues: 227-258 <DIN>
R;Joly, J.C.; Flynn, G.; Purich, D.L.
J. Cell Biol. 109, 2289-2294, 1989
A;Title: The microtubule-binding fragment of microtubule-associated protein-2: locat
A;Reference number: A33734; MUID:90037224
A;Accession: A33734
A;Status: preliminary
A;Molecule type: protein
A;Residues: 121-139 <JOL>
C;Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
C;Keywords: microtubule binding; tandem repeat
F;165-195/Domain: MAP2/tau repeat homology <MT1>
F;227-258/Domain: MAP2/tau repeat homology <MT2>


  Query Match             72.0%;  Score 36;  DB 2;  Length 323;
  Best Local Similarity   72.7%;  Pred. No. 1.2e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 YSS--PGSPGT 9
           |||  ||:|||
Db     105 YSSRTPGTPGT 115


RESULT  39
T32783
hypothetical protein C50D2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C;Accession: T32783
R;Sammons, L.; Wohldmann, P.; Bauer, C.
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submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid C50D2.
A;Reference number: Z21224
A;Accession: T32783
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-329 <SAM>
A;Cross-references: EMBL:AF040642; PIDN:AAB94952.1; GSPDB:GN00020; CESP:C50D2.4
A;Experimental source: strain Bristol N2; clone C50D2
C;Genetics:
A;Gene: CESP:C50D2.4
A;Map position: 2
A;Introns: 27/1; 59/3; 76/3; 237/1
C;Superfamily: unassigned collagens

Query Match 72.0%; Score 36; DB 2; Length 329;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SPGSPGT 9
||:|||
Db 160 SPGNPGT 166

RESULT 40
A75621
TorS-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: A75621
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
A;Accession: A75621
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-351 <WHI>
A;Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12581.1; PID:g6460877; TIGR:DRB00
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRB0027
A;Map position: megaplasmid
A;Genome: plasmid
A;Note: plasmid MP1

Query Match 72.0%; Score 36; DB 2; Length 351;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||: |:|||
Db 95 YSTAGTPGT 103

Search completed: May 21, 2002, 11:19:10
Job time: 205 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 21, 2002, 11:18:40 ; Search time 13.48 Seconds
(without alignments)
25.851 Million cell updates/sec

Title: US-09-734-281-1
Perfect score: 50
Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	382	1	TAU_PAPHA	Q9myx8 papio hamad
2	50	100.0	402	1	TAU_CAPHI	O02828 capra hircu
3	50	100.0	447	1	TAU_BOVIN	P29172 bos taurus
4	50	100.0	458	1	TAU_MACMU	P57786 macaca mula
5	50	100.0	732	1	TAU_MOUSE	P10637 mus musculu
6	50	100.0	751	1	TAU_RAT	P19332 rattus norv
7	50	100.0	757	1	TAU_HUMAN	P10636 homo sapien
8	39	78.0	639	1	P2B1_CRYNE	O42773 cryptococcu
9	38	76.0	710	1	PET1_RAT	P51574 rattus norv
10	38	76.0	756	1	PID1_HUMAN	P51178 homo sapien
11	38	76.0	3122	1	DPOZ_MOUSE	Q61493 mus musculu
12	37	74.0	164	1	CDN1_FELCA	O19002 felis silve
13	37	74.0	387	1	TIZ2_MOUSE	Q9eqn3 mus musculu
14	37	74.0	395	1	TIZ2_HUMAN	Q9y3q8 homo sapien
15	37	74.0	415	1	VE2_PAPVE	P11329 european el
16	37	74.0	418	1	NTR1_HUMAN	P30989 homo sapien
17	37	74.0	420	1	IL5R_HUMAN	Q01344 homo sapien
18	37	74.0	515	1	DHAL_DEIRA	Q9ryg9 deinococcus
19	37	74.0	542	1	ZYX_CHICK	Q04584 gallus gall
20	37	74.0	963	1	YQ36_CAEEL	Q09457 caenorhabdi
21	37	74.0	1387	1	RGSC_RAT	O08774 rattus norv
22	37	74.0	1986	1	WA_EMENI	Q03149 emericella
23	36	72.0	305	1	SAX1_MOUSE	P42580 mus musculu
24	36	72.0	501	1	PYCA_METJA	Q58626 methanococc
25	36	72.0	511	1	GUNB_PSEFL	P18126 pseudomonas
26	36	72.0	603	1	BUD8_YEAST	P41698 saccharomyc
27	36	72.0	680	1	CA1A_MOUSE	Q05306 mus musculu
28	36	72.0	1171	1	TRI2_STRCO	Q9rkb9 streptomyce
29	36	72.0	1827	1	MAP2_HUMAN	P11137 homo sapien
30	36	72.0	1828	1	MAP2_MOUSE	P20357 mus musculu
31	36	72.0	1861	1	MAP2_RAT	P15146 rattus norv
32	35	70.0	159	1	CDN1_MOUSE	P39689 mus musculu
33	35	70.0	386	1	UR2R_RAT	P49684 rattus norv
34	35	70.0	415	1	IL5R_MOUSE	P21183 mus musculu
35	35	70.0	495	1	HXKG_ASPNG	Q92407 aspergillus
36	35	70.0	573	1	AMH2_HUMAN	Q16671 homo sapien
37	35	70.0	828	1	MRKC_KLEPN	P21647 klebsiella
38	35	70.0	903	1	VGLB_HSV1F	P06436 herpes simp
39	35	70.0	904	1	VGLB_HSV11	P10211 herpes simp
40	35	70.0	904	1	VGLB_HSV1P	P08665 herpes simp
41	35	70.0	956	1	RRPO_SBMV	P21405 southern be
42	35	70.0	1464	1	CA13_MOUSE	P08121 mus musculu
43	35	70.0	1690	1	CA44_HUMAN	P53420 homo sapien
44	35	70.0	1835	1	CCAI_RAT	Q9z0y8 rattus norv
45	34	68.0	114	1	ET3_RABIT	P19998 oryctolagus
46	34	68.0	238	1	ET3_HUMAN	P14138 homo sapien
47	34	68.0	239	1	CALD_MELGA	P13505 meleagris g
48	34	68.0	239	1	MABA_MOUSE	P39039 mus musculu
49	34	68.0	249	1	PSPA_PIG	P49874 sus scrofa
50	34	68.0	298	1	34KD_MYCPA	Q04959 mycobacteri
51	34	68.0	467	1	RPB1_CRIGR	P11414 cricetulus
52	34	68.0	492	1	DYJ2_HUMAN	O43237 homo sapien
53	34	68.0	508	1	CILA_KLEPN	P45413 klebsiella
54	34	68.0	520	1	MRCO_HUMAN	Q9uew3 homo sapien
55	34	68.0	547	1	CD19_MOUSE	P25918 mus musculu

ALIGNMENTS

```
RESULT   1
TAU_PAPHA
ID   TAU_PAPHA      STANDARD;      PRT;   382 AA.
AC   Q9MYX8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR TAU.
OS   Papio hamadryas (Hamadryas baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Papio.
OX   NCBI_TaxID=9557;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Frontal cortex;
RA   Wang X.L., Wang J., Schultz C., Hubbard G.B.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC       BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC       POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC       TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC       TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC       CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS (BY
CC       SIMILARITY).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
CC   -!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC       CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC       MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC       MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
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CC   ----------------------------------------------------------------------
DR   EMBL; AF281310; AAF97596.1; -.
DR   InterPro; IPR002955; Tau_protein.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 4.
DR   PRINTS; PR01261; TAUPROTEIN.
DR   PROSITE; PS00229; TAU_MAP; 4.
KW   Microtubules; Cytoskeleton; Repeat; Acetylation; Phosphorylation.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   REPEAT      185    215       TAU/MAP MOTIF 1.
FT   REPEAT      216    246       TAU/MAP MOTIF 2.
FT   REPEAT      247    277       TAU/MAP MOTIF 3.
FT   REPEAT      278    309       TAU/MAP MOTIF 4.
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   DISULFID    232    263       BY SIMILARITY.
SQ   SEQUENCE   382 AA;  39879 MW;  D2D15A53AA00E8E7 CRC64;


  Query Match             100.0%;  Score 50;  DB 1;  Length 382;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     138 YSSPGSPGT 146


RESULT   2
TAU_CAPHI
ID   TAU_CAPHI      STANDARD;      PRT;   402 AA.
AC   O02828;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR TAU.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC   TISSUE=Brain cortex;
RX   MEDLINE=97012131; PubMed=8858947;
RA   Nelson P.T., Stefansson K., Gulcher J., Saper C.B.;
RT   "Molecular evolution of tau protein: implications for Alzheimer's
RT   disease.";
RL   J. Neurochem. 67:1622-1632(1996).
CC   -!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC       BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC       POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC       TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC       TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
CC       ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
CC       ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC       CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; TAU-A (SHOWN HERE) AND
CC       TAU-B; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER FROM EACH
CC       OTHER BY THE PRESENCE OR ABSENCE OF TWO EXONS. ONE OF THESE
CC       OPTIONAL EXONS CONTAINS THE ADDITIONAL TAU/MAP REPEAT.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
CC   -!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
CC       CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC       CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC       MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC       MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S83347; AAB50785.1; -.
DR   InterPro; IPR002955; Tau_protein.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 4.
DR   PRINTS; PR01261; TAUPROTEIN.
DR   PROSITE; PS00229; TAU_MAP; 4.
KW   Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
KW   Phosphorylation.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   REPEAT      205    235       TAU/MAP MOTIF 1.
FT   REPEAT      236    266       TAU/MAP MOTIF 2.
FT   REPEAT      267    297       TAU/MAP MOTIF 3.
FT   REPEAT      298    329       TAU/MAP MOTIF 4.
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   DISULFID    252    283       BY SIMILARITY.
FT   VARSPLIC     33     61       MISSING (IN ISOFORM TAU-B).
FT   VARSPLIC    236    266       MISSING (IN ISOFORM TAU-B).
SQ   SEQUENCE   402 AA;  41716 MW;  3E623B684E9F8AEF CRC64;


  Query Match             100.0%;  Score 50;  DB 1;  Length 402;
  Best Local Similarity   100.0%;  Pred. No. 0.32;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     158 YSSPGSPGT 166


RESULT   3
TAU_BOVIN
ID   TAU_BOVIN      STANDARD;      PRT;   447 AA.
AC   P29172; P29173; Q28185; Q28186; Q28187; Q28188; Q28189; Q28190;
DT   01-DEC-1992 (Rel. 24, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR TAU.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-A; TAU-B; TAU-G AND TAU-H).
RC   TISSUE=Brain;
RX   MEDLINE=89261765; PubMed=2498649;
RA   Himmler A., Drechsel D., Kirschner M.W., Martin D.W. Jr.;
RT   "Tau consists of a set of proteins with repeated C-terminal
RT   microtubule-binding domains and variable N-terminal domains.";
RL   Mol. Cell. Biol. 9:1381-1388(1989).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-A TO TAU-F AND TAU-I TO TAU-T).
RC   TISSUE=Brain;
RX   MEDLINE=89261766; PubMed=2498650;
RA   Himmler A.;
RT   "Structure of the bovine tau gene: alternatively spliced transcripts
RT   generate a protein family.";
RL   Mol. Cell. Biol. 9:1389-1396(1989).
RN   [3]
RP   GLYCOSYLATION.
RX   MEDLINE=97067111; PubMed=8910513;
```

```
RA   Arnold C.S., Johnson G.V.W., Cole R.N., Dong D.L.-Y., Lee M.,
RA   Hart G.W.;
RT   "The microtubule-associated protein tau is extensively modified with
RT   O-linked N-acetylglucosamine.";
RL   J. Biol. Chem. 271:28741-28744(1996).
CC   -!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC       BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC       POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC       TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC       TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
CC       ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
CC       ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE.
CC       CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 20 ISOFORMS; TAU-A/PBT43I12 (SHOWN
CC       HERE), TAU-B/PBT43-12, TAU-C, TAU-D, TAU-E, TAU-F, TAU-G/PBT4,
CC       TAU-H/PBT7, TAU-I, TAU-J, TAU-K, TAU-L, TAU-M, TAU-N, TAU-O, TAU-
CC       P, TAU-Q, TAU-R, TAU-S AND TAU-T; ARE PRODUCED BY ALTERNATIVE
CC       SPLICING. THEY DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE
CC       OF UP TO 6 OF THE 14 EXONS. ONE OF THESE OPTIONAL EXONS CONTAINS
CC       THE ADDITIONAL TAU/MAP REPEAT. TAU-A CDNA HAS BEEN CONSTRUCTED
CC       FROM TWO OVERLAPPING CDNAS BY THE AUTHORS OF REF.1. TAU-G AND TAU-
CC       H SEQUENCES BEGIN WITH EXON 6 OR A PART OF IT (EXON 6 IS MISSING
CC       IN ISOFORMS THAT BEGIN WITH EXON 1). 3 DIFFERENT C-TERMINI ARE
CC       OBTAINED EITHER BY THE RETENTION OR THE SPLICING OF INTRON 13/14
CC       (2 DIFFERENT 5' SPLICE DONORS).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
CC   -!- INDUCTION: DURING NEURITE OUTGROWTH.
CC   -!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
CC       CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC       CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC       MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC       MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC   -!- PTM: O-LINKED N-ACETYLGLUCOSAMINATION AT MORE THAN 4 SITES PER
CC       PROTEIN. SITE-SPECIFIC OR STOICHIOMETRIC CHANGES IN GLYCOSYLATION
CC       MAY MODULATE TAU FUNCTION AND ALSO PLAY A ROLE IN PHF'S FORMATION.
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L34953; AAA51609.1; -.
DR   EMBL; L34940; AAA51609.1; JOINED.
DR   EMBL; L34941; AAA51609.1; JOINED.
DR   EMBL; L34942; AAA51609.1; JOINED.
DR   EMBL; L34943; AAA51609.1; JOINED.
DR   EMBL; L34944; AAA51609.1; JOINED.
DR   EMBL; L34946; AAA51609.1; JOINED.
DR   EMBL; L34947; AAA51609.1; JOINED.
DR   EMBL; L34948; AAA51609.1; JOINED.
DR   EMBL; L34949; AAA51609.1; JOINED.
DR   EMBL; L34950; AAA51609.1; JOINED.
DR   EMBL; L34951; AAA51609.1; JOINED.
DR   EMBL; L34952; AAA51609.1; JOINED.
DR   EMBL; M26157; AAA30770.1; -.
DR   EMBL; M26158; AAA30771.1; -.
DR   EMBL; M26178; AAA51601.1; ALT_SEQ.
DR   EMBL; L34940; AAA51601.1; JOINED.
DR   EMBL; L34941; AAA51601.1; JOINED.
DR   EMBL; L34942; AAA51601.1; JOINED.
DR   EMBL; L34943; AAA51601.1; JOINED.
DR   EMBL; L34944; AAA51601.1; JOINED.
DR   EMBL; L34946; AAA51601.1; JOINED.
DR   EMBL; L34947; AAA51601.1; JOINED.
DR   EMBL; L34948; AAA51601.1; JOINED.
DR   EMBL; L34949; AAA51601.1; JOINED.
DR   EMBL; L34950; AAA51601.1; JOINED.
DR   EMBL; L34951; AAA51601.1; JOINED.
DR   EMBL; M26178; AAA51602.1; ALT_SEQ.
DR   EMBL; L34940; AAA51602.1; JOINED.
DR   EMBL; L34941; AAA51602.1; JOINED.
DR   EMBL; L34943; AAA51602.1; JOINED.
DR   EMBL; L34944; AAA51602.1; JOINED.
DR   EMBL; L34946; AAA51602.1; JOINED.
DR   EMBL; L34948; AAA51602.1; JOINED.
DR   EMBL; L34949; AAA51602.1; JOINED.
DR   EMBL; L34950; AAA51602.1; JOINED.
DR   EMBL; L34951; AAA51602.1; JOINED.
DR   EMBL; M26178; AAA51603.1; ALT_SEQ.
DR   EMBL; L34940; AAA51603.1; JOINED.
DR   EMBL; L34941; AAA51603.1; JOINED.
DR   EMBL; L34943; AAA51603.1; JOINED.
DR   EMBL; L34944; AAA51603.1; JOINED.
DR   EMBL; L34946; AAA51603.1; JOINED.
DR   EMBL; L34948; AAA51603.1; JOINED.
DR   EMBL; L34950; AAA51603.1; JOINED.
DR   EMBL; L34951; AAA51603.1; JOINED.
DR   EMBL; M26178; AAA51604.1; ALT_SEQ.
DR   EMBL; L34940; AAA51604.1; JOINED.
DR   EMBL; L34941; AAA51604.1; JOINED.
DR   EMBL; L34944; AAA51604.1; JOINED.
DR   EMBL; L34946; AAA51604.1; JOINED.
DR   EMBL; L34947; AAA51604.1; JOINED.
DR   EMBL; L34948; AAA51604.1; JOINED.
DR   EMBL; L34949; AAA51604.1; JOINED.
DR   EMBL; L34950; AAA51604.1; JOINED.
DR   EMBL; L34951; AAA51604.1; JOINED.
DR   EMBL; M26178; AAA51605.1; ALT_SEQ.
DR   EMBL; L34940; AAA51605.1; JOINED.
DR   EMBL; L34941; AAA51605.1; JOINED.
DR   EMBL; L34944; AAA51605.1; JOINED.
DR   EMBL; L34946; AAA51605.1; JOINED.
DR   EMBL; L34948; AAA51605.1; JOINED.
DR   EMBL; L34949; AAA51605.1; JOINED.
DR   EMBL; L34950; AAA51605.1; JOINED.
DR   EMBL; L34951; AAA51605.1; JOINED.
DR   EMBL; M26178; AAA51606.1; ALT_SEQ.
DR   EMBL; L34940; AAA51606.1; JOINED.
DR   EMBL; L34941; AAA51606.1; JOINED.
DR   EMBL; L34944; AAA51606.1; JOINED.
DR   EMBL; L34946; AAA51606.1; JOINED.
DR   EMBL; L34948; AAA51606.1; JOINED.
DR   EMBL; L34950; AAA51606.1; JOINED.
DR   EMBL; L34951; AAA51606.1; JOINED.
DR   PIR; A31939; QRBOT1.
DR   InterPro; IPR002955; Tau_protein.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 4.
DR   PRINTS; PR01261; TAUPROTEIN.
DR   PROSITE; PS00229; TAU_MAP; 4.
KW   Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
KW   Phosphorylation; Glycoprotein.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   REPEAT      250    280       TAU/MAP MOTIF 1.
FT   REPEAT      281    311       TAU/MAP MOTIF 2.
FT   REPEAT      312    342       TAU/MAP MOTIF 3.
FT   REPEAT      343    374       TAU/MAP MOTIF 4.
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   DISULFID    297    328       BY SIMILARITY.
FT   VARSPLIC      1    130       AEPRQEFDVMEDHAQGDYTLQDQEGDMDPGLKESPLQTPAD
FT                                DGSEEPGSETSDAKSTPTAEDATAPLVDEGAPGEQAAAQAP
FT                                AEIPEGTAAEEAGIGDTSNLEDQAAGHVTQARMVSKGKDGT
FT                                GPDDKKT -> PLNHYLPYLFLVSVLFQFVPFSHVLTFILI
FT                                LFMFMFKPSTPSSAKTLKNRPCLSPKRPTPGSSDPLIKPSS
FT                                PAVCPEPSSSPKHVSSVTPRTGNSGAKEMKV (IN
FT                                ISOFORM TAU-G).
FT   VARSPLIC      1    130       AEPRQEFDVMEDHAQGDYTLQDQEGDMDPGLKESPLQTPAD
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FT                                   DGSEEPGSETSDAKSTPTAEDATAPLVDEGAPGEQAAAQAP
FT                                   AEIPEGTAAEEAGIGDTSNLEDQAAGHVTQARMVSKGKDGT
FT                                   GPDDKKT -> KV (IN ISOFORM TAU-H).
FT   VARSPLIC      62      90       MISSING (IN ISOFORM TAU-D, ISOFORM TAU-E,
FT                                   ISOFORM TAU-F, ISOFORM TAU-J, ISOFORM
FT                                   TAU-K, ISOFORM TAU-L, ISOFORM TAU-M,
FT                                   ISOFORM TAU-N, ISOFORM TAU-P, ISOFORM
FT                                   TAU-Q, ISOFORM TAU-R, ISOFORM TAU-S AND
FT                                   ISOFORM TAU-T).
FT   VARSPLIC      91     112       MISSING (IN ISOFORM TAU-L, ISOFORM TAU-M,
FT                                   ISOFORM TAU-N, ISOFORM TAU-R, ISOFORM
FT                                   TAU-S AND ISOFORM TAU-T).
FT   VARSPLIC     174     191       MISSING (IN ISOFORM TAU-B, ISOFORM TAU-C,
FT                                   ISOFORM TAU-E, ISOFORM TAU-F, ISOFORM
FT                                   TAU-G, ISOFORM TAU-H, ISOFORM TAU-J,
FT                                   ISOFORM TAU-K, ISOFORM TAU-M, ISOFORM
FT                                   TAU-N, ISOFORM TAU-P, ISOFORM TAU-Q,
FT                                   ISOFORM TAU-S AND ISOFORM TAU-T).
FT   VARSPLIC     281     311       MISSING (IN ISOFORM TAU-C, ISOFORM TAU-F,
FT                                   ISOFORM TAU-K, ISOFORM TAU-N, ISOFORM
FT                                   TAU-Q AND ISOFORM TAU-T).
FT   VARSPLIC     438     447       VSASLAKQGL -> PCVCPHHACVSAVRSLVTACPLTTSCC

  Query Match             100.0%;  Score 50;  DB 1;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 0.36;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     203 YSSPGSPGT 211


RESULT   4
TAU_MACMU
ID   TAU_MACMU      STANDARD;      PRT;   458 AA.
AC   P57786;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR TAU.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D).
RC   TISSUE=Brain;
RX   MEDLINE=97012131; PubMed=8858947;
RA   Nelson P.T., Stefansson K., Gulcher J., Saper C.B.;
RT   "Molecular evolution of tau protein: implications for Alzheimer's
RT   disease.";
RL   J. Neurochem. 67:1622-1632(1996).
CC   -!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC       BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC       POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC       TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC       TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
CC       ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
CC       ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC       CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; TAU A (SHOWN HERE),
CC       TAU-B, TAU-C AND TAU-D; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY
CC       DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE OF UP TO 4
CC       EXONS. ONE OF THESE OPTIONAL EXONS CONTAINS THE ADDITIONAL TAU/MAP
CC       REPEAT. THE SEQUENCE SHOWN HERE IS THAT OF THE COMPLETE ISOFORM
CC       NOT YET CHARACTERIZED.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
CC   -!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
CC       CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC       CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC       MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC       MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
DR   InterPro; IPR002955; Tau_protein.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 4.
DR   PRINTS; PR01261; TAUPROTEIN.
DR   PROSITE; PS00229; TAU_MAP; 4.
KW   Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
KW   Phosphorylation.
FT   INIT_MET      0       0       BY SIMILARITY.
FT   REPEAT      261     291       TAU/MAP MOTIF 1.
FT   REPEAT      292     322       TAU/MAP MOTIF 2.
FT   REPEAT      323     353       TAU/MAP MOTIF 3.
FT   REPEAT      354     385       TAU/MAP MOTIF 4.
FT   MOD_RES       1       1       ACETYLATION (BY SIMILARITY).
FT   DISULFID    308     339       BY SIMILARITY.
FT   VARSPLIC     44     101       MISSING (IN ISOFORM TAU-B AND ISOFORM
FT                                  TAU-C).
FT   VARSPLIC    185     202       MISSING (IN ISOFORM TAU-C AND ISOFORM
FT                                  TAU-D).
FT   VARSPLIC    292     322       MISSING (IN ISOFORM TAU-B).
SQ   SEQUENCE   458 AA;  47841 MW;  68BE63DBA30665A8 CRC64;

  Query Match             100.0%;  Score 50;  DB 1;  Length 458;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     214 YSSPGSPGT 222


RESULT   5
TAU_MOUSE
ID   TAU_MOUSE      STANDARD;      PRT;   732 AA.
AC   P10637; P10638; Q60684; Q60685; Q60686; Q62286;
DT   01-JUL-1989 (Rel. 11, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR MTAPT OR TAU.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM PNS-TAU).
RC   TISSUE=Neuroblastoma;
RX   MEDLINE=92262443; PubMed=1374898;
RA   Couchie D., Mavilia C., Georgieff I.S., Liem R.K.H., Shelanski M.L.,
RA   Nunez J.;
RT   "Primary structure of high molecular weight tau present in the
RT   peripheral nervous system.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:4378-4381(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-A; TAU-D AND TAU-E).
RC   STRAIN=Him OF1; TISSUE=Liver, Kidney, and Brain;
RX   MEDLINE=95012085; PubMed=7927211;
RA   Kenner L., el-Shabrawi Y., Hutter H., Forstner M., Zatloukal K.,
RA   Hoefler G., Preisegger K.-H., Kurzbauer R., Denk H.;
RT   "Expression of three- and four-repeat tau isoforms in mouse liver.";
RL   Hepatology 20:1086-1089(1994).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-B AND TAU-C).
RC   TISSUE=Brain;
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RX   MEDLINE=88099510; PubMed=3122323;
RA   Lee G., Cowan N.J., Kirschner M.;
RT   "The primary structure and heterogeneity of tau protein from mouse
RT   brain.";
RL   Science 239:285-288(1988).
RN   [4]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM B).
RC   STRAIN=ICR; TISSUE=Brain;
RX   MEDLINE=95182802; PubMed=7877441;
RA   Sawa A., Oyama F., Matsushita M., Ihara Y.;
RT   "Molecular diversity at the carboxyl terminus of human and rat tau.";
RL   Brain Res. Mol. Brain Res. 27:111-117(1994).
RN   [5]
RP   CHARACTERIZATION.
RX   MEDLINE=94005827; PubMed=8402267;
RA   Couchie D., Gache Y., Mavilia C., Guilleminot J., Bridoux A.-M.,
RA   Nivez M.-P., Nunez J.;
RT   "High molecular weight tau proteins and acquisition of neuronal
RT   polarity in peripheral nervous system.";
RL   C. R. Acad. Sci., III, Sci. Vie 316:404-409(1993).
CC   -!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC       BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC       POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC       TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC       TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
CC       ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
CC       ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC       CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; PNS-TAU (SHOWN HERE),
CC       TAU-A, TAU-B, TAU-C, TAU-D AND TAU-E; ARE PRODUCED BY ALTERNATIVE
CC       SPLICING. THEY DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE
CC       OF UP TO 5 OF THE 14 EXONS. ONE OF THESE OPTIONAL EXONS CONTAINS
CC       THE ADDITIONAL TAU/MAP REPEAT. TWO DIFFERENT C-TERMINI ARE
CC       OBTAINED EITHER BY THE RETENTION OR THE SPLICING OF INTRON 13/14.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS AND AT A LOWER LEVEL IN
CC       THE LIVER AND KIDNEY. PNS-TAU IS EXPRESSED IN THE PERIPHERAL
CC       NERVOUS SYSTEM WHILE THE OTHERS ARE EXPRESSED IN THE CENTRAL
CC       NERVOUS SYSTEM.
CC   -!- DEVELOPMENTAL STAGE: SHORTER FORMS OR LOW MOLECULAR WEIGHT TAU
CC       (LMW-TAU) ARE GENERALLY EXPRESSED AT EARLY DEVELOPMENT STAGES AND
CC       LONGER FORMS OR HIGH MOLECULAR WEIGHT TAU (HMW-TAU) IN THE ADULT
CC       BRAIN.
CC   -!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
CC       CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC       CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC       MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC       MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC   -!- DISEASE: MAY BE INVOLVED IN THE PATHOGENESIS OF CYTOPLASMIC
CC       INCLUSIONS (AS MALLORY BODIES) IN LIVERS OF MICE CHRONICALLY
CC       INTOXICATED WITH GRISEOFULVIN OR DDC (3,5-DIETHOXYCARBONYL-2,4-
CC       DIHYDROCOLLIDINE), A MODEL FOR HUMAN ALCOHOLIC HEPATITIS.
CC       ALTERATION OF TAU (ABNORMAL PHOSPHORYLATION AND CROSSLINKING)
CC       COULD CONTRIBUTE TO MALLORY BODIES FORMATION AND DISTURBANCE OF
CC       MICROTUBULE FUNCTION IN ALCOHOLIC LIVER DISEASE.
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U12914; AAA58343.1; -.
DR   EMBL; U12915; AAA58344.1; -.
DR   EMBL; U12916; AAA58345.1; -.
DR   EMBL; Z12133; CAA78121.1; -.
DR   EMBL; M93266; -; NOT_ANNOTATED_CDS.
DR   EMBL; M18775; AAA40165.1; -.
DR   EMBL; M18776; AAA40166.1; -.
DR   EMBL; D30627; BAA18878.1; -.
DR   PIR; A28820; A28820.
DR   PIR; B28820; B28820.
DR   MGD; MGI:97180; Mapt.
DR   InterPro; IPR002955; Tau_protein.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 7.
DR   PRINTS; PR01261; TAUPROTEIN.
DR   PROSITE; PS00229; TAU_MAP; 3.
KW   Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
KW   Phosphorylation.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   REPEAT      535    565       TAU/MAP MOTIF 1.
FT   REPEAT      566    596       TAU/MAP MOTIF 2.
FT   REPEAT      597    627       TAU/MAP MOTIF 3.
FT   REPEAT      628    659       TAU/MAP MOTIF 4.
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   DISULFID    582    613       BY SIMILARITY.
FT   VARSPLIC     33     90       MISSING (IN ISOFORM TAU-B, ISOFORM TAU-C,
FT                                ISOFORM TAU-D AND ISOFORM TAU-E).
FT   VARSPLIC     91    112       MISSING (IN ISOFORM TAU-E).
FT   VARSPLIC    113    349       MISSING (IN ISOFORM TAU-A, ISOFORM TAU-B,
FT                                ISOFORM TAU-C, ISOFORM TAU-D AND ISOFORM
FT                                TAU-E).
FT   VARSPLIC    367    432       MISSING (IN ISOFORM TAU-A, ISOFORM TAU-B,
FT                                ISOFORM TAU-C, ISOFORM TAU-D AND ISOFORM
FT                                TAU-E).
FT   VARSPLIC    566    596       MISSING (IN ISOFORM TAU-B AND ISOFORM
FT                                TAU-C).
FT   VARSPLIC    732    732       L -> KAALLSSQVWNYSHDLATITDLGL (IN
FT                                ISOFORM TAU-B).
FT   CONFLICT      2      2       D -> N (IN REF. 1).
FT   CONFLICT      8      8       D -> N (IN REF. 1).
FT   CONFLICT    527    527       P -> T (IN REF. 2; CAA78121).
FT   CONFLICT    671    671       E -> Q (IN REF. 1).
SQ   SEQUENCE   732 AA;  76112 MW;  BFDF0767E41C7A3A CRC64;


  Query Match           100.0%;  Score 50;  DB 1;  Length 732;
  Best Local Similarity  100.0%;  Pred. No. 0.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     488 YSSPGSPGT 496


RESULT   6
TAU_RAT
ID   TAU_RAT        STANDARD;      PRT;   751 AA.
AC   P19332; Q63567; Q9QW06; Q63677;
DT   01-NOV-1990 (Rel. 16, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR MTAPT OR TAU.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM TAU-B).
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=92179305; PubMed=1542696;
RA   Goedert M., Spillantini M.G., Crowther R.A.;
RT   "Cloning of a big tau microtubule-associated protein characteristic of
RT   the peripheral nervous system.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:1983-1987(1992).
RN   [2]
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RP   SEQUENCE FROM N.A. (ISOFORM TAU-B).
RC   TISSUE=Dorsal root ganglion;
RX   MEDLINE=94013081; PubMed=8408300;
RA   Georgieff I.S., Liem R.K.H., Couchie D., Mavilia C., Nunez J.,
RA   Shelanski M.L.;
RT   "Expression of high molecular weight tau in the central and peripheral
RT   nervous systems.";
RL   J. Cell Sci. 105:729-737(1993).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM TAU-F).
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=94334997; PubMed=8057376;
RA   Sadot E., Marx R., Barg J., Behar L., Ginzburg I.;
RT   "Complete sequence of 3'-untranslated region of tau from rat central
RT   nervous system. Implications for mRNA heterogeneity.";
RL   J. Mol. Biol. 241:325-331(1994).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-E AND TAU-G).
RC   TISSUE=Brain;
RX   MEDLINE=90180457; PubMed=2560640;
RA   Kosik K.S., Orecchio L.D., Bakalis S., Neve R.L.;
RT   "Developmentally regulated expression of specific tau sequences.";
RL   Neuron 2:1389-1397(1989).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-E AND TAU-C).
RX   MEDLINE=89359509; PubMed=2504728;
RA   Kanai Y., Takemura R., Oshima T., Mori H., Ihara Y., Yanagisawa M.,
RA   Masaki T., Hirokawa N.;
RT   "Expression of multiple tau isoforms and microtubule bundle formation
RT   in fibroblasts transfected with a single tau cDNA.";
RL   J. Cell Biol. 109:1173-1184(1989).
RN   [6]
RP   SEQUENCE OF 359-460 FROM N.A. (ISOFORM TAU-A), AND SEQUENCE OF 105-112
RP   AND 367-460 FROM N.A. (ISOFORM TAU-D).
RC   TISSUE=Spinal cord;
RX   MEDLINE=95054048; PubMed=7964751;
RA   Mavilia C., Couchie D., Nunez J.;
RT   "Diversity of high-molecular-weight tau proteins in different regions
RT   of the nervous system.";
RL   J. Neurochem. 63:2300-2306(1994).
RN   [7]
RP   SEQUENCE OF 696-751 FROM N.A. (ISOFORMS TAU-A TO TAU-G), AND SEQUENCE
RP   OF 751-774 FROM N.A. (ISOFORM TAU-H).
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=95182802; PubMed=7877441;
RA   Sawa A., Oyama F., Matsushita M., Ihara Y.;
RT   "Molecular diversity at the carboxyl terminus of human and rat tau.";
RL   Brain Res. Mol. Brain Res. 27:111-117(1994).
CC   -!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC       BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC       POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC       TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC       TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
CC       ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
CC       ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC       CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 8 ISOFORMS; TAU-A/SC1 (SHOWN HERE),
CC       TAU-B/BIG-TAU/HMW-TAU, TAU-C, TAU-D/SC2, TAU-E, TAU-F, TAU-
CC       G/FETAL-TAU AND TAU-H; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY
CC       DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE OF UP TO 4 OF
CC       THE 14 EXONS. TWO DIFFERENT C-TERMINI ARE OBTAINED EITHER BY THE
CC       RETENTION OR THE SPLICING OF INTRON 13/14.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS. THE LARGER FORMS (TAU-A
CC       AND TAU-B) ARE PREFERENTIALLY EXPRESSED IN THE PERIPHERAL NERVOUS
CC       SYSTEM WHILE THE OTHERS ARE EXPRESSED IN THE CENTRAL NERVOUS
CC       SYSTEM. LOW AMOUNTS OF THE LARGER FORMS ARE ALSO FOUND IN LIMITED
CC       AREAS OF THE CNS.
CC   -!- DEVELOPMENTAL STAGE: DURING THE IMMEDIATE POSTNATAL PERIOD, THE
CC       DORSAL ROOT GANGLIA EXPRESS ALL ISOFORMS WHEREAS ONLY THE LARGER
CC       FORMS PERSIST IN THE ADULTS.
CC   -!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
CC       CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC       CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC       MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC       MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M84156; AAA42204.1; -.
DR   EMBL; X79321; CAA55889.1; -.
DR   EMBL; D30628; -; NOT_ANNOTATED_CDS.
DR   EMBL; D30629; -; NOT_ANNOTATED_CDS.
DR   PIR; JS0306; JS0306.
DR   PIR; A33574; A33574.
DR   InterPro; IPR002955; Tau_protein.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 8.
DR   PRINTS; PR01261; TAUPROTEIN.
DR   PROSITE; PS00229; TAU_MAP; 4.
KW   Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
KW   Phosphorylation.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   REPEAT      554    584       TAU/MAP MOTIF 1.
FT   REPEAT      585    615       TAU/MAP MOTIF 2.
FT   REPEAT      616    646       TAU/MAP MOTIF 3.
FT   REPEAT      647    678       TAU/MAP MOTIF 4.
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   DISULFID    601    632       BY SIMILARITY.
FT   VARSPLIC     33     90       MISSING (IN ISOFORM TAU-F).
FT   VARSPLIC     62     90       MISSING (IN ISOFORM TAU-C AND ISOFORM
FT                                TAU-G).
FT   VARSPLIC    113    366       MISSING (IN ISOFORM TAU-C, ISOFORM TAU-D,
FT                                ISOFORM TAU-E, ISOFORM TAU-F AND ISOFORM
FT                                TAU-G).
FT   VARSPLIC    386    451       MISSING (IN ISOFORM TAU-B, ISOFORM TAU-C,
FT                                ISOFORM TAU-E, ISOFORM TAU-F AND ISOFORM
FT                                TAU-G).
FT   VARSPLIC    585    615       MISSING (IN ISOFORM TAU-G).
FT   VARSPLIC    751    751       L -> KPVLLSSEVWNYSHDFGHHTDLGL (IN ISOFORM
FT                                TAU-H).
FT   CONFLICT    254    254       F -> L (IN REF. 2).
FT   CONFLICT    283    283       G -> A (IN REF. 2).
FT   CONFLICT    291    291       H -> D (IN REF. 2).
FT   CONFLICT    617    617       H -> Q (IN REF. 2, 3 AND 4).
FT   CONFLICT    704    704       Y -> H (IN REF. 3).
FT   CONFLICT    733    733       P -> A (IN REF. 2).
SQ   SEQUENCE   751 AA;  78432 MW;  B96B7329444D44B2 CRC64;


  Query Match             100.0%;  Score 50;  DB 1;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 0.62;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     507 YSSPGSPGT 515


RESULT   7
TAU_HUMAN
ID   TAU_HUMAN      STANDARD;      PRT;   757 AA.
AC   P10636; P18518; Q14799; Q15551; Q9UQ96; Q15549; Q15550; Q9UDJ3;
AC   Q9UMH0;
DT   01-JUL-1989 (Rel. 11, Created)
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DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR MTBT1 OR TAU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS PNS-TAU; TAU-A AND TAU-F).
RA   Andreadis A.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM TAU-A).
RC   TISSUE=Brain;
RX   MEDLINE=88234557; PubMed=3131773;
RA   Goedert M., Wischik C., Crowther R., Walker J., Klug A.;
RT   "Cloning and sequencing of the cDNA encoding a core protein of the
RT   paired helical filament of Alzheimer disease: identification as the
RT   microtubule-associated protein tau.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-B; TAU-C; TAU-E AND TAU-F).
RC   TISSUE=Brain;
RX   MEDLINE=90380393; PubMed=2484340;
RA   Goedert M., Spillantini M.G., Jakes R., Rutherford D., Crowther R.A.;
RT   "Multiple isoforms of human microtubule-associated protein tau:
RT   sequences and localization in neurofibrillary tangles of Alzheimer's
RT   disease.";
RL   Neuron 3:519-526(1989).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM TAU-D).
RC   TISSUE=Brain;
RX   MEDLINE=89251564; PubMed=2498079;
RA   Goedert M., Spillantini M.G., Potier M.C., Ulrich J., Crowther R.A.;
RT   "Cloning and sequencing of the cDNA encoding an isoform of
RT   microtubule-associated protein tau containing four tandem repeats:
RT   differential expression of tau protein mRNAs in human brain.";
RL   EMBO J. 8:393-399(1989).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-A AND FETAL-TAU).
RC   TISSUE=Fetal brain;
RX   MEDLINE=90180482; PubMed=2516729;
RA   Lee G., Neve R.L., Kosik K.S.;
RT   "The microtubule binding domain of tau protein.";
RL   Neuron 2:1615-1624(1989).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM TAU-F), AND ALTERNATIVE SPLICING.
RX   MEDLINE=93041757; PubMed=1420178;
RA   Andreadis A., Brown W.M., Kosik K.S.;
RT   "Structure and novel exons of the human tau gene.";
RL   Biochemistry 31:10626-10633(1992).
RN   [7]
RP   SEQUENCE OF 591-621 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=89193714; PubMed=2495000;
RA   Mori H., Hamada Y., Kawaguchi M., Honda T., Kondo J., Ihara Y.;
RT   "A distinct form of tau is selectively incorporated into Alzheimer's
RT   paired helical filaments.";
RL   Biochem. Biophys. Res. Commun. 159:1221-1226(1989).
RN   [8]
RP   SEQUENCE OF 1-72; 102-380; 467-496; 507-570; 576-582; 591-606;
RP   615-633; 638-656; 660-663; 670-699 AND 702-757.
RC   TISSUE=Brain;
RX   MEDLINE=92381012; PubMed=1512244;
RA   Hasegawa M., Morishima-Kawashima M., Takio K., Suzuki M., Titani K.,
RA   Ihara Y.;
RT   "Protein sequence and mass spectrometric analyses of tau in the
RT   Alzheimer's disease brain.";
RL   J. Biol. Chem. 267:17047-17054(1992).
RN   [9]
RP   SEQUENCE OF 576-583; 607-610; 615-627; 638-647 AND 670-685,
RP   PHOSPHORYLATION, AND MUTAGENESIS.
RX   MEDLINE=95221434; PubMed=7706316;
RA   Drewes G., Trinczek B., Illenberger S., Biernat J., Schmitt-Ulms G.,
RA   Meyer H.E., Mandelkow E.-M., Mandelkow E.;
RT   "Microtubule-associated protein/microtubule affinity-regulating kinase
RT   (p110mark). A novel protein kinase that regulates tau-microtubule
RT   interactions and dynamic instability by phosphorylation at the
RT   Alzheimer-specific site serine 262.";
RL   J. Biol. Chem. 270:7679-7688(1995).
RN   [10]
RP   REVIEW.
RX   MEDLINE=91320377; PubMed=1713721;
RA   Goedert M., Crowther R.A., Garner C.C.;
RT   "Molecular characterization of microtubule-associated proteins tau and
RT   MAP2.";
RL   Trends Neurosci. 14:193-199(1991).
RN   [11]
RP   SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
RX   MEDLINE=20283597; PubMed=10747907;
RA   Maas T., Eidenmueller J., Brandt R.;
RT   "Interaction of tau with the neural membrane cortex is regulated by
RT   phosphorylation at sites that are modified in paired helical
RT   filaments.";
RL   J. Biol. Chem. 275:15733-15740(2000).
RN   [12]
RP   PHOSPHORYLATION, AND MUTAGENESIS.
RX   MEDLINE=98413833; PubMed=9735171;
RA   Sengupta A., Kabat J., Novak M., Wu Q., Grundke-Iqbal I., Iqbal K.;
RT   "Phosphorylation of tau at both Thr 231 and Ser 262 is required for
RT   maximal inhibition of its binding to microtubules.";
RL   Arch. Biochem. Biophys. 357:299-309(1998).
RN   [13]
RP   PHOSPHORYLATION, AND MUTAGENESIS.
RX   MEDLINE=98278959; PubMed=9614189;
RA   Illenberger S., Zheng-Fischhofer Q., Preuss U., Stamer K., Baumann K.,
RA   Trinczek B., Biernat J., Godemann R., Mandelkow E.-M., Mandelkow E.;
RT   "The endogenous and cell cycle-dependent phosphorylation of tau
RT   protein in living cells: implications for Alzheimer's disease.";
RL   Mol. Biol. Cell 9:1495-1512(1998).
RN   [14]
RP   GLYCATION.
RX   MEDLINE=97465580; PubMed=9326300;
RA   Nacharaju P., Ko L., Yen S.H.;
RT   "Characterization of in vitro glycation sites of tau.";
RL   J. Neurochem. 69:1709-1719(1997).
RN   [15]
RP   REVIEW ON VARIANTS.
RX   MEDLINE=20437008; PubMed=10899436;
RA   Goedert M., Spillantini M.G.;
RT   "Tau mutations in frontotemporal dementia FTDP-17 and their relevance
RT   for Alzheimer's disease.";
RL   Biochim. Biophys. Acta 1502:110-121(2000).
RN   [16]
RP   VARIANT FTDP17 M-653, AND VARIANTS N-284; A-288; Y-440 AND P-446.
RX   MEDLINE=98291804; PubMed=9629852;
RA   Poorkaj P., Bird T.D., Wijsman E., Nemens E., Garruto R.M.,
RA   Anderson L., Andreadis A., Wiederholt W.C., Raskind M.,
RA   Schellenberg G.D.;
RT   "Tau is a candidate gene for chromosome 17 frontotemporal dementia.";
RL   Ann. Neurol. 43:815-825(1998).
RN   [17]
RP   ERRATUM.
RA   Poorkaj P., Bird T.D., Wijsman E., Nemens E., Garruto R.M.,
RA   Anderson L., Andreadis A., Wiederholt W.C., Raskind M.,
RA   Schellenberg G.D.;
RL   Ann. Neurol. 44:428-428(1998).
RN   [18]
RP   VARIANT FTDP17 LEU-617.
RX   MEDLINE=98409513; PubMed=9736786;
RA   Dumanchin C., Camuzat A., Campion D., Verpillat P., Hannequin D.,
RA   Dubois B., Saugier-Veber P., Martin C., Penet C., Charbonnier F.,
RA   Agid Y., Frebourg T., Brice A.;
RT   "Segregation of a missense mutation in the microtubule-associated
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RT   protein tau gene with familial frontotemporal dementia and
RT   parkinsonism.";
RL   Hum. Mol. Genet. 7:1825-1829(1998).
RN   [19]
RP   VARIANTS FTDP17 VAL-588; LEU-617 AND TRP-722.
RX   MEDLINE=98303385; PubMed=9641683;
RA   Hutton M., Lendon C.L., Rizzu P., Baker M., Froelich S., Houlden H.,
RA   Pickering-Brown S., Chakraverty S., Isaacs A., Grover A., Hackett J.,
RA   Adamson J., Lincoln S., Dickson D., Davies P., Petersen R.C.,
RA   Stevens M., de Graaff E., Wauters E., van Baren J., Hillebrand M.,
RA   Joosse M., Kwon J.M., Nowotny P., Che L.K., Norton J., Morris J.C.,
RA   Reed L.A., Trojanowski J., Basun H., Lannfelt L., Neystat M., Fahn S.,
RA   Dark F., Tannenberg T., Dodd P.R., Hayward N., Kwok J.B.J.,
RA   Schofield P.R., Andreadis A., Snowden J., Craufurd D., Neary D.,
RA   Owen F., Oostra B.A., Hardy J., Goate A., van Swieten J., Mann D.,
RA   Lynch T., Heutink P.;
RT   "Association of missense and 5'-splice-site mutations in tau with the
RT   inherited dementia FTDP-17.";
RL   Nature 393:702-705(1998).
RN   [20]
RP   VARIANT PPND LYS-595, AND VARIANT FTDP17 LEU-617.
RX   MEDLINE=99007274; PubMed=9789048;
RA   Clark L.N., Poorkaj P., Wszolek Z., Geschwind D.H., Nasreddine Z.S.,
RA   Miller B., Li D., Payami H., Awert F., Markopoulou K., Andreadis A.,
RA   D'Souza I., Lee V.M.-Y., Reed L., Trojanowski J.Q., Zhukareva V.,
RA   Bird T., Schellenberg G., Wilhelmsen K.C.;
RT   "Pathogenic implications of mutations in the tau gene in
RT   pallido-ponto-nigral degeneration and related neurodegenerative
RT   disorders linked to chromosome 17.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:13103-13107(1998).
RN   [21]
RP   VARIANTS FTDP17 VAL-588; LYS-596 DEL; LEU-617 AND TRP-722.
RX   MEDLINE=99138654; PubMed=9973279;
RA   Rizzu P., Van Swieten J.C., Joosse M., Hasegawa M., Stevens M.,
RA   Tibben A., Niermeijer M.F., Hillebrand M., Ravid R., Oostra B.A.,
RA   Goedert M., van Duijn C.M., Heutink P.;
RT   "High prevalence of mutations in the microtubule-associated protein
RT   tau in a population study of frontotemporal dementia in the
RT   Netherlands.";
RL   Am. J. Hum. Genet. 64:414-421(1999).
RN   [22]
RP   VARIANTS FTDP17 LEU-617; MET-653 AND TRP-722.
RX   MEDLINE=99229757; PubMed=10214944;
RA   Nacharaju P., Lewis J., Easson C., Yen S., Hackett J., Hutton M.,
RA   Yen S.H.;
RT   "Accelerated filament formation from tau protein with specific FTDP-17
RT   missense mutations.";
RL   FEBS Lett. 447:195-199(1999).
RN   [23]
RP   VARIANT FTDP17/CBD SER-617.
```

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  Query Match             100.0%;  Score 50;  DB 1;  Length 757;
  Best Local Similarity   100.0%;  Pred. No. 0.62;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     513 YSSPGSPGT 521
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RESULT   8
P2B1_CRYNE
ID   P2B1_CRYNE      STANDARD;       PRT;   639 AA.
AC   O42773;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Serine/threonine protein phosphatase 2B catalytic subunit A1
DE   (EC 3.1.3.16) (Calcineurin A1).
GN   CNA1.
OS   Cryptococcus neoformans (Filobasidiella neoformans).
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=5207;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H99;
RX   MEDLINE=97327538; PubMed=9184205;
RA   Odom A., Muir S., Lim E., Toffaletti D.L., Perfect J., Heitman J.;
RT   "Calcineurin is required for virulence of Cryptococcus neoformans.";
RL   EMBO J. 16:2576-2589(1997).
CC   -!- FUNCTION: CALCIUM-DEPENDENT, CALMODULIN-STIMULATED PROTEIN
CC       PHOSPHATASE. THIS SUBUNIT MAY HAVE A ROLE IN THE CALMODULIN
CC       ACTIVATION OF CALCINEURIN (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
CC       THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC       SENSITIVITY.
CC   -!- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-2B
CC       SUBFAMILY.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AF042082; AAB97372.1; -.
DR   HSSP; P08129; 1FJM.
DR   InterPro; IPR000934; Ser_thr_phosphtse.
DR   Pfam; PF00149; STphosphatase; 1.
DR   PRINTS; PR00114; STPHPHTASE.
DR   SMART; SM00156; PP2Ac; 1.
DR   PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
KW   Hydrolase; Calmodulin-binding; Iron; Manganese.
SQ   SEQUENCE   639 AA;  71499 MW;  4B92EBE361C80579 CRC64;
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  Query Match             78.0%;  Score 39;  DB 1;  Length 639;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db     556 SPGSPGT 562
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RESULT   9
PET1_RAT
ID   PET1_RAT        STANDARD;       PRT;   710 AA.
AC   P51574;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Oligopeptide transporter, small intestine isoform (Peptide transporter
DE   1) (Intestinal H+/peptide cotransporter) (Proton-coupled dipeptide
DE   cotransporter).
GN   SLC15A1 OR PEPT1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Small intestine;
RX   MEDLINE=96180982; PubMed=8605246;
RA   Miyamoto K., Shiraga T., Morita K., Yamamoto H., Haga H.,
RA   Taketani Y., Tamai I., Sai Y., Tsuji A., Takeda E.;
RT   "Sequence, tissue distribution and developmental changes in rat
RT   intestinal oligopeptide transporter.";
RL   Biochim. Biophys. Acta 1305:34-38(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
```

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RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney;
RX   MEDLINE=96108664; PubMed=8531138;
RA   Saito H., Okuda M., Terada T., Sasaki S., Inui K.;
RT   "Cloning and characterization of a rat H+/peptide cotransporter
RT   mediating absorption of beta-lactam antibiotics in the intestine and
RT   kidney.";
RL   J. Pharmacol. Exp. Ther. 275:1631-1637(1995).
CC   -!- FUNCTION: PROTON-COUPLED INTAKE OF OLIGOPEPTIDES OF 2 TO 4
CC       AMINO ACIDS WITH A PREFERENCE FOR DIPEPTIDES. MAY CONSTITUTE
CC       A MAJOR ROUTE FOR THE ABSORPTION OF PROTEIN DIGESTION END-
CC       PRODUCTS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE PTR2 FAMILY OF TRANSPORTERS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D50664; BAA09318.1; -.
DR   EMBL; D50306; BAA08844.1; -.
DR   InterPro; IPR000109; PTR2.
DR   Pfam; PF00854; PTR2; 2.
DR   PROSITE; PS01022; PTR2_1; 1.
DR   PROSITE; PS01023; PTR2_2; 1.
KW   Peptide transport; Transport; Transmembrane; Symport; Glycoprotein.
FT   TRANSMEM      1     21       POTENTIAL.
FT   DOMAIN       22     53       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     54     74       POTENTIAL.
FT   DOMAIN       75     82       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     83    103       POTENTIAL.
FT   DOMAIN      104    118       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    119    139       POTENTIAL.
FT   DOMAIN      140    161       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    162    182       POTENTIAL.
FT   DOMAIN      183    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    219       POTENTIAL.
FT   DOMAIN      220    276       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    277    297       POTENTIAL.
FT   DOMAIN      298    327       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    328    348       POTENTIAL.
FT   DOMAIN      349    361       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    362    382       POTENTIAL.
FT   DOMAIN      383    586       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    587    607       POTENTIAL.
FT   DOMAIN      608    621       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    622    642       POTENTIAL.
FT   DOMAIN      643    647       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    648    668       POTENTIAL.
FT   DOMAIN      669    710       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    415    415       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    439    439       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    510    510       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    532    532       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    539    539       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    241    241       R -> G (IN REF. 2).
FT   CONFLICT    259    259       N -> E (IN REF. 2).
FT   CONFLICT    279    280       IM -> MV (IN REF. 2).
SQ   SEQUENCE   710 AA;  78928 MW;  435727A6C76F2D7B CRC64;


  Query Match          76.0%;  Score 38;  DB 1;  Length 710;
  Best Local Similarity  100.0%;  Pred. No. 52;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
           |||||||
Db     441 SSPGSPG 447
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RESULT  10
PID1_HUMAN
ID   PID1_HUMAN      STANDARD;      PRT;   756 AA.
AC   P51178;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1
DE   (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-III).
GN   PLCD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=95197554; PubMed=7890667;
RA   Cheng H.F., Jiang M.J., Chen C.L., Liu S.M., Wong L.P.,
RA   Lomasney J.W., King K.;
RT   "Cloning and identification of amino acid residues of human
RT   phospholipase C delta 1 essential for catalysis.";
RL   J. Biol. Chem. 270:5495-5505(1995).
CC   -!- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC       DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC       MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC       C ENZYMES.
CC   -!- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC       diacylglycerol.
CC   -!- COFACTOR: REQUIRES CALCIUM.
CC   -!- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC       PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC   -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U09117; AAA73567.1; -.
DR   HSSP; P10688; 1MAI.
DR   MIM; 602142; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR001192; PI_PLC.
DR   InterPro; IPR000909; PI_PLC_X.
DR   InterPro; IPR001711; PI_PLC_Y.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00036; efhand; 2.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00388; PI-PLC-X; 1.
DR   Pfam; PF00387; PI-PLC-Y; 1.
DR   PRINTS; PR00360; C2DOMAIN.
DR   PRINTS; PR00390; PHPHLIPASEC.
DR   ProDom; PD001202; PI_PLC_Y; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00148; PLCXc; 1.
DR   SMART; SM00149; PLCYc; 1.
DR   PROSITE; PS00018; EF_HAND; 2.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR   PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
KW   Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat.
FT   DOMAIN       21    130       PH.
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FT   CA_BIND      153    164       EF-HAND 1 (POTENTIAL).
FT   CA_BIND      189    200       EF-HAND 2 (POTENTIAL).
FT   DOMAIN       296    440       DOMAIN X.
FT   DOMAIN       492    609       DOMAIN Y.
FT   DOMAIN       616    720       C2 DOMAIN.
FT   ACT_SITE     311    311       BY SIMILARITY.
FT   ACT_SITE     356    356       BY SIMILARITY.
SQ   SEQUENCE   756 AA;  85763 MW;  AD9A4251C5EBADFB CRC64;
```

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  Query Match             76.0%;  Score 38;  DB 1;  Length 756;
  Best Local Similarity   75.0%;  Pred. No. 56;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           :||||:||
Db     507 FSSPGTPG 514
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RESULT  11
DPOZ_MOUSE
ID   DPOZ_MOUSE     STANDARD;      PRT;  3122 AA.
AC   Q61493; Q9QWX6; Q9JMD6;
DT   30-MAY-2000 (Rel. 39, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   DNA polymerase zeta catalytic subunit (EC 2.7.7.7) (Seizure related
DE   protein 4).
GN   REV3L OR POLZ OR SEZ4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/OLA; TISSUE=Testis;
RX   MEDLINE=99202265; PubMed=10102037;
RA   Van Sloun P.P.H., Romeijn R.J., Eeken J.C.J.;
RT   "Molecular cloning, expression and chromosomal localisation of the
RT   mouse Rev3l gene, encoding the catalytic subunit of polymerase zeta.";
RL   Mutat. Res. 433:109-116(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kajiwara K.;
RT   "Molecular analyses of Sez4 encoding murine homologue of yeast REV3 in
RT   brain neurons.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 2368-3122 FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryonic brain;
RX   MEDLINE=96216731; PubMed=8645260;
RA   Kajiwara K., Nagawawa H., Shimizu-Nishikawa K., Ookura T., Kimura M.,
RA   Sugaya E.;
RT   "Molecular characterization of seizure-related genes isolated by
RT   differential screening.";
RL   Biochem. Biophys. Res. Commun. 219:795-799(1996).
CC   -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC       + {DNA}(N).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF083464; AAC98785.1; -.
DR   EMBL; AB031049; BAA90768.1; -.
DR   EMBL; D78644; BAA11461.1; -.
DR   MGD; MGI:1337131; Rev31.
DR   InterPro; IPR002064; DNA_pol_B.
DR   Pfam; PF00136; DNA_pol_B; 2.
DR   Pfam; PF03104; DNA_pol_B_exo; 1.
DR   PRINTS; PR00106; DNAPOLB.
DR   SMART; SM00486; POLBc; 1.
DR   PROSITE; PS00116; DNA_POLYMERASE_B; 1.
KW   Transferase; DNA-directed DNA polymerase; DNA replication;
KW   DNA-binding; DNA repair; Nuclear protein; Zinc-finger.
FT   ZN_FING    3034   3049       C4-TYPE (POTENTIAL).
FT   ZN_FING    3078   3096       C4-TYPE (POTENTIAL).
FT   CONFLICT     92     92       G -> A (IN REF. 2).
FT   CONFLICT    294    294       A -> T (IN REF. 2).
FT   CONFLICT    578    578       E -> Q (IN REF. 2).
FT   CONFLICT    609    609       R -> Q (IN REF. 2).
FT   CONFLICT   1278   1278       L -> P (IN REF. 2).
FT   CONFLICT   1298   1298       L -> F (IN REF. 2).
FT   CONFLICT   1416   1416       P -> L (IN REF. 2).
FT   CONFLICT   1848   1848       A -> T (IN REF. 2).
FT   CONFLICT   2368   2368       V -> G (IN REF. 3).
SQ   SEQUENCE   3122 AA;  350654 MW;  A39846CAF7365BA8 CRC64;
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  Query Match             76.0%;  Score 38;  DB 1;  Length 3122;
  Best Local Similarity   87.5%;  Pred. No. 2.5e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           |||| |||
Db    2108 YSSPDSPG 2115
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RESULT  12
CDN1_FELCA
ID   CDN1_FELCA     STANDARD;      PRT;   164 AA.
AC   O19002;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Cyclin-dependent kinase inhibitor 1 (P21) (CDK-interacting protein 1).
GN   CDKN1A OR CIP1 OR WAF1.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph node;
RX   MEDLINE=98036042; PubMed=9370275;
RA   Okuda M., Minehata K., Setoguchi.A., Cho K.-W., Nakamura N.,
RA   Nishigaki K., Watari T., Cevario S., O'Brien S.J., Tsujimoto H.,
RA   Hasegawa A.;
RT   "Cloning and chromosome mapping of the feline genes p21WAF1 and
RT   p27Kip1.";
RL   Gene 198:141-147(1997).
CC   -!- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES
CC       ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO
CC       DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
CC       ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
CC       KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D84650; BAA23168.1; -.
DR   HSSP; P46527; 1JSU.
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DR   InterPro; IPR003175; CDI.
DR   Pfam; PF02234; CDI; 1.
KW   Cell cycle; Nuclear protein; Zinc-finger.
FT   ZN_FING      13     41       C4-TYPE (POTENTIAL).
FT   DOMAIN       141    156      NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ   SEQUENCE   164 AA;  18315 MW;  0F7912A76C78BF38 CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 164;
  Best Local Similarity   75.0%;  Pred. No. 16;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            :|||:|||
Db     129 ASPGAPGT 136


RESULT  13
TIZ2_MOUSE
ID   TIZ2_MOUSE      STANDARD;      PRT;   387 AA.
AC   Q9EQN3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   TSC22-related inducible leucine zipper protein 2.
GN   TIL22.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ershler M.A., Belyavsky A.V., Visser J.W.M.;
RT   "Identification and characterization of a family of leucine zipper
RT   genes related to TSC22.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: TRANSCRIPTIONAL REPRESSOR (BY SIMILARITY).
CC   -!- SUBUNIT: FORMS HOMODIMER OR HETERODIMER. CAN FORM AN HETERODIMER
CC       WITH TSC-22.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: BELONGS TO THE TSC-22/DIP/BUN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF201286; AAG41219.1; -.
DR   InterPro; IPR000580; TSC-22_Dip_Bun.
DR   Pfam; PF01166; TSC22; 1.
DR   ProDom; PD007152; TSC-22_Dip_Bun; 1.
DR   PROSITE; PS01289; TSC22; 1.
KW   Transcription regulation; Repressor; Nuclear protein.
FT   DOMAIN      336    357      LEUCINE-ZIPPER.
SQ   SEQUENCE   387 AA;  39987 MW;  C78BB96B5B2DFB90 CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 387;
  Best Local Similarity   75.0%;  Pred. No. 40;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
            |  |||||
Db      19 YEGPGSPG 26


RESULT  14
TIZ2_HUMAN
ID   TIZ2_HUMAN      STANDARD;      PRT;   395 AA.
AC   Q9Y3Q8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   TSC22-related inducible leucine zipper protein 2 (Tsc-22-like protein
DE   THG-1).
GN   TIL22.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99419018; PubMed=10488076;
RA   Kester H.A., Blanchetot C., den Hertog J., van der Saag P.T.,
RA   van der Burg B.;
RT   "Transforming growth factor-beta-stimulated clone-22 is a member of a
RT   family of leucine zipper proteins that can homo- and heterodimerize
RT   and has transcriptional repressor activity.";
RL   J. Biol. Chem. 274:27439-27447(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cervix;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: TRANSCRIPTIONAL REPRESSOR.
CC   -!- SUBUNIT: FORMS HOMODIMER OR HETERODIMER. CAN FORM AN HETERODIMER
CC       WITH TSC-22.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: BELONGS TO THE TSC-22/DIP/BUN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ133115; CAB43491.1; -.
DR   EMBL; BC001966; AAH01966.1; -.
DR   InterPro; IPR000580; TSC-22_Dip_Bun.
DR   Pfam; PF01166; TSC22; 1.
DR   ProDom; PD007152; TSC-22_Dip_Bun; 1.
DR   PROSITE; PS01289; TSC22; 1.
KW   Transcription regulation; Repressor; Nuclear protein.
FT   DOMAIN      344    365      LEUCINE-ZIPPER.
FT   CONFLICT    355    356      NA -> KR (IN REF. 1).
SQ   SEQUENCE   395 AA;  41026 MW;  DA08B5617C9BB151 CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 395;
  Best Local Similarity   75.0%;  Pred. No. 41;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
            |  |||||
Db      19 YEGPGSPG 26


RESULT  15
VE2_PAPVE
ID   VE2_PAPVE      STANDARD;      PRT;   415 AA.
AC   P11329;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Probable regulatory protein E2.
GN   E2.
OS   European elk papillomavirus (EEPV).
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10565;
RN   [1]
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RP   SEQUENCE FROM N.A.
RX   MEDLINE=87219878; PubMed=3034730;
RA   Ahola H., Bergman P., Stroem A.C., Moreno-Lopez J., Petterson U.;
RT   "Organization and expression of the transforming region from the
RT   European elk papillomavirus (EEPV).";
RL   Gene 50:195-205(1986).
CC   -!- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC       IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNNNNNGGT-3') PRESENT
CC       IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC       ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
CC       WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC       BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC       INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC       REPLICATION.
CC   -!- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M15953; AAA66854.1; -.
DR   PIR; D29499; W2WLEP.
DR   HSSP; P03122; 2BOP.
DR   InterPro; IPR001866; E2_N.
DR   InterPro; IPR000427; Early2_C.
DR   Pfam; PF00511; E2_C; 1.
DR   Pfam; PF00508; E2_N; 1.
DR   ProDom; PD000672; Early2_C; 1.
DR   ProDom; PD000678; E2_N; 1.
KW   Early protein; Transcription regulation; Activator; DNA-binding;
KW   Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SQ   SEQUENCE   415 AA;  46245 MW;  0B7BF6AEEF0AC80C CRC64;
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  Query Match             74.0%;  Score 37;  DB 1;  Length 415;
  Best Local Similarity   66.7%;  Pred. No. 43;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           ||:| |||:
Db     268 YSAPSSPGS 276
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RESULT  16
NTR1_HUMAN
ID   NTR1_HUMAN     STANDARD;      PRT;   418 AA.
AC   P30989; Q9H4T5; Q9H4H1;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Neurotensin receptor type 1 (NT-R-1) (High-affinity levocabastine-
DE   insensitive neurotensin receptor) (NTRH).
GN   NTSR1 OR NTRR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93154505; PubMed=8381365;
RA   Vita N., Laurent P., Lefort S., Chalon P., Dumont X., Kaghad M.,
RA   Gully D., le Fur G., Ferrara P., Caput D.;
RT   "Cloning and expression of a complementary DNA encoding a high
RT   affinity human neurotensin receptor.";
RL   FEBS Lett. 317:139-142(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaslaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
CC   -!- FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. IT IS
CC       ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC       CALCIUM SECOND MESSENGER SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC       HIGHEST TO TACHYKININS RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X70070; CAA49675.1; -.
DR   EMBL; AL357033; CAC14923.1; -.
DR   EMBL; AL035669; CAC12747.1; -.
DR   PIR; S29506; S29506.
DR   GCRDb; GCR_0577; -.
DR   GCRDb; GCR_2067; -.
DR   MIM; 162651; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003985; NT1_rec.
DR   InterPro; IPR003984; NT_rec.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01479; NEUROTENSINR.
DR   PRINTS; PR01480; NEUROTENSN1R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN       1     63       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    64     86       1 (POTENTIAL).
FT   DOMAIN      87     95       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    96    120       2 (POTENTIAL).
FT   DOMAIN     121    142       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   143    164       3 (POTENTIAL).
FT   DOMAIN     165    187       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   188    209       4 (POTENTIAL).
FT   DOMAIN     210    234       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   235    259       5 (POTENTIAL).
FT   DOMAIN     260    303       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   304    325       6 (POTENTIAL).
FT   DOMAIN     326    343       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   344    367       7 (POTENTIAL).
FT   DOMAIN     368    418       CYTOPLASMIC (POTENTIAL).
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FT   CARBOHYD      4      4       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     41     41       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    141    224       BY SIMILARITY.
FT   LIPID       383    383       PALMITATE (POTENTIAL).
FT   CONFLICT    200    200       T -> A (IN REF. 2).
SQ   SEQUENCE   418 AA;  46288 MW;  BBBD1EEC2BE6E390 CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 418;
  Best Local Similarity   75.0%;  Pred. No. 44;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           |:||:|||
Db       6 SAPGTPGT 13


RESULT  17
IL5R_HUMAN
ID   IL5R_HUMAN     STANDARD;      PRT;   420 AA.
AC   Q01344;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-5 receptor alpha chain precursor (IL-5R-alpha) (CD125
DE   antigen).
GN   IL5RA OR IL5R.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92372031; PubMed=1505961;
RA   Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT   "Structure and sequence of the human alpha-L-iduronidase gene.";
RL   Genomics 13:1311-1313(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92357767; PubMed=1495999;
RA   Tavernier J., Tuypens T., Plaetinck G., Verhee A., Fiers W.,
RA   Devos R.;
RT   "Molecular basis of the membrane-anchored and two soluble isoforms of
RT   the human interleukin 5 receptor alpha subunit.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
RN   [3]
RP   SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
RX   MEDLINE=92005669; PubMed=1833065;
RA   Tavernier J., Devos R., Cornelis S., Tuypens T., van der Heyden J.,
RA   Fiers W., Plaetinck G.;
RT   "A human high affinity interleukin-5 receptor (IL5R) is composed of
RT   an IL5-specific alpha chain and a beta chain shared with the receptor
RT   for GM-CSF.";
RL   Cell 66:1175-1184(1991).
CC   -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC       BINDS TO IL-5.
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC       CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN
CC       HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY
CC       ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CDw125 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw125.htm".
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M96652; AAA59152.1; -.
DR   EMBL; M96651; AAA59151.1; -.
DR   EMBL; M75914; AAA36110.1; -.
DR   EMBL; A26249; CAA01793.1; -.
DR   EMBL; A24587; CAA01731.1; -.
DR   EMBL; A26251; CAA01794.1; -.
DR   PIR; A40267; A40267.
DR   MIM; 147851; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003532; Hematopo_receptor_S_F2.
DR   PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW   Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    420       INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT   DOMAIN       21    342       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    343    362       POTENTIAL.
FT   DOMAIN      363    420       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     35     35       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    131    131       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    216    216       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    244    244       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    333    335       NDE -> FSR (IN SOLUBLE ISOFORM S1).
FT   VARSPLIC    336    420       MISSING (IN SOLUBLE ISOFORM S1).
FT   VARSPLIC    333    333       N -> K (IN SOLUBLE ISOFORM S2).
FT   VARSPLIC    334    420       MISSING (IN SOLUBLE ISOFORM S2).
SQ   SEQUENCE   420 AA;  47700 MW;  420681FBC6B51700 CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 420;
  Best Local Similarity   66.7%;  Pred. No. 44;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 HAPPGSPGT 127


RESULT  18
DHAL_DEIRA
ID   DHAL_DEIRA     STANDARD;      PRT;   515 AA.
AC   Q9RYG9; O32502;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Aldehyde dehydrogenase (EC 1.2.1.3).
GN   ALDA OR DRA0348.
OS   Deinococcus radiodurans.
OC   Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX   NCBI_TaxID=1299;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R1;
RX   MEDLINE=20036896; PubMed=10567266;
RA   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA   Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA   Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA   Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA   Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA   Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA   Fraser C.M.;
RT   "Genome sequence of the radioresistant bacterium Deinococcus
RT   radiodurans R1.";
RL   Science 286:1571-1577(1999).
RN   [2]
RP   SEQUENCE OF 1-258 FROM N.A.
RC   STRAIN=KD8301;
RA   Narumi I., Du Z., Alatas Z., Kitayama S., Watanabe H.;
RT   "Isolation and characterization of pprA, a novel Deinococcus
RT   radiodurans gene involved in DNA repair.";
```

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RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
CC   -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE001863; AAF12436.1; -.
DR   EMBL; AB003475; BAA21372.1; -.
DR   HSSP; P05091; 1CW3.
DR   TIGR; DRA0348; -.
DR   InterPro; IPR002086; Aldehyde_dehydr.
DR   Pfam; PF00171; aldedh; 1.
DR   PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
DR   PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
KW   Oxidoreductase; NAD; Complete proteome.
FT   NP_BIND     228    234       NAD (ADP PART) (BY SIMILARITY).
FT   ACT_SITE    272    272       BY SIMILARITY.
FT   ACT_SITE    311    311       BY SIMILARITY.
SQ   SEQUENCE   515 AA;  56409 MW;  D8BB5DDF7D2DBBC0 CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 515;
  Best Local Similarity   55.6%;  Pred. No. 54;
  Matches    5;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            |::||:||:
Db      13 YANPGTPGS 21


RESULT  19
ZYX_CHICK
ID   ZYX_CHICK      STANDARD;      PRT;   542 AA.
AC   Q04584;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Zyxin.
GN   ZYX.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93107157; PubMed=1469049;
RA   Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.;
RT   "Zyxin and cCRP: two interactive LIM domain proteins associated with
RT   the cytoskeleton.";
RL   J. Cell Biol. 119:1573-1587(1992).
CC   -!- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP
CC       PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT
CC       MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN
CC       CYTOSKELETON NEAR THE ADHESION PLAQUES.
CC   -!- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2
CC       ZINC IONS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X69190; CAA48936.1; -.
DR   PIR; A44358; A44358.
DR   InterPro; IPR001781; LIM.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00412; LIM; 3.
DR   ProDom; PD000094; LIM; 3.
DR   SMART; SM00132; LIM; 3.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR   PROSITE; PS50023; LIM_DOMAIN_2; 3.
KW   Repeat; LIM domain; Metal-binding; Zinc; Cell adhesion.
FT   DOMAIN       83     90       PRO-RICH.
FT   DOMAIN      103    130       PRO-RICH.
FT   DOMAIN      352    411       LIM 1.
FT   DOMAIN      412    471       LIM 2.
FT   DOMAIN      472    538       LIM 3.
FT   VARIANT     463    463       D -> V.
SQ   SEQUENCE   542 AA;  58537 MW;  9D898AC180C680FC CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 542;
  Best Local Similarity   75.0%;  Pred. No. 57;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            :|||:|||
Db       2 ASPGTPGT 9


RESULT  20
YQ36_CAEEL
ID   YQ36_CAEEL     STANDARD;      PRT;   963 AA.
AC   Q09457;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Putative cuticle collagen C09G5.6.
GN   C09G5.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Palmer S.;
RL   Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE
CC       PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A
CC       BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT (BY SIMILARITY).
CC   -!- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
CC       CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
CC       LINKS (BY SIMILARITY).
CC   -!- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE
CC       COLLAGENS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z46791; CAA86755.1; -.
DR   WormPep; C09G5.6; CE01486.
DR   InterPro; IPR002486; Col_cuticle_N.
DR   InterPro; IPR000087; Collagen.
DR   Pfam; PF01391; Collagen; 2.
DR   Pfam; PF01484; Col_cuticle_N; 1.
KW   Hypothetical protein; Cuticle; Connective tissue; Repeat;
KW   Multigene family; Collagen.
FT   DOMAIN      392    423       TRIPLE-HELICAL REGION.
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FT   DOMAIN       441    503       TRIPLE-HELICAL REGION.
FT   DOMAIN       506    567       TRIPLE-HELICAL REGION.
FT   DOMAIN       663    666       POLY-PRO.
FT   DOMAIN       685    688       POLY-PRO.
SQ   SEQUENCE   963 AA;  107031 MW;  AFF895A75909F66E CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 963;
  Best Local Similarity   75.0%;  Pred. No. 1e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            |:||:|||
Db     559 SAPGAPGT 566


RESULT  21
RGSC_RAT
ID   RGSC_RAT       STANDARD;      PRT;  1387 AA.
AC   O08774; O88383;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Regulator of G-protein signaling 12 (RGS12).
GN   RGS12.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97312490; PubMed=9168931;
RA   Snow B.E., Antonio L., Suggs S., Gutstein H.B., Siderovski D.P.;
RT   "Molecular cloning and expression analysis of rat Rgs12 and Rgs14.";
RL   Biochem. Biophys. Res. Commun. 233:770-777(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98316347; PubMed=9651375;
RA   Snow B.E., Hall R.A., Krumins A.M., Brothers G.M., Bouchard D.,
RA   Brothers C.A., Chung S., Mangion J., Gilman A.G., Lefkowitz R.J.,
RA   Siderovski D.P.;
RT   "GTPase activating specificity of RGS12 and binding specificity of an
RT   alternatively spliced PDZ (PSD-95/Dlg/ZO-1) domain.";
RL   J. Biol. Chem. 273:17749-17755(1998).
CC   -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC       ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC       THEIR INACTIVE GDP-BOUND FORM.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO ISOFORMS THAT ARISE
CC       FROM ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN AND LUNG
CC       AND LOWER LEVELS IN TESTIS, HEART, AND SPLEEN.
CC   -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 PID DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U92280; AAC53176.1; -.
DR   EMBL; AF035151; AAC40154.1; -.
DR   HSSP; P49799; 1AGR.
DR   InterPro; IPR003109; GoLoco.
DR   InterPro; IPR001478; PDZ.
DR   InterPro; IPR000050; PID_domain.
DR   InterPro; IPR003116; RBD.
DR   InterPro; IPR000342; RGS.
DR   Pfam; PF02188; GoLoco; 1.
DR   Pfam; PF00595; PDZ; 1.
DR   Pfam; PF00640; PID; 1.
DR   Pfam; PF02196; RBD; 2.
DR   Pfam; PF00615; RGS; 1.
DR   PRINTS; PR01301; RGSPROTEIN.
DR   ProDom; PD001580; RGS; 1.
DR   SMART; SM00390; GoLoco; 1.
DR   SMART; SM00228; PDZ; 1.
DR   SMART; SM00462; PTB; 1.
DR   SMART; SM00455; RBD; 2.
DR   SMART; SM00315; RGS; 1.
DR   PROSITE; PS50106; PDZ; 1.
DR   PROSITE; PS01179; PID; 1.
DR   PROSITE; PS50132; RGS; 1.
KW   Signal transduction inhibitor; Nuclear protein; Alternative splicing.
FT   DOMAIN        21     97       PDZ.
FT   DOMAIN       227    339       PID.
FT   DOMAIN       715    832       RGS.
FT   DOMAIN      1368   1373       POLY-PRO.
FT   VARSPLIC       1    648       MISSING (IN ISOFORM PDZ-LESS).
FT   VARSPLIC     649    666       SFGRSRRFSLTRSLDDLE -> MNLEKGLSDDSDVFIDQQ
FT                                 (IN ISOFORM PDZ-LESS).
SQ   SEQUENCE   1387 AA;  150468 MW;  958047D106B08310 CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 1387;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
             :|:|| |||
Db    1296 HSTPGPPGT 1304


RESULT  22
WA_EMENI
ID   WA_EMENI       STANDARD;      PRT;  1986 AA.
AC   Q03149;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Conidial green pigment synthase (EC 2.3.1.-).
GN   WA.
OS   Emericella nidulans (Aspergillus nidulans).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=5072;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93101122; PubMed=1465094;
RA   Mayorga M.E., Timberlake W.E.;
RT   "The developmentally regulated Aspergillus nidulans wA gene encodes a
RT   polypeptide homologous to polyketide and fatty acid synthases.";
RL   Mol. Gen. Genet. 235:205-212(1992).
CC   -!- FUNCTION: THIS PROTEIN CONDENSES CARBON UNITS TO FORM AN
CC       INTERMEDIATE YELLOW POLYKETIDE PIGMENT THAT IS POLYMERIZED
CC       BY CONIDIAL LACCASE TO FORM THE GREEN PIGMENT IN MATURE
CC       ASEXUAL SPORES (CONIDIA).
CC   -!- COFACTOR: CONTAINS 2 COVALENTLY BOUND PHOSPHOPANTETHEINES
CC       (POTENTIAL).
CC   -!- PATHWAY: BIOSYNTHESIS OF CONIDIAL GREEN PIGMENT.
CC   -!- SIMILARITY: CONTAINS 2 ACYL CARRIER DOMAINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
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DR   EMBL; X65866; CAA46695.1; -.
DR   PIR; S28353; S28353.
DR   InterPro; IPR001227; Acyltransf_domain.
DR   InterPro; IPR000794; Ketoacyl-synt.
DR   InterPro; IPR003880; Phosphopant_attach.
DR   Pfam; PF00698; Acyl_transf; 1.
DR   Pfam; PF00109; ketoacyl-synt; 1.
DR   Pfam; PF02801; ketoacyl-synt_C; 1.
DR   Pfam; PF00550; pp-binding; 2.
DR   PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
DR   PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR   PROSITE; PS50075; ACP_DOMAIN; 2.
KW   Transferase; Phosphopantetheine; Multifunctional enzyme; Repeat.
FT   DOMAIN      529    582       BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT   DOMAIN      991   1024       ACYL/MALONYL TRANSFERASES
FT                                (BY SIMILARITY).
FT   DOMAIN     1650   1719       ACYL CARRIER (ACP) 1.
FT   DOMAIN     1772   1841       ACYL CARRIER (ACP) 2.
FT   ACT_SITE    548    548       BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT   ACT_SITE   1001   1001       ACYL/MALONYL TRANSFERASES (BY
FT                                SIMILARITY).
FT   BINDING    1682   1682       PHOSPHOPANTETHEINE (BY SIMILARITY).
FT   BINDING    1804   1804       PHOSPHOPANTETHEINE (BY SIMILARITY).
SQ   SEQUENCE   1986 AA;  216634 MW;  74EF0940FF40EE9A CRC64;
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Query Match 74.0%; Score 37; DB 1; Length 1986;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2 SSPGSPGT 9
            ||| ||||
Db    1749 SSPASPGT 1756
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RESULT  23
SAX1_MOUSE
ID   SAX1_MOUSE     STANDARD;      PRT;   305 AA.
AC   P42580;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Homeobox protein SAX-1 (NKX-1.1).
GN   SAX1 OR NKX1-1 OR NKX-1.1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=95399317; PubMed=7669696;
RA   Schubert F.R., Fainsod A., Gruenbaum Y., Gruss P.;
RT   "Expression of the novel murine homeobox gene Sax-1 in the developing
RT   nervous system.";
RL   Mech. Dev. 51:99-114(1995).
RN   [2]
RP   SEQUENCE OF 289-305 FROM N.A.
RC   STRAIN=BALB/C;
RA   Hong S.B., Kim S.J., Noh M.J., Lee Y.M., Kim Y.S., Yoo O.J.;
RL   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY FUNCTION IN CELL SPECIFICATION, PARTICULARLY IN THE
CC       CNS.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING POSTERIOR CENTRAL
CC       NERVOUS SYSTEM. FIRST SEEN IN THE ECTODERM LATERAL TO THE
CC       PRIMITIVE STREAK, LATER IT ENCOMPASSES THE NEURAL PLATE. STARTING
CC       AT DAY 9.5 PC, IT IS EXPRESSED IN DISTINCT AREAS OF SPINAL CORD,
CC       HINDBRAIN, MIDBRAIN AND FOREBRAIN.
CC   -!- SIMILARITY: BELONGS TO THE NK-1 FAMILY OF HOMEOBOX PROTEINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X75384; CAA53153.1; -.
DR   EMBL; U58137; AAB06948.1; -.
DR   HSSP; P02836; 3HDD.
DR   MGD; MGI:104806; Sax1.
DR   InterPro; IPR001356; Homeobox.
DR   Pfam; PF00046; homeobox; 1.
DR   PRINTS; PR00024; HOMEOBOX.
DR   SMART; SM00389; HOX; 1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
KW   Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT   DOMAIN       88     96       POLY-GLU.
FT   DOMAIN      143    148       POLY-ARG.
FT   DNA_BIND    156    215       HOMEOBOX.
FT   DOMAIN      239    242       POLY-GLY.
SQ   SEQUENCE   305 AA;  32012 MW;  E02E09A40453FF1B CRC64;
```

Query Match 72.0%; Score 36; DB 1; Length 305;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy       2 SSPGSPGT 9
            :||||||:
Db    134 ASPGSPGS 141
```

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RESULT  24
PYCA_METJA
ID   PYCA_METJA     STANDARD;      PRT;   501 AA.
AC   Q58626;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
GN   PYCA OR MJ1229.
OS   Methanococcus jannaschii.
OC   Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC   Methanococcus.
OX   NCBI_TaxID=2190;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX   MEDLINE=96337999; PubMed=8688087;
RA   Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA   Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA   Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA   Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA   Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA   Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA   Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA   Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT   "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT   jannaschii.";
RL   Science 273:1058-1073(1996).
RN   [2]
RP   SEQUENCE OF 1-12, AND FUNCTION.
RX   MEDLINE=21034791; PubMed=11195096;
RA   Mukhopadhyay B., Patel V.J., Wolfe R.S.;
RT   "A stable archaeal pyruvate carboxylase from the hyperthermophile
RT   Methanococcus jannaschii.";
RL   Arch. Microbiol. 174:406-414(2000).
CC   -!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
CC       INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
CC       ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL
CC       GROUP TO PYRUVATE IN THE SECOND.
CC   -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
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CC       oxaloacetate.
CC    -!- COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND
CC       BICARBONATE.
CC    -!- ENZYME REGULATION: INHIBITED BY MAGNESIUM, WHEN ITS CONCENTRATION
CC       EXCEEDED THE ATP ONE, AND BY HIGH CONCENTRATION OF ATP AND ALPHA-
CC       KETOGLUTARATE.
CC    -!- PATHWAY: GLUCONEOGENESIS.
CC    -!- SUBUNIT: HETEROOCTAMER OF FOUR A AND FOUR B SUBUNITS.
CC    -!- MASS SPECTROMETRY: MW=55500; METHOD=MALDI.
CC    -!- MISCELLANEOUS: ITS OPTIMUM PH IS 8.5 AND THE OPTIMUM TEMPERATURE
CC       IS 80-90 DEGREES CELSIUS.
CC    -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC       AND CARBAMYL PHOSPHATE SYNTHETASES.
CC    ---------------------------------------------------------------------
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CC    ---------------------------------------------------------------------
DR    EMBL; U67563; AAB99232.1; -.
DR    HSSP; P24182; 1BNC.
DR    TIGR; MJ1229; -.
DR    InterPro; IPR000901; CPSase.
DR    Pfam; PF02785; Biotin_carb_C; 1.
DR    Pfam; PF00289; CPSase_L_chain; 1.
DR    Pfam; PF02786; CPSase_L_D2; 1.
DR    PROSITE; PS00866; CPSASE_1; 1.
DR    PROSITE; PS00867; CPSASE_2; 1.
KW    Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
KW    ATP-binding; Complete proteome.
FT    NP_BIND     162    167       ATP (POTENTIAL).
FT    ACT_SITE    291    291       POTENTIAL.
SQ    SEQUENCE   501 AA;  55402 MW;  04D2E401892F872F CRC64;


  Query Match             72.0%;  Score 36;  DB 1;  Length 501;
  Best Local Similarity   75.0%;  Pred. No. 77;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           | ||| ||
Db     357 YRSPGGPG 364


RESULT  25
GUNB_PSEFL
ID    GUNB_PSEFL     STANDARD;      PRT;   511 AA.
AC    P18126;
DT    01-NOV-1990 (Rel. 16, Created)
DT    01-NOV-1990 (Rel. 16, Last sequence update)
DT    15-DEC-1998 (Rel. 37, Last annotation update)
DE    Endoglucanase B precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
DE    (Cellulase) (EGB).
GN    CELB.
OS    Pseudomonas fluorescens.
OC    Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC    Pseudomonas.
OX    NCBI_TaxID=294;
RN    [1]
RP    SEQUENCE FROM N.A., AND SEQUENCE OF 30-48.
RC    STRAIN=SP. CELLULOSA;
RX    MEDLINE=90355836; PubMed=2117693;
RA    Gilbert H.J., Hall J., Hazlewood G.P., Ferreira L.M.A.;
RT    "The N-terminal region of an endoglucanase from Pseudomonas
RT    fluorescens subspecies cellulosa constitutes a cellulose-binding
RT    domain that is distinct from the catalytic centre.";
RL    Mol. Microbiol. 4:759-767(1990).
CC    -!- FUNCTION: THIS ENZYME CATALYZES THE ENDOHYDROLYSIS OF 1,4-BETA-
CC       GLUCOSIDIC LINKAGES IN CELLULOSE, LICHENIN AND CEREAL BETA-D-
CC       GLUCANS. EGB IS MOST ACTIVE AGAINST BARLEY BETA-GLUCAN, BUT SHOWED
CC       SIGNIFICANT ACTIVITY AGAINST AMORPHOUS AND CRISTALLINE CELLULOSE.
CC    -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC       linkages in cellulose.
CC    -!- SUBCELLULAR LOCATION: Periplasmic.
CC    -!- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
CC       (CBD).
CC    -!- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
CC       HYDROLASES).
CC    ---------------------------------------------------------------------
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CC    ---------------------------------------------------------------------
DR    EMBL; X52615; CAA36844.1; -.
DR    PIR; S10527; S10527.
DR    HSSP; P43316; 2ENG.
DR    InterPro; IPR001919; CBD_2.
DR    InterPro; IPR002883; CBD_5.
DR    InterPro; IPR000334; Glyco_hydro_45.
DR    Pfam; PF00553; CBD_2; 1.
DR    Pfam; PF02013; CBD_5; 1.
DR    Pfam; PF02015; Glyco_hydro_45; 1.
DR    PROSITE; PS00561; CBD_BACTERIAL; 1.
DR    PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.
KW    Cellulose degradation; Hydrolase; Glycosidase; Signal; Periplasmic.
FT    SIGNAL       1     29
FT    CHAIN       30    511       ENDOGLUCANASE B.
FT    DOMAIN      30    131       CELLULOSE-BINDING (BY SIMILARITY).
FT    DOMAIN     132    173       SER-RICH (LINKER).
FT    DOMAIN     223    259       SER-RICH.
FT    DISULFID    32    127       BY SIMILARITY.
FT    ACT_SITE   276    276       NUCLEOPHILE (BY SIMILARITY).
FT    ACT_SITE   393    393       PROTON DONOR (BY SIMILARITY).
SQ    SEQUENCE   511 AA;  52078 MW;  3C3119D998291D8E CRC64;


  Query Match             72.0%;  Score 36;  DB 1;  Length 511;
  Best Local Similarity   55.6%;  Pred. No. 78;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |::|| ||:
Db     360 YNAPGDPGS 368


RESULT  26
BUD8_YEAST
ID    BUD8_YEAST     STANDARD;      PRT;   603 AA.
AC    P41698; Q06482;
DT    01-NOV-1995 (Rel. 32, Created)
DT    15-JUL-1998 (Rel. 36, Last sequence update)
DT    15-JUL-1998 (Rel. 36, Last annotation update)
DE    Bud site selection protein BUD8.
GN    BUD8 OR YLR353W OR L9638.3.
OS    Saccharomyces cerevisiae (Baker's yeast).
OC    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC    Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX    NCBI_TaxID=4932;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Harkins H.A., Pringle J.R.;
RL    Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN    [2]
RP    SEQUENCE FROM N.A.
RC    STRAIN=S288C / AB972;
RA    Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA    Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA    Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA    Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
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RA   Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA   Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
RA   Wilson R., Waterston R.;
RL   Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO YEAST BUD9.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; L37016; AAA64518.1; -.
DR   EMBL; U19102; AAB67749.1; -.
DR   SGD; S0004345; BUD8.
FT   DOMAIN       84     95       POLY-SER.
FT   CONFLICT    140    140       R -> W (IN REF. 1).
FT   CONFLICT    145    145       V -> M (IN REF. 1).
FT   CONFLICT    221    221       Y -> C (IN REF. 1).
FT   CONFLICT    350    350       S -> N (IN REF. 1).
FT   CONFLICT    354    354       T -> M (IN REF. 1).
FT   CONFLICT    422    422       MISSING (IN REF. 1).
FT   CONFLICT    602    602       R -> L (IN REF. 1).
SQ   SEQUENCE   603 AA;  66288 MW;  83F8843CA476E6C4 CRC64;


  Query Match             72.0%;  Score 36;  DB 1;  Length 603;
  Best Local Similarity   85.7%;  Pred. No. 93;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||:|||
Db     299 SPGAPGT 305


RESULT  27
CA1A_MOUSE
ID   CA1A_MOUSE     STANDARD;      PRT;   680 AA.
AC   Q05306;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Collagen alpha 1(X) chain precursor.
GN   COL10A1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=93143676; PubMed=8424763;
RA   Elima K., Eerola I., Rosati R., Metsaranta M., Garofalo S., Perala M.,
RA   de Crombrugghe B., Vuorio E.;
RT   "The mouse collagen X gene: complete nucleotide sequence, exon
RT   structure and expression pattern.";
RL   Biochem. J. 289:247-253(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=Liver;
RX   MEDLINE=93238750; PubMed=8477738;
RA   Kong R.Y.C., Kwan K.M., Lau E.T., Thomas J.T., Boot-Handford R.P.,
RA   Grant M.E., Cheah K.S.E.;
RT   "Intron-exon structure, alternative use of promoter and expression of
RT   the mouse collagen X gene, Col10a-1.";
RL   Eur. J. Biochem. 213:99-111(1993).
RN   [3]
RP   SEQUENCE OF 51-680 FROM N.A.
RC   STRAIN=DBA/2J;
RX   MEDLINE=92267014; PubMed=1587271;
RA   Apte S.S., Seldin M.F., Hayashi M., Olsen B.R.;
RT   "Cloning of the human and mouse type X collagen genes and mapping of
RT   the mouse type X collagen gene to chromosome 10.";
RL   Eur. J. Biochem. 206:217-224(1992).
RN   [4]
RP   SEQUENCE OF 385-627 FROM N.A.
RC   STRAIN=C57BL;
RX   MEDLINE=92182017; PubMed=1543751;
RA   Elima K., Metsaeranta M., Kallio J., Peraelae M., Eerola I.,
RA   Garofalo S., de Crombrugghe B., Vuorio E.;
RT   "Specific hybridization probes for mouse alpha 2(IX) and alpha 1(X)
RT   collagen mRNAs.";
RL   Biochim. Biophys. Acta 1130:78-80(1992).
CC   -!- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC
CC       CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
CC       MINERALIZATION ZONES OF HYALINE CARTILAGE.
CC   -!- SUBUNIT: HOMOTRIMER.
CC   -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC       UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC   -!- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
CC   -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; X67348; CAA47763.1; -.
DR   EMBL; X65121; CAA46237.1; -.
DR   EMBL; X63013; CAA44741.1; -.
DR   EMBL; Z21610; CAA79736.1; -.
DR   PIR; S28807; S28807.
DR   PIR; S31216; S31216.
DR   PIR; S22215; S22215.
DR   MGD; MGI:88445; Col10a1.
DR   InterPro; IPR001073; C1q.
DR   InterPro; IPR000087; Collagen.
DR   Pfam; PF00386; C1q; 1.
DR   Pfam; PF01391; Collagen; 6.
DR   PRINTS; PR00007; COMPLEMNTC1Q.
DR   SMART; SM00110; C1Q; 1.
DR   PROSITE; PS01113; C1Q; 1.
KW   Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW   Cartilage; Collagen; Signal.
FT   SIGNAL       1     18       POTENTIAL.
FT   CHAIN       19    680       COLLAGEN ALPHA 1(X) CHAIN.
FT   DOMAIN      19     56       NONHELICAL REGION (NC2).
FT   DOMAIN      57    519       TRIPLE-HELICAL REGION.
FT   DOMAIN     520    680       NONHELICAL REGION (NC1).
FT   DOMAIN     545    680       C1Q.
FT   CONFLICT   248    248       P -> L (IN REF. 3).
FT   CONFLICT   286    286       A -> S (IN REF. 2).
FT   CONFLICT   306    306       L -> F (IN REF. 3).
FT   CONFLICT   417    417       T -> S (IN REF. 3).
FT   CONFLICT   451    451       R -> K (IN REF. 4).
FT   CONFLICT   500    500       H -> L (IN REF. 3).
FT   CONFLICT   567    567       A -> C (IN REF. 3).
FT   CONFLICT   569    569       I -> H (IN REF. 3).
FT   CONFLICT   571    572       FD -> IY (IN REF. 3).
FT   CONFLICT   635    635       Q -> T (IN REF. 3).
SQ   SEQUENCE   680 AA;  66775 MW;  FE984CA99AF708E2 CRC64;


  Query Match             72.0%;  Score 36;  DB 1;  Length 680;
  Best Local Similarity   75.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           | ||| ||
Db     193 YGSPGRPG 200
```

```
RESULT  28
TRI2_STRCO
ID   TRI2_STRCO     STANDARD;      PRT;  1171 AA.
AC   Q9RKB9;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Putative Tricorn protease homolog 2 (EC 3.4.21.-).
GN   TRI2 OR SCE87.19.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Seeger K.J., Harris D., Thomson N.R., Parkhill J., Barrell B.G.,
RA   Rajandream M.A.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Degrades oligopeptides in a sequential manner
CC       (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S41 (SERINE PROTEASE).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AL132674; CAB59664.1; -.
DR   MEROPS; S41A; -.
DR   InterPro; IPR003581; TSPc.
DR   SMART; SM00245; TSPc; 1.
KW   Hydrolase; Serine protease.
FT   DOMAIN      842    941       PDZ-LIKE.
FT   SITE       1022   1022       SUBSTRATE SPECIFICITY SWITCH (BY
FT                                SIMILARITY).
FT   ACT_SITE    827    827       BY SIMILARITY.
FT   ACT_SITE   1051   1051       SUBSTRATE-BINDING (BY SIMILARITY).
FT   ACT_SITE   1052   1052       NUCLEOPHILE (BY SIMILARITY).
SQ   SEQUENCE   1171 AA;  125660 MW;  9C53019CEC0B0A25 CRC64;


  Query Match             72.0%;  Score 36;  DB 1;  Length 1171;
  Best Local Similarity   85.7%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           :||||||
Db     487 TPGSPGT 493


RESULT  29
MAP2_HUMAN
ID   MAP2_HUMAN     STANDARD;      PRT;  1827 AA.
AC   P11137; Q99976; Q99975;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein 2 (MAP 2) (MAP2B) [Contains: MAP2C].
GN   MAP2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Price R.;
RL   Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain;
RX   MEDLINE=94124038; PubMed=8294038;
RA   Albala J.S., Kalcheva N., Shafit-Zagardo B.;
RT   "Characterization of the transcripts encoding two isoforms of human
RT   microtubule-associated protein-2 (MAP-2).";
RL   Gene 136:377-378(1993).
RN   [3]
RP   SEQUENCE OF 493-1562 FROM N.A.
RX   MEDLINE=88274407; PubMed=2455776;
RA   Kosik K.S., Orecchio L.D., Bakalis S., Duffy L., Neve R.L.;
RT   "Partial sequence of MAP2 in the region of a shared epitope with
RT   Alzheimer neurofibrillary tangles.";
RL   J. Neurochem. 51:587-598(1988).
CC   -!- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
CC       STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
CC       SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
CC   -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
CC       FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
CC   -!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U01828; AAA03354.1; -.
DR   EMBL; U89330; AAB48098.1; -.
DR   EMBL; U89329; AAB48097.1; -.
DR   EMBL; M25668; AAA59552.1; -.
DR   PIR; PL0024; QRHUMT.
DR   MIM; 157130; -.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 3.
DR   PROSITE; PS00229; TAU_MAP; 2.
KW   Microtubules; Repeat; Alternative splicing; Calmodulin-binding.
FT   DOMAIN     1447   1467       CALMODULIN-BINDING (POTENTIAL).
FT   REPEAT     1661   1691       TAU/MAP MOTIF.
FT   REPEAT     1692   1722       TAU/MAP MOTIF.
FT   REPEAT     1723   1754       TAU/MAP MOTIF.
FT   VARSPLIC    152   1507       MISSING (IN ISOFORM MAP2C).
FT   CONFLICT      9      9       A -> G (IN REF. 2).
FT   CONFLICT     37     37       R -> A (IN REF. 2).
FT   CONFLICT    108    108       A -> G (IN REF. 2).
FT   CONFLICT    152    155       MISSING (IN REF. 2).
FT   CONFLICT    187    187       S -> K (IN REF. 2).
FT   CONFLICT   1655   1655       A -> GL (IN REF. 2).
FT   CONFLICT   1736   1736       V -> A (IN REF. 2).
SQ   SEQUENCE   1827 AA;  199610 MW;  BAC36D0030F5F455 CRC64;


  Query Match             72.0%;  Score 36;  DB 1;  Length 1827;
  Best Local Similarity   72.7%;  Pred. No. 3e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 YSS--PGSPGT 9
           |||  ||:|||
Db    1609 YSSRTPGTPGT 1619


RESULT  30
MAP2_MOUSE
ID   MAP2_MOUSE     STANDARD;      PRT;  1828 AA.
AC   P20357;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein 2 (MAP 2).
```

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GN   MAP2 OR MTAP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89083571; PubMed=3205744;
RA   Wang D., Lewis S.A., Cowan N.J.;
RT   "Complete sequence of a cDNA encoding mouse MAP2.";
RL   Nucleic Acids Res. 16:11369-11370(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89043973; PubMed=3142041;
RA   Lewis S.A., Wang D., Cowan N.J.;
RT   "Microtubule-associated protein MAP2 shares a microtubule binding
RT   motif with tau protein.";
RL   Science 242:936-939(1988).
CC   -!- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
CC       STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
CC       SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
CC   -!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M21041; AAA39490.1; -.
DR   PIR; S06467; S06467.
DR   PIR; A40115; A40115.
DR   MGD; MGI:97175; Mtap2.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 3.
DR   PROSITE; PS00229; TAU_MAP; 2.
KW   Microtubules; Repeat; Calmodulin-binding.
FT   DOMAIN      1452   1472       CALMODULIN-BINDING (POTENTIAL).
FT   REPEAT      1662   1692       TAU/MAP MOTIF.
FT   REPEAT      1693   1723       TAU/MAP MOTIF.
FT   REPEAT      1724   1755       TAU/MAP MOTIF.
SQ   SEQUENCE   1828 AA;  198980 MW;  200BC59E360538CA CRC64;
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  Query Match             72.0%;  Score 36;  DB 1;  Length 1828;
  Best Local Similarity   72.7%;  Pred. No. 3e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 YSS--PGSPGT 9
           |||  ||:|||
Db    1613 YSSRTPGTPGT 1623
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RESULT  31
MAP2_RAT
ID   MAP2_RAT       STANDARD;      PRT;  1861 AA.
AC   P15146;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein 2 (MAP 2) (MAP2B) [Contains: MAP2C].
GN   MAP2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Brain;
RX   MEDLINE=90251471; PubMed=2339070;
RA   Kindler S., Schwanke B., Schulz B., Garner C.C.;
RT   "Complete cDNA sequence encoding rat high and low molecular weight
RT   MAP2.";
RL   Nucleic Acids Res. 18:2822-2822(1990).
RN   [2]
RP   SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Brain;
RX   MEDLINE=91060576; PubMed=2174050;
RA   Kindler S., Schulz B., Goedert M., Garner C.C.;
RT   "Molecular structure of microtubule-associated protein 2b and 2c from
RT   rat brain.";
RL   J. Biol. Chem. 265:19679-19684(1990).
RN   [3]
RP   SEQUENCE OF 1-151; 1515-1694 AND 1726-1861 FROM N.A.
RX   MEDLINE=90221819; PubMed=2326166;
RA   Doll T., Papandrikopoulou A., Matus A.;
RT   "Nucleotide and amino acid sequences of embryonic rat MAP2c.";
RL   Nucleic Acids Res. 18:361-361(1990).
RN   [4]
RP   DISCUSSION OF SEQUENCE.
RX   MEDLINE=89365159; PubMed=2770869;
RA   Papandrikopoulou A., Doll T., Tucker R.P., Garner C.C., Matus A.;
RT   "Embryonic MAP2 lacks the cross-linking sidearm sequences and
RT   dendritic targeting signal of adult MAP2.";
RL   Nature 340:650-652(1989).
RN   [5]
RP   SEQUENCE OF 1695-1725 FROM N.A.
RX   MEDLINE=94110302; PubMed=8282767;
RA   Doll T., Meichsner M., Riederer B.M., Honegger P., Matus A.;
RT   "An isoform of microtubule-associated protein 2 (MAP2) containing
RT   four repeats of the tubulin-binding motif.";
RL   J. Cell Sci. 106:633-640(1993).
CC   -!- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
CC       STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
CC       SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
CC   -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
CC       FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
CC   -!- DEVELOPMENTAL STAGE: MAP2C IS EXPRESSED DURING EMBRYONIC BRAIN
CC       DEVELOPMENT AND UNTIL POSTANATAL DAY 10. MAP2B IS EXPRESSED
CC       THROUGHOUT BRAIN DEVELOPMENT.
CC   -!- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X51842; CAA36135.1; -.
DR   EMBL; X17682; CAA35667.1; -.
DR   EMBL; X71487; CAA50588.1; -.
DR   PIR; S07887; S07887.
DR   PIR; S10003; S10003.
DR   PIR; A37981; A37981.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 4.
DR   PROSITE; PS00229; TAU_MAP; 3.
KW   Microtubules; Repeat; Alternative splicing; Calmodulin-binding.
FT   DOMAIN      1454   1474       CALMODULIN-BINDING (POTENTIAL).
FT   REPEAT      1664   1694       TAU/MAP MOTIF.
FT   REPEAT      1695   1725       TAU/MAP MOTIF.
FT   REPEAT      1726   1756       TAU/MAP MOTIF.
FT   REPEAT      1757   1788       TAU/MAP MOTIF.
FT   VARSPLIC     152   1514       MISSING (IN ISOFORM MAP2C).
FT   VARSPLIC    1695   1725       MISSING (IN ISOFORM WITH 3 TAU/MAP
FT                                 REPEATS).
SQ   SEQUENCE   1861 AA;  202409 MW;  42DCF116D21EF54E CRC64;
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  Query Match             72.0%;  Score 36;  DB 1;  Length 1861;
  Best Local Similarity   72.7%;  Pred. No. 3.1e+02;
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  Matches    8;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 YSS--PGSPGT 9
           |||  ||:|||
Db    1615 YSSRTPGTPGT 1625


RESULT  32
CDN1_MOUSE
ID   CDN1_MOUSE      STANDARD;      PRT;   159 AA.
AC   P39689;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Cyclin-dependent kinase inhibitor 1 (Melanoma differentiation
DE   associated protein) (P21) (CDK-interacting protein 1).
GN   CDKN1A OR CIP1 OR WAF1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BXSB; TISSUE=Spleen;
RX   MEDLINE=94366751; PubMed=8084607;
RA   Huppi K., Siwarski D., Dosik J., Michieli P., Chedid M., Reed S.,
RA   Mock B., Givol D., Mushinski J.F.;
RT   "Molecular cloning, sequencing, chromosomal localization and
RT   expression of mouse p21 (Waf1).";
RL   Oncogene 9:3017-3020(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95316868; PubMed=7796420;
RA   El-Deiry W.S., Tokino T., Waldman T., Velculescu V., Oliner J.D.,
RA   Burell M., Hill D.E., Rees J.L., Hamilton S.R., Kinzler K.W.,
RA   Vogelstein B.;
RT   "Topological control of p21WAF1/CIP1 expression in normal and
RT   neoplastic tissues.";
RL   Cancer Res. 55:2910-2919(1995).
RN   [3]
RP   SEQUENCE OF 1-143 FROM N.A.
RX   MEDLINE=94061997; PubMed=8242752;
RA   El-Deiry W.S., Tokino T., Velculescu V.E., Levy D.B., Parsons R.,
RA   Trent J.M., Lin D., Mercer W.E., Kinzler K.W., Vogelstein B.;
RT   "WAF1, a potential mediator of p53 tumor suppression.";
RL   Cell 75:817-825(1993).
CC   -!- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES
CC       ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO
CC       DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
CC       ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
CC       KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- INDUCTION: BY P53, MEZEREIN (ANTILEUKEMIC COMPOUND) AND INTERFERON
CC       BETA.
CC   -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U09507; AAB60456.1; -.
DR   EMBL; U24173; AAC52220.1; -.
DR   PIR; A49438; A49438.
DR   HSSP; P46527; 1JSU.
DR   MGD; MGI:104556; Cdkn1a.
DR   InterPro; IPR003175; CDI.
DR   Pfam; PF02234; CDI; 1.
KW   Cell cycle; Nuclear protein; Zinc-finger.
FT   ZN_FING      12     40       C4-TYPE (POTENTIAL).
FT   CONFLICT     30     30       R -> S (IN REF. 3).
FT   CONFLICT     56     57       TP -> RQ (IN REF. 3).
SQ   SEQUENCE   159 AA;  17785 MW;  37B7C22B9A2FD089 CRC64;


  Query Match             70.0%;  Score 35;  DB 1;  Length 159;
  Best Local Similarity   85.7%;  Pred. No. 33;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           ||| |||
Db     125 SPGGPGT 131


RESULT  33
UR2R_RAT
ID   UR2R_RAT       STANDARD;      PRT;   386 AA.
AC   P49684; P48041;
DT   01-FEB-1996 (Rel. 33, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Urotensin II receptor (UR-II-R) (G protein-coupled sensory epithelial
DE   neuropeptide-like receptor) (SENR).
GN   GPR14.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96115583; PubMed=8666380;
RA   Marchese A., Heiber M., Nguyen T., Heng H.H.Q., Saldivia V.R.,
RA   Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R.,
RA   O'Dowd B.F., Docherty J.M.;
RT   "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
RT   and GPR14, encoding receptors related to interleukin 8, neuropeptide
RT   Y, and somatostatin receptors.";
RL   Genomics 29:335-344(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Circumvallate papillae;
RX   MEDLINE=95251679; PubMed=7733947;
RA   Tal M., Ammar D.A., Karpuj M., Krizhanovsky V., Naim M.,
RA   Thompson D.A.;
RT   "A novel putative neuropeptide receptor expressed in neural tissue,
RT   including sensory epithelia.";
RL   Biochem. Biophys. Res. Commun. 209:752-759(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Urinary bladder;
RA   Suga H., Takao K.;
RT   "Expression of the rat SENR in the urinary bladder tissues.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: HIGH AFINITY RECEPTOR FOR UROTENSIN II. THE ACTIVITY OF
CC       THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATE A
CC       PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN NEURAL AND SENSORY
CC       TISSUES.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U32673; AAC52593.1; -.
DR   EMBL; U23483; AAA80111.1; -.
DR   EMBL; AB012210; BAA25251.1; -.
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DR   HSSP; P34996; 1DDD.
DR   GCRDb; GCR_1427; -.
DR   GCRDb; GCR_1443; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN       1     54       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     55    77       1 (POTENTIAL).
FT   DOMAIN       78    87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    113      2 (POTENTIAL).
FT   DOMAIN       114   124      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     125   146      3 (POTENTIAL).
FT   DOMAIN       147   167      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     168   186      4 (POTENTIAL).
FT   DOMAIN       187   209      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     210   232      5 (POTENTIAL).
FT   DOMAIN       233   258      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     259   284      6 (POTENTIAL).
FT   DOMAIN       285   299      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     300   321      7 (POTENTIAL).
FT   DOMAIN       322   386      CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     29    29       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     33    33       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     123   199      BY SIMILARITY.
FT   CONFLICT     315   315      F -> L (IN REF. 1).
SQ   SEQUENCE   386 AA;  42707 MW;  FA4E95CC6A4CA27C CRC64;
```

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  Query Match             70.0%;  Score 35;  DB 1;  Length 386;
  Best Local Similarity   85.7%;  Pred. No. 85;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           ||||||:
Db     341 SPGSPGS 347
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RESULT  34
IL5R_MOUSE
ID   IL5R_MOUSE     STANDARD;      PRT;   415 AA.
AC   P21183;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Interleukin-5 receptor alpha chain precursor (IL-5R-alpha).
GN   IL5RA OR IL5R.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91092260; PubMed=2265612;
RA   Takaki S., Tominaga A., Mita S., Sonoda E., Yamaguchi N.,
RA   Takatsu K.;
RT   "Molecular cloning and expression of the murine interleukin-5
RT   receptor.";
RL   EMBO J. 9:4367-4374(1990).
CC   -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC       BINDS TO IL-5.
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC       CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO
CC       ON B-CELLS.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D90205; BAA14231.1; -.
DR   PIR; S12357; S12357.
DR   MGD; MGI:96558; Il5ra.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003532; Hematopo_receptor_S_F2.
DR   PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW   Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL       1     17
FT   CHAIN        18    415      INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT   DOMAIN       18    339      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     340   361      POTENTIAL.
FT   DOMAIN       362   415      CYTOPLASMIC (POTENTIAL).
FT   DISULFID     131   152      BY SIMILARITY.
FT   DISULFID     179   193      BY SIMILARITY.
FT   CARBOHYD     32    32       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     128   128      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     213   213      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     241   241      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   415 AA;  46989 MW;  A4326D2922571C08 CRC64;
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  Query Match             70.0%;  Score 35;  DB 1;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 PGSPGT 9
           ||||||
Db     119 PGSPGT 124
```

```
RESULT  35
HXKG_ASPNG
ID   HXKG_ASPNG     STANDARD;      PRT;   495 AA.
AC   Q92407;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Glucokinase (EC 2.7.1.2) (Glucose kinase) (GLK).
GN   GLKA.
OS   Aspergillus niger.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5061;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CBS 120.49 / N400;
RX   MEDLINE=97008939; PubMed=8856049;
RA   Panneman H., Ruijter G.J.G., van den Broeck H.C., Driever E.T.M.,
RA   Visser J.;
RT   "Cloning and biochemical characterisation of an Aspergillus niger
RT   glucokinase. Evidence for the presence of separate glucokinase and
RT   hexokinase enzymes.";
RL   Eur. J. Biochem. 240:518-525(1996).
CC   -!- FUNCTION: THE ENZYME HAS GREAT AFFINITY FOR GLUCOSE. MANNOSE, 2-
CC       DEOXYGLUCOSE AND GLUCOSAMINE CAN SERVE AS SUBSTRATES. ACTIVITY IS
CC       RELATIVELY CONSTANT BETWEEN PH 7.5 AND PH 9.0. BELOW PH 7.5, THE
CC       ACTIVITY DECREASES WITH PH.
CC   -!- CATALYTIC ACTIVITY: ATP + D-glucose = ADP + D-glucose 6-phosphate.
CC   -!- SUBUNIT: MONOMER (PROBABLE).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X99626; CAA67949.1; -.
DR   HSSP; Q26609; 1BDG.
DR   InterPro; IPR001312; Hexokinase.
DR   Pfam; PF00349; hexokinase; 1.
DR   PRINTS; PR00475; HEXOKINASE.
DR   ProDom; PD001109; Hexokinase; 1.
DR   PROSITE; PS00378; HEXOKINASES; 1.
KW   Transferase; Kinase; Glycolysis; ATP-binding.
FT   BINDING      93     93       ATP (POTENTIAL).
FT   DOMAIN      149    175       GLUCOSE-BINDING (POTENTIAL).
FT   NP_BIND     472    477       ATP (POTENTIAL).
SQ   SEQUENCE   495 AA;  54536 MW;  02C94EF07D1809F8 CRC64;


  Query Match             70.0%;  Score 35;  DB 1;  Length 495;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |:|||  ||
Db     218 YTSPGETGT 226


RESULT  36
AMH2_HUMAN
ID   AMH2_HUMAN     STANDARD;      PRT;   573 AA.
AC   Q16671; Q13762;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Anti-mullerian hormone type II receptor precursor (EC 2.7.1.37) (AMH
DE   type II receptor) (MIS type II receptor) (MISRII) (MRII).
GN   AMHR2 OR AMHR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96083584; PubMed=7493017;
RA   Imbeaud S., Faure E., Lamarre I., Mattei M.-G., di Clemente N.,
RA   Tizard R., Carre-Eusebe D., Belville C., Tragethon L., Tonkin C.,
RA   Nelson J., McAuliffe M., Bidart J.-M., Lababidi A., Josso N.,
RA   Cate R.L., Picard J.-Y.;
RT   "Insensitivity to anti-mullerian hormone due to a mutation in the
RT   human anti-mullerian hormone receptor.";
RL   Nat. Genet. 11:382-388(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96028015; PubMed=7488027;
RA   Visser J.A., McLuskey A., van Beers T., Weghuis D.O., van Kessel A.G.,
RA   Grootegoed J.A., Themmen A.P.N.;
RT   "Structure and chromosomal localization of the human anti-mullerian
RT   hormone type II receptor gene.";
RL   Biochem. Biophys. Res. Commun. 215:1029-1036(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=20055680; PubMed=10589763;
RA   Masiakos P.T., MacLaughlin D.T., Maheswaran S., Teixeira J.,
RA   Fuller A.F. Jr., Shah P.C., Kehas D.J., Kenneally M.K.,
RA   Dombkowski D.M., Ha T.U., Preffer F.I., Donahoe P.K.;
RT   "Human ovarian cancer, cell lines, and primary ascites cells express
RT   the human Mullerian inhibiting substance (MIS) type II receptor,
RT   bind, and are responsive to MIS.";
RL   Clin. Cancer Res. 5:3488-3499(1999).
CC   -!- FUNCTION: RECEPTOR FOR ANTI-MULLERIAN HORMONE.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DISEASE: DEFECTS IN AMHR2 ARE THE CAUSE OF PERSISTENT MULLERIAN
CC       DUCT SYNDROME TYPE II (PMDS-2); A FORM OF MALE
CC       PSEUDOHERMAPHRODITISM CHARACTERIZED BY A FAILURE OF MUELLERIAN
CC       DUCT REGRESSION IN OTHERWISE NORMAL MALES.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       TGFB RECEPTOR SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X89013; CAA61418.1; -.
DR   EMBL; U29700; AAC50328.1; -.
DR   EMBL; X91156; CAA62593.1; -.
DR   EMBL; X91157; CAA62593.1; JOINED.
DR   EMBL; X91158; CAA62593.1; JOINED.
DR   EMBL; X91159; CAA62593.1; JOINED.
DR   EMBL; X91160; CAA62593.1; JOINED.
DR   EMBL; X91161; CAA62593.1; JOINED.
DR   EMBL; X91162; CAA62593.1; JOINED.
DR   EMBL; X91163; CAA62593.1; JOINED.
DR   EMBL; X91164; CAA62593.1; JOINED.
DR   EMBL; X91165; CAA62593.1; JOINED.
DR   EMBL; X91166; CAA62593.1; JOINED.
DR   EMBL; AF172932; AAD48497.1; -.
DR   MIM; 600956; -.
DR   InterPro; IPR000472; Activin_rec.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Transmembrane; Glycoprotein; Signal; Pseudohermaphroditism.
FT   SIGNAL       1     17       POTENTIAL.
FT   CHAIN       18    573       ANTI-MULLERIAN HORMONE TYPE II RECEPTOR.
FT   DOMAIN      18    149       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   150    170       POTENTIAL.
FT   DOMAIN     171    573       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     203    518       PROTEIN KINASE.
FT   NP_BIND    209    217       ATP (BY SIMILARITY).
FT   BINDING    230    230       ATP (BY SIMILARITY).
FT   ACT_SITE   333    333       BY SIMILARITY.
FT   CARBOHYD    66     66       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   119    119       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   161    161       L -> V (IN REF. 2; CAA62593).
SQ   SEQUENCE  573 AA;  62749 MW;  1347C10C2942FDBA CRC64;


  Query Match             70.0%;  Score 35;  DB 1;  Length 573;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 PGSPGT 9
           ||||||
Db     126 PGSPGT 131


RESULT  37
MRKC_KLEPN
ID   MRKC_KLEPN     STANDARD;      PRT;   828 AA.
AC   P21647;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Outer membrane usher protein mrkC precursor.
GN   MRKC.
OS   Klebsiella pneumoniae.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Klebsiella.
OX   NCBI_TaxID=573;
```

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RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IA565;
RX   MEDLINE=91100388; PubMed=1670938;
RA   Allen B.L., Gerlach G.-F., Clegg S.;
RT   "Nucleotide sequence and functions of mrk determinants necessary for
RT   expression of type 3 fimbriae in Klebsiella pneumoniae.";
RL   J. Bacteriol. 173:916-920(1991).
CC   -!- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF THE TYPE 3
CC       FIMBRIAL SUBUNIT (MRKA).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC       (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
CC   ---------------------------------------------------------------------
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M55912; AAA25095.1; -.
DR   PIR; D39142; D39142.
DR   InterPro; IPR000015; Fimb_usher.
DR   Pfam; PF00577; Usher; 1.
DR   PROSITE; PS01151; FIMBRIAL_USHER; 1.
KW   Outer membrane; Transmembrane; Fimbria; Transport; Signal.
FT   SIGNAL       1     18       POTENTIAL.
FT   CHAIN       19    828       OUTER MEMBRANE USHER PROTEIN MRKC.
FT   DISULFID   813    827       POTENTIAL.
SQ   SEQUENCE   828 AA;  91049 MW;  B30EDF5798249FC9 CRC64;
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  Query Match             70.0%;  Score 35;  DB 1;  Length 828;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 PGSPGT 9
           ||||||
Db     693 PGSPGT 698
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RESULT  38
VGLB_HSV1F
ID   VGLB_HSV1F     STANDARD;      PRT;   903 AA.
AC   P06436;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Glycoprotein B precursor.
GN   GB OR UL27.
OS   Herpes simplex virus (type 1 / strain F).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=10304;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85083254; PubMed=2981343;
RA   Pellett P.E., Kousoulas K.G., Pereira L., Roizman B.;
RT   "Anatomy of the herpes simplex virus 1 strain F glycoprotein B gene:
RT   primary sequence and predicted protein structure of the wild type and
RT   of monoclonal antibody-resistant mutants.";
RL   J. Virol. 53:243-253(1985).
RN   [2]
RP   SEQUENCE OF 1-176 FROM N.A.
RX   MEDLINE=88306232; PubMed=2457278;
RA   Hammerschmidt W., Conraths F., Mankertz J., Buhk H.-J., Pauli G.,
RA   Ludwig H.;
RT   "Common epitopes of glycoprotein B map within the major DNA-binding
RT   proteins of bovine herpesvirus type 2 (BHV-2) and herpes simplex
RT   virus type 1 (HSV-1).";
RL   Virology 165:406-418(1988).
CC   -!- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,
CC       GB, GC, GG, GD, GI, AND GE.
CC   -!- MISCELLANEOUS: GB IS THE ONLY GLYCOPROTEIN THAT IS KNOWN TO BE
CC       REQUIRED FOR VIRAL GROWTH.
CC   -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
CC   ---------------------------------------------------------------------
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14164; AAA45776.1; -.
DR   EMBL; M21633; AAA45788.1; -.
DR   PIR; A03750; VGBEB1.
DR   InterPro; IPR000234; Glycoprot_B.
DR   Pfam; PF00606; Glycoprotein_B; 1.
DR   ProDom; PD000693; Glycoprot_B; 1.
KW   Glycoprotein; Transmembrane; Signal.
FT   SIGNAL       1     29
FT   CHAIN       30    903       GLYCOPROTEIN B.
FT   DOMAIN      31    729       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   730    745       POTENTIAL.
FT   TRANSMEM   751    770       POTENTIAL.
FT   TRANSMEM   774    794       POTENTIAL.
FT   DOMAIN     795    903       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   140    140       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   397    397       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   429    429       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   488    488       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   673    673       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   903 AA;  100104 MW;  73BDCA7813DB35E8 CRC64;
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  Query Match             70.0%;  Score 35;  DB 1;  Length 903;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
           ||||:||
Db      32 SSPGTPG 38
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RESULT  39
VGLB_HSV11
ID   VGLB_HSV11     STANDARD;      PRT;   904 AA.
AC   P10211;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Glycoprotein B precursor.
GN   GB OR UL27.
OS   Herpes simplex virus (type 1 / strain 17).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=10299;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88274327; PubMed=2839594;
RA   McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
RA   McNab D., Perry L.J., Scott J.E., Taylor P.;
RT   "The complete DNA sequence of the long unique region in the genome of
RT   herpes simplex virus type 1.";
RL   J. Gen. Virol. 69:1531-1574(1988).
CC   -!- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,
CC       GB, GC, GG, GD, GI, AND GE.
CC   -!- MISCELLANEOUS: GB IS THE ONLY GLYCOPROTEIN THAT IS KNOWN TO BE
CC       REQUIRED FOR VIRAL GROWTH.
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CC   -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10879; BAA01673.1; -.
DR   EMBL; X14112; CAA32320.1; -.
DR   PIR; I30084; VGBEW7.
DR   InterPro; IPR000234; Glycoprot_B.
DR   Pfam; PF00606; Glycoprotein_B; 1.
DR   ProDom; PD000693; Glycoprot_B; 1.
KW   Glycoprotein; Transmembrane; Signal.
FT   SIGNAL        1     30
FT   CHAIN        31    904       GLYCOPROTEIN B.
FT   DOMAIN       31    730       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    731    746       POTENTIAL.
FT   TRANSMEM    752    771       POTENTIAL.
FT   TRANSMEM    775    795       POTENTIAL.
FT   DOMAIN      796    904       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     87     87       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    398    398       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    430    430       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    489    489       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    674    674       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   904 AA;  100292 MW;  2C14E8B1284C1F3A CRC64;

  Query Match             70.0%;  Score 35;  DB 1;  Length 904;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
           ||||:||
Db      33 SSPGTPG 39


RESULT  40
VGLB_HSV1P
ID   VGLB_HSV1P     STANDARD;      PRT;   904 AA.
AC   P08665;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Glycoprotein B precursor.
GN   GB OR UL27.
OS   Herpes simplex virus (type 1 / strain Patton).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=10308;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87112925; PubMed=3027364;
RA   Stuve L.L., Brown-Shimer S., Pachl C., Najarian R., Dina D.,
RA   Burke R.L.;
RT   "Structure and expression of the herpes simplex virus type 2
RT   glycoprotein gB gene.";
RL   J. Virol. 61:326-335(1987).
CC   -!- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,
CC       GB, GC, GG, GD, GI, AND GE.
CC   -!- MISCELLANEOUS: GB IS THE ONLY GLYCOPROTEIN THAT IS KNOWN TO BE
CC       REQUIRED FOR VIRAL GROWTH.
CC   -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K03541; AAA45778.1; -.
DR   InterPro; IPR000234; Glycoprot_B.
DR   Pfam; PF00606; Glycoprotein_B; 1.
DR   ProDom; PD000693; Glycoprot_B; 1.
KW   Glycoprotein; Transmembrane; Signal.
FT   SIGNAL        1     30
FT   CHAIN        31    904       GLYCOPROTEIN B.
FT   DOMAIN       31    730       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    731    746       POTENTIAL.
FT   TRANSMEM    752    772       POTENTIAL.
FT   TRANSMEM    775    795       POTENTIAL.
FT   DOMAIN      796    904       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     87     87       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    398    398       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    430    430       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    489    489       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    674    674       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   904 AA;  100115 MW;  7825E1DC830A626F CRC64;

  Query Match             70.0%;  Score 35;  DB 1;  Length 904;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
           ||||:||
Db      33 SSPGTPG 39


Search completed: May 21, 2002, 11:24:11
Job time: 331 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 21, 2002, 11:18:10 ; Search time 41.2 Seconds
(without alignments)
37.790 Million cell updates/sec

Title: US-09-734-281-1
Perfect score: 50
Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	372	11	Q91WK4	Q91wk4 mus musculu
2	42	84.0	641	3	Q9Y879	Q9y879 cryptococcu
3	41	82.0	15	6	Q9TRE5	Q9tre5 bos taurus
4	41	82.0	626	10	Q9ZRY1	Q9zry1 glycine max
5	40	80.0	376	4	Q96CK9	Q96ck9 homo sapien
6	40	80.0	435	2	O68641	O68641 oerskovia x
7	39	78.0	150	2	Q9XAE0	Q9xae0 streptomyce
8	39	78.0	272	2	Q9S283	Q9s283 streptomyce
9	39	78.0	389	6	Q9BEG5	Q9beg5 bos taurus
10	39	78.0	391	6	Q9BEG6	Q9beg6 bos taurus
11	39	78.0	405	4	Q9NWV9	Q9nwv9 homo sapien
12	39	78.0	424	4	Q9UKS6	Q9uks6 homo sapien
13	39	78.0	424	4	Q9H331	Q9h331 homo sapien
14	39	78.0	513	4	Q9BRM0	Q9brm0 homo sapien
15	39	78.0	651	4	Q9P2L4	Q9p214 homo sapien
16	39	78.0	2232	5	P91365	P91365 caenorhabdi
17	38	76.0	280	5	Q95TC5	Q95tc5 drosophila
18	38	76.0	453	11	Q63422	Q63422 rattus norv
19	38	76.0	517	17	Q974W1	Q974w1 sulfolobus
20	38	76.0	711	5	Q9U5M3	Q9u5m3 podocoryne
21	38	76.0	1019	5	Q961G7	Q961g7 drosophila
22	38	76.0	1345	1	Q54437	Q54437 staphylothe
23	37	74.0	168	5	O17289	O17289 caenorhabdi
24	37	74.0	238	4	Q9H4T5	Q9h4t5 homo sapien
25	37	74.0	302	3	O43060	O43060 schizosacch
26	37	74.0	333	4	Q15469	Q15469 homo sapien
27	37	74.0	387	11	Q9D2V9	Q9d2v9 mus musculu
28	37	74.0	387	11	Q99PD5	Q99pd5 mus musculu
29	37	74.0	393	6	Q99147	Q99147 oryctolagus
30	37	74.0	396	4	Q14631	Q14631 homo sapien
31	37	74.0	406	3	O74658	O74658 candida alb
32	37	74.0	406	3	Q9URP9	Q9urp9 candida alb
33	37	74.0	407	3	O74661	O74661 candida alb
34	37	74.0	420	4	Q14633	Q14633 homo sapien
35	37	74.0	539	4	O95196	O95196 homo sapien
36	37	74.0	539	11	Q9QY32	Q9qy32 mus musculu
37	37	74.0	541	6	Q01106	Q01106 oryctolagus
38	37	74.0	723	11	Q9D677	Q9d677 mus musculu
39	37	74.0	734	4	O75112	O75112 homo sapien
40	37	74.0	742	11	Q9CW54	Q9cw54 mus musculu
41	37	74.0	847	4	Q16584	Q16584 homo sapien
42	37	74.0	850	11	Q9JJ15	Q9jj15 mus musculu
43	37	74.0	1523	3	Q9HFX4	Q9hfx4 candida alb
44	37	74.0	3494	4	Q96RU9	Q96ru9 homo sapien
45	37	74.0	3620	6	Q9TU53	Q9tu53 canis famil
46	37	74.0	3623	4	O60494	O60494 homo sapien
47	37	74.0	6875	6	Q28733	Q28733 oryctolagus
48	37	74.0	26926	4	Q10466	Q10466 homo sapien
49	36	72.0	114	10	Q9ATC9	Q9atc9 malus domes
50	36	72.0	119	10	Q43548	Q43548 malus domes
51	36	72.0	149	11	Q9JKX0	Q9jkx0 mus musculu
52	36	72.0	179	11	Q9JKW9	Q9jkw9 mus musculu
53	36	72.0	209	16	Q98K79	Q98k79 rhizobium l
54	36	72.0	216	11	Q9JKX1	Q9jkx1 mus musculu
55	36	72.0	221	2	Q9RJC5	Q9rjc5 streptomyce

ALIGNMENTS

RESULT 1
Q91WK4
ID Q91WK4 PRELIMINARY; PRT; 372 AA.
AC Q91WK4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN TAU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE, AND RETINA;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC014748; AAH14748.1; -.
SQ SEQUENCE 372 AA; 38861 MW; B027745D23BC62A2 CRC64;

Query Match 100.0%; Score 50; DB 11; Length 372;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 128 YSSPGSPGT 136

```
RESULT   2
Q9Y879
ID   Q9Y879      PRELIMINARY;      PRT;   641 AA.
AC   Q9Y879;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CALCINEURIN A CATALYTIC SUBUNIT.
GN   CNA1.
OS   Cryptococcus neoformans var. neoformans.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=40410;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JEC21;
RX   MEDLINE=20107115; PubMed=10639477;
RA   Cruz M.C., Sia R.A.L., Olson M., Cox G.M., Heitman J.;
RT   "Comparison of the Roles of Calcineurin in Physiology and Virulence in
RT   Serotype D and Serotype A Strains of Cryptococcus neoformans.";
RL   Infect. Immun. 68:982-985(2000).
CC   -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC       ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC   -!- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
DR   EMBL; AF159511; AAD44336.1; -.
DR   HSSP; P48452; 1TCO.
DR   InterPro; IPR000934; Ser_thr_phosphtse.
DR   Pfam; PF00149; STphosphatase; 1.
DR   PRINTS; PR00114; STPHPHTASE.
DR   SMART; SM00156; PP2Ac; 1.
DR   PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW   Hydrolase; Iron; Manganese.
SQ   SEQUENCE   641 AA;  71813 MW;  DD68607843D8E6DB CRC64;

  Query Match             84.0%;  Score 42;  DB 3;  Length 641;
  Best Local Similarity   77.8%;  Pred. No. 18;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           : |||||||
Db     554 FGSPGSPGT 562


RESULT   3
Q9TRE5
ID   Q9TRE5      PRELIMINARY;      PRT;    15 AA.
AC   Q9TRE5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   TAU PROTEIN (FRAGMENT).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94043150; PubMed=8226879;
RA   Paudel H.K., Lew J., Ali Z., Wang J.H.;
RT   "Brain proline-directed protein kinase phosphorylates tau on sites
RT   that are abnormally phosphorylated in tau associated with Alzheimer's
RT   paired helical filaments.";
RL   J. Biol. Chem. 268:23512-23518(1993).
SQ   SEQUENCE   15 AA;  1449 MW;  FBCBEEFEEBC2B342 CRC64;

  Query Match             82.0%;  Score 41;  DB 6;  Length 15;
  Best Local Similarity   87.5%;  Pred. No. 0.5;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           ||||| ||
Db       3 YSSPGXPG 10


RESULT   4
Q9ZRY1
ID   Q9ZRY1      PRELIMINARY;      PRT;   626 AA.
AC   Q9ZRY1;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   NDX1 HOMEOBOX PROTEIN (FRAGMENT).
GN   NDX1.
OS   Glycine max (Soybean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jorgensen J.E., Gronlund M., Pallisgaard N., Larsen K., Marcker K.A.,
RA   Jensen E.;
RT   "A new class of plant homeobox genes is expressed in specific regions
RT   of determinate symbiotic root nodules.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ011831; CAA09794.1; -.
DR   InterPro; IPR001356; Homeobox.
DR   SMART; SM00389; HOX; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
KW   Homeobox; DNA-binding; Nuclear protein.
FT   NON_TER       1      1
SQ   SEQUENCE   626 AA;  69101 MW;  0DCF8C371CD61B11 CRC64;

  Query Match             82.0%;  Score 41;  DB 10;  Length 626;
  Best Local Similarity   87.5%;  Pred. No. 26;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           | ||||||
Db     498 YDSPGSPG 505


RESULT   5
Q96CK9
ID   Q96CK9      PRELIMINARY;      PRT;   376 AA.
AC   Q96CK9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SIMILAR TO ZINC FINGER PROTEIN 16 (KOX 9).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG CARCINOMA;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC014165; AAH14165.1; -.
SQ   SEQUENCE   376 AA;  41145 MW;  68B1A638CC0758BC CRC64;

  Query Match             80.0%;  Score 40;  DB 4;  Length 376;
  Best Local Similarity   87.5%;  Pred. No. 23;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||:|||
Db      20 SSPGTPGT 27
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```
RESULT   6
O68641
ID   O68641      PRELIMINARY;      PRT;   435 AA.
AC   O68641;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BETA-1,3-GLUCANASE II.
GN   BGLII.
OS   Oerskovia xanthineolytica.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Micrococcineae; Cellulomonadaceae; Oerskovia.
OX   NCBI_TaxID=1826;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LL G109;
RA   Ventom A.M., Asenjo J.A.;
RT   "Characterization of yeast lytic enzymes from Oerskovia
RT   xanthineolytica LL-G109.";
RL   Enzyme Microb. Technol. 13:71-75(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LL G109;
RX   MEDLINE=96409238; PubMed=8814220;
RA   Parrado J., Escuredo P.R., Conejero-Lara F., Kotik M., Ponting C.P.,
RA   Asenjo J.A., Dobson C.M.;
RT   "Molecular characterisation of a thermoactive beta-1,3-glucanase from
RT   Oerskovia xanthineolytica.";
RL   Biochim. Biophys. Acta 1296:145-151(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LL G109;
RX   MEDLINE=96250169; PubMed=8659924;
RA   Ferrer P., Hedegaard L., Halkier T., Diers I., Savva D., Asenjo J.A.;
RT   "Molecular cloning of a lytic beta-1,3-glucanase gene from Oerskovia
RT   xanthineolytica LL G109.";
RL   Ann. N. Y. Acad. Sci. 782:555-566(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LL G109;
RA   Ferrer P., Andrews B.A., Asenjo J.A., Hedegaard L., Diers I.;
RT   "BglII codes for a yeast-lytic beta-1,3-glucanase from Oerskovia
RT   xanthineolytica LL G109 (Cellulomonas cellulans) having a mannose-
RT   binding domain.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF052745; AAC38290.1; -.
DR   HSSP; P23904; 1AJK.
DR   InterPro; IPR000757; Glyco_hydro_16.
DR   InterPro; IPR000772; Ricin_B_lectin.
DR   Pfam; PF00722; Glyco_hydro_16; 1.
DR   Pfam; PF00652; Ricin_B_lectin; 1.
DR   SMART; SM00458; RICIN; 1.
DR   PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
DR   PROSITE; PS50231; RICIN_B_LECTIN; 1.
SQ   SEQUENCE   435 AA;  46097 MW;  00F087BE644C0F58 CRC64;

  Query Match             80.0%;  Score 40;  DB 2;  Length 435;
  Best Local Similarity   87.5%;  Pred. No. 27;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||:|||
Db     297 SSPGNPGT 304


RESULT   7
Q9XAE0
ID   Q9XAE0      PRELIMINARY;      PRT;   150 AA.
AC   Q9XAE0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 16.1 KDA PROTEIN.
GN   SC6G9.42C.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Seeger K.J., Harris D.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=97000351; PubMed=8843436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA   Kinashi H., Hopwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
DR   EMBL; AL079356; CAB45633.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   150 AA;  16072 MW;  7A8D93D1C6A48A0D CRC64;

  Query Match             78.0%;  Score 39;  DB 2;  Length 150;
  Best Local Similarity   87.5%;  Pred. No. 13;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           |||| |||
Db       3 SSPGKPGT 10


RESULT   8
Q9S283
ID   Q9S283      PRELIMINARY;      PRT;   272 AA.
AC   Q9S283;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PUTATIVE EXPRESSION REGULATOR (FRAGMENT).
GN   SCI11.37C.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Saunders D., Harris D.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=97000351; PubMed=8843436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA   Kinashi H., Hopwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
DR   EMBL; AL096849; CAB50963.1; -.
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DR   InterPro; IPR001450; 4Fe4S_ferredoxin.
DR   InterPro; IPR000561; EGF-like.
DR   PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
FT   NON_TER       1       1
SQ   SEQUENCE   272 AA;  27508 MW;  6E8523635D929BB5 CRC64;


  Query Match             78.0%;  Score 39;  DB 2;  Length 272;
  Best Local Similarity   66.7%;  Pred. No. 25;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            |: ||:|||
Db     170 YAPPGAPGT 178


RESULT   9
Q9BEG5
ID   Q9BEG5      PRELIMINARY;      PRT;   389 AA.
AC   Q9BEG5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   ECTODYSPLASIN 1, ISOFORM A2.
GN   ED1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HOLSTEIN;
RA   Droegemueller C., Distl O., Leeb T.;
RT   "Identification of a highly polymorphic microsatellite within the
RT   bovine ectodysplasin A (ED1) gene on BTA Xq22-24.";
RL   Anim. Genet. 31:416-416(2000).
DR   EMBL; AJ300468; CAC29152.1; -.
DR   EMBL; AJ300469; CAC29152.1; JOINED.
DR   EMBL; AJ278907; CAC29152.1; JOINED.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR000478; TNF_family.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   389 AA;  41339 MW;  60BE0077C7C83986 CRC64;


  Query Match             78.0%;  Score 39;  DB 6;  Length 389;
  Best Local Similarity   66.7%;  Pred. No. 36;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            :| ||:|||
Db      78 FSGPGTPGT 86


RESULT  10
Q9BEG6
ID   Q9BEG6      PRELIMINARY;      PRT;   391 AA.
AC   Q9BEG6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   ECTODYSPLASIN 1, ISOFORM A1.
GN   ED1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HOLSTEIN;
RA   Droegemueller C., Distl O., Leeb T.;
RT   "Identification of a highly polymorphic microsatellite within the
RT   bovine ectodysplasin A (ED1) gene on BTA Xq22-24.";
RL   Anim. Genet. 31:416-416(2000).
DR   EMBL; AJ300468; CAC29151.1; -.
DR   EMBL; AJ300469; CAC29151.1; JOINED.
DR   EMBL; AJ278907; CAC29151.1; JOINED.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR000478; TNF_family.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   391 AA;  41567 MW;  1F87AD67A04EB7AA CRC64;


  Query Match             78.0%;  Score 39;  DB 6;  Length 391;
  Best Local Similarity   66.7%;  Pred. No. 36;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            :| ||:|||
Db      78 FSGPGTPGT 86


RESULT  11
Q9NWV9
ID   Q9NWV9      PRELIMINARY;      PRT;   405 AA.
AC   Q9NWV9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   CDNA FLJ20570 FIS, CLONE REC00956 (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,
RA   Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T.,
RA   Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK000577; BAA91267.1; -.
DR   InterPro; IPR001060; FCH.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00611; FCH; 1.
DR   SMART; SM00055; FCH; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50002; SH3; 1.
FT   NON_TER     405     405
SQ   SEQUENCE   405 AA;  46494 MW;  6EA81D7782B53D92 CRC64;


  Query Match             78.0%;  Score 39;  DB 4;  Length 405;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
            |||||||
Db     341 SPGSPGT 347


RESULT  12
Q9UKS6
ID   Q9UKS6      PRELIMINARY;      PRT;   424 AA.
AC   Q9UKS6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   SH3 DOMAIN-CONTAINING PROTEIN 6511.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20002705; PubMed=10531379;
RA   Howard L., Nelson K.K., Maciewicz R.A., Blobel C.P.;
RT   "Interaction of the metalloprotease disintegrins MDC9 and MDC15 with
RT   two SH3 domain-containing proteins, endophilin I and SH3PX1.";
RL   J. Biol. Chem. 274:31693-31699(1999).
DR   EMBL; AF130979; AAF04472.1; -.
DR   HSSP; P29355; 1SEM.
DR   InterPro; IPR001060; FCH.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00611; FCH; 1.
DR   Pfam; PF00018; SH3; 1.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   SMART; SM00055; FCH; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   424 AA;  48515 MW;  924A7BF79C8DC395 CRC64;


  Query Match             78.0%;  Score 39;  DB 4;  Length 424;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 SPGSPGT 9
          |||||||
Db    341 SPGSPGT 347


RESULT  13
Q9H331
ID   Q9H331      PRELIMINARY;      PRT;   424 AA.
AC   Q9H331;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PACSIN3 (PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE 3) (UNKNOWN)
DE   (PROTEIN FOR MGC:19935) (PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE
DE   IN NEURONS 3).
GN   PACSIN3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=11082044;
RA   Modregger J., Ritter B., Witter B., Paulsson M., Plomann M.;
RT   "All three PACSIN isoforms bind to endocytic proteins and inhibit
RT   endocytosis.";
RL   J. Cell Sci. 113:4511-4521(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21100457; PubMed=11179684;
RA   Sumoy L., Pluvinet R., Andreu N., Estivill X., Escarceller M.;
RT   "PACSIN 3 is a novel SH3 domain cytoplasmic adapter protein of the
RT   pacsin-syndapin-FAP52 gene family.";
RL   Gene 262:199-205(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MELANOMA;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=UTERUS, LEIOMYOSARCOMA;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF149825; AAG31023.1; -.
DR   EMBL; AF242530; AAK29207.1; -.
DR   EMBL; BC011889; AAH11889.1; -.
DR   EMBL; BC007914; AAH07914.1; -.
DR   HSSP; P29355; 1SEM.
DR   InterPro; IPR001060; FCH.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00018; SH3; 1.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   SMART; SM00055; FCH; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   424 AA;  48486 MW;  6DBD940AE6D1F352 CRC64;


  Query Match             78.0%;  Score 39;  DB 4;  Length 424;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 SPGSPGT 9
          |||||||
Db    341 SPGSPGT 347


RESULT  14
Q9BRM0
ID   Q9BRM0      PRELIMINARY;      PRT;   513 AA.
AC   Q9BRM0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   HYPOTHETICAL PROTEIN (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=UTERUS, AND LEIOMYOSARCOMA;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006174; AAH06174.1; -.
DR   InterPro; IPR001798; Kelch.
DR   Pfam; PF01344; Kelch; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   513 AA;  54599 MW;  21FD050215015520 CRC64;


  Query Match             78.0%;  Score 39;  DB 4;  Length 513;
  Best Local Similarity   87.5%;  Pred. No. 48;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 SSPGSPGT 9
          |||||||:
Db    379 SSPGSPGS 386


RESULT  15
Q9P2L4
ID   Q9P2L4      PRELIMINARY;      PRT;   651 AA.
AC   Q9P2L4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   KIAA1332 PROTEIN (FRAGMENT).
GN   KIAA1332.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=20181126; PubMed=10718198;
RA   Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
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RT   "Prediction of the coding sequences of unidentified human genes.XVI.
RT   The complete sequences of 150 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 7:65-73(2000).
DR   EMBL; AB037753; BAA92570.1; -.
DR   InterPro; IPR001798; Kelch.
DR   Pfam; PF01344; Kelch; 2.
FT   NON_TER       1       1
SQ   SEQUENCE   651 AA;  70304 MW;  1CF1DEB5F03DCB3C CRC64;
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  Query Match             78.0%;  Score 39;  DB 4;  Length 651;
  Best Local Similarity   87.5%;  Pred. No. 62;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           |||||||:
Db     517 SSPGSPGS 524
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RESULT  16
P91365
ID   P91365      PRELIMINARY;      PRT;  2232 AA.
AC   P91365;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   K06A9.1 PROTEIN.
GN   K06A9.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Geisel C., Gattung S.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) MAY BE PRODUCED BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN IS THAT
CC       OF THE A FORM.
DR   EMBL; U80846; AAC70889.1; -.
DR   EMBL; U80846; AAC70890.1; -.
KW   Alternative splicing.
FT   VARSPLIC    842    866       VASSSPAPSTSQNPNPSTSSGSSMI -> LATTSAPKPSVT
FT                                CLFMYD (IN ISOFORM B).
FT   VARSPLIC    870   1051       PYPSQSTSPVESSTTPSPGSPGTTLTSTSPSPSQSTTIGST
FT                                QGSTSPGISTTSEEMTSQGSTQTPGSTGSTVTQPSTVSDST
FT                                SSGSTVTVGSTEGSSSPIPSTSQNTNPSTSSGSSMSTQTPQ
FT                                SSQSTSPVESSTSGATSSSGSPGTTLTSISPSPSPSSTIGS
FT                                SQGSTSPVVSTISQGSTE -> KEIDQTAINTYKTYFNFAL
FT                                LVASKLNNESILTGYIDNFGYSAGLNDHQYYPTDDYNGIKS
FT                                VPFPIDGTDDDIDLDLKDVDKSLATADWTPPVADQTCMIFI
FT                                SAAPEDEYGGTTIKSTYTYFETVVGVLVGGAKSIPGLSIDK
FT                                NIVITNNTMNDRDASAVVSKLLELLPTA (IN ISOFORM
FT                                B).
SQ   SEQUENCE   2232 AA;  213840 MW;  08D69FA638E14CC8 CRC64;
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```
  Query Match             78.0%;  Score 39;  DB 5;  Length 2232;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db     886 SPGSPGT 892
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RESULT  17
Q95TC5
ID   Q95TC5      PRELIMINARY;      PRT;  280 AA.
AC   Q95TC5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   GH02414P.
GN   CG3960.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Y, CN BW SP;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA   Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA   Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA   Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY060231; AAL25270.1; -.
SQ   SEQUENCE   280 AA;  29901 MW;  571CBAAE823B3BE2 CRC64;
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  Query Match             76.0%;  Score 38;  DB 5;  Length 280;
  Best Local Similarity   75.0%;  Pred. No. 38;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           |: |||||
Db     125 YNQPGSPG 132
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RESULT  18
Q63422
ID   Q63422      PRELIMINARY;      PRT;  453 AA.
AC   Q63422;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PROTON-DEPENDENT PEPTIDE TRANSPORTER (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=SMALL INTESTINE;
RX   MEDLINE=96067558; PubMed=7488096;
RA   Erickson R.H., Gum J.R. Jr., Lindstrom M.M., McKean D., Kim Y.S.;
RT   "Regional expression and dietary regulation of rat small intestinal
RT   peptide and amino acid transporter mRNAs.";
RL   Biochem. Biophys. Res. Commun. 216:249-257(1995).
DR   EMBL; L46873; AAC42076.1; -.
DR   InterPro; IPR002637; Ham1p_like.
DR   InterPro; IPR000109; PTR2.
DR   Pfam; PF00854; PTR2; 1.
DR   PROSITE; PS01022; PTR2_1; 1.
DR   PROSITE; PS01023; PTR2_2; 1.
FT   NON_TER       1       1
FT   NON_TER     453     453
SQ   SEQUENCE   453 AA;  49905 MW;  0706EE059904B082 CRC64;
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```
  Query Match             76.0%;  Score 38;  DB 11;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
           |||||||
Db     420 SSPGSPG 426
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RESULT  19
Q974W1
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ID   Q974W1      PRELIMINARY;      PRT;   517 AA.
AC   Q974W1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL PROTEIN ST0549.
GN   ST0549.
OS   Sulfolobus tokodaii.
OC   Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX   NCBI_TaxID=111955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JCM 10545 / 7;
RX   PubMed=11572479;
RA   Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA   Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA   Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA   Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA   Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA   Oshima T., Kikuchi H.;
RT   "Complete genome sequence of an aerobic thermoacidophilic
RT   Crenarchaeon, Sulfolobus tokodaii strain7.";
RL   DNA Res. 8:123-140(2001).
DR   EMBL; AP000982; BAB65546.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   517 AA;  57965 MW;  E129448C73A27A24 CRC64;

  Query Match             76.0%;  Score 38;  DB 17;  Length 517;
  Best Local Similarity   66.7%;  Pred. No. 73;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |:|| :|||
Db     204 YASPSTPGT 212


RESULT  20
Q9U5M3
ID   Q9U5M3      PRELIMINARY;      PRT;   711 AA.
AC   Q9U5M3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PAIRED BOX PROTEIN.
GN   PAX-B.
OS   Podocoryne carnea.
OC   Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC   Hydractiniidae; Podocoryne.
OX   NCBI_TaxID=6096;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20302558; PubMed=10842067;
RA   Groeger H., Callaerts P., Gehring W.J., Schmid V.;
RT   "Characterization and expression analysis of an ancestor-type Pax gene
RT   in the hydrozoan jellyfish Podocoryne carnea.";
RL   Mech. Dev. 94:157-169(2000).
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
CC   -!- SIMILARITY: WITH OTHER HOMEOBOX PROTEINS.
DR   EMBL; AJ249563; CAB61522.1; -.
DR   HSSP; P26367; 6PAX.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR001523; Paired_box.
DR   Pfam; PF00046; homeobox; 1.
DR   Pfam; PF00292; PAX; 1.
DR   PRINTS; PR00027; PAIREDBOX.
DR   SMART; SM00389; HOX; 1.
DR   SMART; SM00351; PAX; 1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
DR   PROSITE; PS00034; PAIRED_BOX; 1.
KW   DNA-binding; Developmental protein; Homeobox; Nuclear protein;
KW   Paired box; Transcription regulation.
SQ   SEQUENCE   711 AA;  79326 MW;  AC1D9099E25249B1 CRC64;

  Query Match             76.0%;  Score 38;  DB 5;  Length 711;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
             |||||||
Db     211 SSPGSPG 217


RESULT  21
Q961G7
ID   Q961G7      PRELIMINARY;      PRT;  1019 AA.
AC   Q961G7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   GH23906P.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Y, CN BW SP;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA   Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA   Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA   Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY051598; AAK93022.1; -.
SQ   SEQUENCE   1019 AA;  112156 MW;  207885C035945EAF CRC64;

  Query Match             76.0%;  Score 38;  DB 5;  Length 1019;
  Best Local Similarity   75.0%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           |: |||||
Db     864 YNQPGSPG 871


RESULT  22
Q54437
ID   Q54437      PRELIMINARY;      PRT;  1345 AA.
AC   Q54437;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   STABLE PROTEASE PRECURSOR.
OS   Staphylothermus marinus.
OC   Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC   Staphylothermus.
OX   NCBI_TaxID=2280;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=F1;
RX   MEDLINE=95139068; PubMed=7837271;
RA   Peters J., Nitsch M., Kuhlmorgen B., Golbik R., Lupas A.,
RA   Kellermann J., Engelhardt H., Pfander J.-P., Muller S., Goldie K.,
RA   Engel A., Stetter K.-O., Baumeister W.;
RT   "Tetrabrachion: a filamentous archaebacterial surface protein assembly
RT   of unusual structure and extreme stability.";
RL   J. Mol. Biol. 245:385-401(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=F1;
```

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RA   Mayr J., Lupas A., Kellermann J., Eckerskorn C., Baumeister W.,
RA   Peters J.;
RT   "A hyperthermostable protease of the subtilisin family bound to the
RT   surface layer of the archaeon Staphylothermus marinus.";
RL   Curr. Biol. 0:0-0(1996).
DR   EMBL; U57968; AAB02323.1; -.
DR   MEROPS; S08.096; -.
DR   InterPro; IPR000209; Peptidase_S8.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00082; Peptidase_S8; 3.
DR   PRINTS; PR00723; SUBTILISIN.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
DR   PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
DR   PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.
KW   Signal; Protease.
FT   SIGNAL        1     24       POTENTIAL.
SQ   SEQUENCE   1345 AA;  148446 MW;  D40878E437A52EC3 CRC64;


  Query Match             76.0%;  Score 38;  DB 1;  Length 1345;
  Best Local Similarity   77.8%;  Pred. No. 2e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
             ||| |:|||
Db     596 YSSNGAPGT 604


RESULT  23
O17289
ID   O17289      PRELIMINARY;      PRT;   168 AA.
AC   O17289;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 18.6 KDA PROTEIN.
GN   R52.4.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Du Z., Goela D., Ozersky P.;
RT   "The sequence of C. elegans cosmid R52.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RT   "Direct Submission.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF025471; AAB71062.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   168 AA;  18604 MW;  4D72C56A94F38F88 CRC64;


  Query Match             74.0%;  Score 37;  DB 5;  Length 168;
  Best Local Similarity   75.0%;  Pred. No. 34;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ::|||||
Db      40 TTPGSPGT 47


RESULT  24
Q9H4T5
ID   Q9H4T5      PRELIMINARY;      PRT;   238 AA.
AC   Q9H4T5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BA93B14.3 (NEUROTENSIN RECEPTOR 1 (HIGH AFFINITY)(NTR))
DE   (FRAGMENT).
GN   NTSR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Heath P.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL357033; CAC14923.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
FT   NON_TER     238    238
SQ   SEQUENCE   238 AA;  25503 MW;  258BE57EACCF6EF0 CRC64;


  Query Match             74.0%;  Score 37;  DB 4;  Length 238;
  Best Local Similarity   75.0%;  Pred. No. 49;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           |:||:|||
Db       6 SAPGTPGT 13


RESULT  25
O43060
ID   O43060      PRELIMINARY;      PRT;   302 AA.
AC   O43060;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   HYPOTHETICAL 33.3 KDA PROTEIN C4C3.07 IN CHROMOSOME II.
GN   SPBC4C3.07.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Wood V., Rajandream M.A., Barrell B.G., Lauber J., Hilbert H.,
RA   Duesterhoeft A.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO PROTEASOME REGULATORY SUBUNIT S12/MOV-34.
DR   EMBL; AL021730; CAA16829.1; -.
DR   InterPro; IPR000555; Mov34.
DR   InterPro; IPR003640; Mov34_2.
DR   Pfam; PF01398; Mov34; 1.
DR   ProDom; PD005425; Mov34_2; 1.
DR   SMART; SM00232; JAB_MPN; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   302 AA;  33251 MW;  A046E087CF083D84 CRC64;


  Query Match             74.0%;  Score 37;  DB 3;  Length 302;
  Best Local Similarity   66.7%;  Pred. No. 63;
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Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 YSSPGSPGT 9
          |:||  |||
Db    123 YASPAEPGT 131
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RESULT  26
Q15469
ID   Q15469      PRELIMINARY;      PRT;   333 AA.
AC   Q15469;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SOLUBLE INTERLEUKIN-5  RECEPTOR PRECURSOR.
GN   HSIL5R4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL BLOOD;
RX   MEDLINE=92121815; PubMed=1732409;
RA   Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT   "Molecular cloning and expression of the human interleukin 5
RT   receptor.";
RL   J. Exp. Med. 175:341-351(1992).
DR   EMBL; X62156; CAA44081.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003532; Hematopo_receptor_S_F2.
DR   PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW   Signal; Receptor.
FT   SIGNAL       1     20       POTENTIAL.
FT   CHAIN       21    333       SOLUBLE INTERLEUKIN-5  RECEPTOR.
SQ   SEQUENCE   333 AA;  37722 MW;  8D9239845E16985B CRC64;
```

Query Match 74.0%; Score 37; DB 4; Length 333;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 YSSPGSPGT 9
          :: ||||||
Db    119 HAPPGSPGT 127
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RESULT  27
Q9D2V9
ID   Q9D2V9      PRELIMINARY;      PRT;   387 AA.
AC   Q9D2V9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   0610009M14RIK PROTEIN.
GN   0610009M14RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK018735; BAB31377.1; -.
DR   HSSP; P80220; 1DIP.
DR   MGD; MGI:1926079; 0610009M14Rik.
DR   InterPro; IPR000580; TSC-22_Dip_Bun.
DR   Pfam; PF01166; TSC22; 1.
DR   ProDom; PD007152; TSC-22_Dip_Bun; 1.
DR   PROSITE; PS01289; TSC22; 1.
SQ   SEQUENCE   387 AA;  39978 MW;  D4160FA3AB2DFB90 CRC64;
```

Query Match 74.0%; Score 37; DB 11; Length 387;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 YSSPGSPG 8
          |  |||||
Db     19 YEGPGSPG 26
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```
RESULT  28
Q99PD5
ID   Q99PD5      PRELIMINARY;      PRT;   387 AA.
AC   Q99PD5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   LEUCINE ZIPPER PROTEIN THG-1PIT.
GN   0610009M14RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Fiorenza M.T., Mukhopdhyay M., Westphal H.;
RT   "Thg-1pit, a putative Lhx3 target gene.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF315352; AAK02018.1; -.
DR   HSSP; P80220; 1DIP.
DR   MGD; MGI:1926079; 0610009M14Rik.
DR   InterPro; IPR000580; TSC-22_Dip_Bun.
DR   Pfam; PF01166; TSC22; 1.
DR   ProDom; PD007152; TSC-22_Dip_Bun; 1.
DR   PROSITE; PS01289; TSC22; 1.
SQ   SEQUENCE   387 AA;  39908 MW;  D047B988643CE237 CRC64;
```

Query Match 74.0%; Score 37; DB 11; Length 387;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 YSSPGSPG 8
          |  |||||
Db     19 YEGPGSPG 26
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RESULT  29
Q99147
ID   Q99147      PRELIMINARY;      PRT;   393 AA.
AC   Q99147;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
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DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TITIN (FRAGMENT).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NEW ZEALAND WHITE; TISSUE=HEART;
RX   MEDLINE=91305130; PubMed=1712941;
RA   Fritz J.D., Greaser M.L., Wolff J.;
RT   "A novel 3' Extension Technique using Random Primers in RNA-PCR.";
RL   Nucleic Acids Res. 19:3747-3747(1991).
DR   EMBL; X59596; CAA42165.1; -.
DR   InterPro; IPR003962; FnIII_repeat.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00041; fn3; 2.
DR   PRINTS; PR00014; FNTYPEIII.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00410; IG_like; 1.
KW   Repeat.
FT   NON_TER       1      1
FT   NON_TER     393    393
SQ   SEQUENCE   393 AA;  43475 MW;  0672492F4091CBE7 CRC64;


  Query Match             74.0%;  Score 37;  DB 6;  Length 393;
  Best Local Similarity   66.7%;  Pred. No. 83;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |  || |||
Db      55 YKEPGPPGT 63


RESULT  30
Q14631
ID   Q14631      PRELIMINARY;      PRT;   396 AA.
AC   Q14631;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-5 RECEPTOR  TYPE 2 PRECURSOR.
GN   HSIL5R2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL BLOOD;
RX   MEDLINE=92121815; PubMed=1732409;
RA   Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT   "Molecular cloning and expression of the human interleukin 5
RT   receptor.";
RL   J. Exp. Med. 175:341-351(1992).
DR   EMBL; X61177; CAA43484.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003532; Hematopo_receptor_S_F2.
DR   PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW   Signal; Receptor.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    396       INTERLEUKIN-5 RECEPTOR  TYPE 2.
SQ   SEQUENCE   396 AA;  44998 MW;  1AB60619842ACDA5 CRC64;


  Query Match             74.0%;  Score 37;  DB 4;  Length 396;
  Best Local Similarity   66.7%;  Pred. No. 83;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 HAPPGSPGT 127


RESULT  31
O74658
ID   O74658      PRELIMINARY;      PRT;   406 AA.
AC   O74658;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AGGLUTININ-LIKE PROTEIN (FRAGMENT).
GN   ALS2.
OS   Candida albicans (Yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=5476;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1161;
RX   MEDLINE=98440424; PubMed=9765564;
RA   Hoyer L.L., Payne T.L., Hecht J.E.;
RT   "Identification of Candida albicans ALS2 and ALS4 and localization of
RT   als proteins to the fungal cell surface.";
RL   J. Bacteriol. 180:5334-5343(1998).
DR   EMBL; AF024581; AAC64236.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   406 AA;  40585 MW;  9A6C92C1B2A93A81 CRC64;


  Query Match             74.0%;  Score 37;  DB 3;  Length 406;
  Best Local Similarity   75.0%;  Pred. No. 86;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           |:||:|||
Db     189 SNPGAPGT 196


RESULT  32
Q9URP9
ID   Q9URP9      PRELIMINARY;      PRT;   406 AA.
AC   Q9URP9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   AGGLUTININ-LIKE PROTEIN (FRAGMENT).
GN   ALS4.
OS   Candida albicans (Yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=5476;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1161;
RX   MEDLINE=98440424; PubMed=9765564;
RA   Hoyer L.L., Payne T.L., Hecht J.E.;
RT   "Identification of Candida albicans ALS2 and ALS4 and localization of
RT   als proteins to the fungal cell surface.";
RL   J. Bacteriol. 180:5334-5343(1998).
DR   EMBL; AF024585; AAC64240.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   406 AA;  40592 MW;  E0117B4CE4ECB4C3 CRC64;


  Query Match             74.0%;  Score 37;  DB 3;  Length 406;
  Best Local Similarity   75.0%;  Pred. No. 86;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           |:||:|||
Db     189 SNPGAPGT 196
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RESULT  33
O74661
ID   O74661      PRELIMINARY;      PRT;   407 AA.
AC   O74661;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AGGLUTININ-LIKE PROTEIN (FRAGMENT).
GN   ALS4.
OS   Candida albicans (Yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=5476;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1161;
RX   MEDLINE=98440424; PubMed=9765564;
RA   Hoyer L.L., Payne T.L., Hecht J.E.;
RT   "Identification of Candida albicans ALS2 and ALS4 and localization of
RT   als proteins to the fungal cell surface.";
RL   J. Bacteriol. 180:5334-5343(1998).
DR   EMBL; AF024587; AAC64242.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   407 AA;  40649 MW;  FC846B7A1640CF44 CRC64;

  Query Match             74.0%;  Score 37;  DB 3;  Length 407;
  Best Local Similarity   75.0%;  Pred. No. 86;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           |:||:|||
Db     189 SNPGAPGT 196


RESULT  34
Q14633
ID   Q14633      PRELIMINARY;      PRT;   420 AA.
AC   Q14633;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-5 RECEPTOR  PRECURSOR.
GN   HSIL5R.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL BLOOD;
RX   MEDLINE=92121815; PubMed=1732409;
RA   Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT   "Molecular cloning and expression of the human interleukin 5
RT   receptor.";
RL   J. Exp. Med. 175:341-351(1992).
DR   EMBL; X61176; CAA43483.1; -.
DR   InterPro; IPR002996; CRIA.
DR   InterPro; IPR003532; Hematopo_receptor_S_F2.
DR   PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW   Signal; Receptor.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    420       INTERLEUKIN-5 RECEPTOR.
SQ   SEQUENCE   420 AA;  47670 MW;  8DC56DFC8BEFF524 CRC64;

  Query Match             74.0%;  Score 37;  DB 4;  Length 420;
  Best Local Similarity   66.7%;  Pred. No. 89;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
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Db     119 HAPPGSPGT 127


RESULT  35
O95196
ID   O95196      PRELIMINARY;      PRT;   539 AA.
AC   O95196;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   NEUROGLYCAN C.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=99133557; PubMed=9950058;
RA   Yasuda Y., Tokita Y., Aono S., Matsui F., Ono T., Sonta S.,
RA   Watanabe E., Nakanishi Y., Oohira A.;
RT   "Cloning and chromosomal mapping of the human gene of neuroglycan C
RT   (NGC), a neural transmembrane chondroitin sulfate proteoglycan with an
RT   EGF module.";
RL   Neurosci. Res. 32:313-322(1998).
DR   EMBL; AF059274; AAC69612.1; -.
DR   InterPro; IPR000561; EGF-like.
DR   SMART; SM00181; EGF; 1.
SQ   SEQUENCE   539 AA;  57024 MW;  5B22E9E8DE34290E CRC64;

  Query Match             74.0%;  Score 37;  DB 4;  Length 539;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           | ||||||
Db     227 SFPGSPGT 234


RESULT  36
Q9QY32
ID   Q9QY32      PRELIMINARY;      PRT;   539 AA.
AC   Q9QY32;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   NEUROGLYCAN C.
GN   CSPG5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BLACK/6; TISSUE=BRAIN;
RX   MEDLINE=20085050; PubMed=10617623;
RA   Aono S., Keino H., Ono T., Yasuda Y., Tokita Y., Matsui F.,
RA   Taniguchi M., Sonta S.-I., Oohira A.;
RT   "Genomic Organization and Expression Pattern of Mouse Neuroglycan C in
RT   the Cerebellar Development.";
RL   J. Biol. Chem. 275:337-342(2000).
DR   EMBL; AF133700; AAF23362.1; -.
DR   MGD; MGI:1352747; Cspg5.
DR   InterPro; IPR000561; EGF-like.
DR   SMART; SM00181; EGF; 1.
SQ   SEQUENCE   539 AA;  57352 MW;  7D566881555460ED CRC64;

  Query Match             74.0%;  Score 37;  DB 11;  Length 539;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       2 SSPGSPGT 9
            | ||||||
Db     228 SFPGSPGT 235


RESULT  37
Q01106
ID   Q01106      PRELIMINARY;      PRT;   541 AA.
AC   Q01106;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TITIN (FRAGMENT).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART MUSCLE;
RX   MEDLINE=92258380; PubMed=1582406;
RA   Labeit S., Gautel M., Lakey A., Trinick J.;
RT   "Towards a molecular understanding of titin.";
RL   EMBO J. 11:1711-1716(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART MUSCLE;
RA   Fritz J.D., Greaser M.L., Wolff J.;
RT   "A novel 3' extension method using random primers.";
RL   Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; M98338; AAA31480.1; -.
DR   InterPro; IPR003962; FnIII_repeat.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00041; fn3; 4.
DR   PRINTS; PR00014; FNTYPEIII.
DR   SMART; SM00060; FN3; 4.
DR   SMART; SM00409; IG; 1.
KW   Repeat.
FT   NON_TER       1       1
SQ   SEQUENCE   541 AA;  60088 MW;  0DAA2541E1318B99 CRC64;


  Query Match             74.0%;  Score 37;  DB 6;  Length 541;
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Qy       1 YSSPGSPGT 9
            |  || |||
Db      55 YKEPGPPGT 63


RESULT  38
Q9D677
ID   Q9D677      PRELIMINARY;      PRT;   723 AA.
AC   Q9D677;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   4632412M04RIK PROTEIN.
GN   4632412M04RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=SKIN;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
DR   EMBL; AK014569; BAB29434.1; -.
DR   HSSP; P49799; 1AGR.
DR   MGD; MGI:1924302; 4632412M04Rik.
DR   InterPro; IPR003109; GoLoco.
DR   InterPro; IPR003116; RBD.
DR   InterPro; IPR000342; RGS.
DR   Pfam; PF02188; GoLoco; 1.
DR   Pfam; PF02196; RBD; 2.
DR   Pfam; PF00615; RGS; 1.
DR   PRINTS; PR01301; RGSPROTEIN.
DR   ProDom; PD001580; RGS; 1.
DR   SMART; SM00390; GoLoco; 1.
DR   SMART; SM00455; RBD; 2.
DR   SMART; SM00315; RGS; 1.
DR   PROSITE; PS50132; RGS; 1.
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  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

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            :|:|| |||
Db     632 HSTPGPPGT 640


RESULT  39
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ID   O75112      PRELIMINARY;      PRT;   734 AA.
AC   O75112;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   KIAA0613 PROTEIN (FRAGMENT).
GN   KIAA0613.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=98403880; PubMed=9734811;
RA   Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA   Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. X.
RT   The complete sequences of 100 new cDNA clones from brain which can
RT   code for large proteins in vitro.";
RL   DNA Res. 5:169-176(1998).
CC   -!- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC       IONS.
DR   EMBL; AB014513; BAA31588.1; -.
DR   HSSP; Q05158; 1QLI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001781; LIM.
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DR   InterPro; IPR001478; PDZ.
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DR   Pfam; PF00412; LIM; 3.
DR   Pfam; PF00595; PDZ; 1.
DR   PRINTS; PR01217; PRICHEXTENSN.
DR   ProDom; PD000094; LIM; 3.
DR   SMART; SM00132; LIM; 3.
DR   SMART; SM00228; PDZ; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR   PROSITE; PS50023; LIM_DOMAIN_2; 3.
DR   PROSITE; PS50106; PDZ; 1.
KW   LIM domain; Metal-binding; Zinc.
FT   NON_TER       1       1
SQ   SEQUENCE   734 AA;  77738 MW;  5CB9AC39CC690FB8 CRC64;


  Query Match             74.0%;  Score 37;  DB 4;  Length 734;
  Best Local Similarity   75.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            :|||:|||
Db     135 ASPGTPGT 142


RESULT  40
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ID   Q9CW54       PRELIMINARY;       PRT;   742 AA.
AC   Q9CW54;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   1200016K18RIK PROTEIN (FRAGMENT).
GN   1200016K18RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=LUNG;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
DR   EMBL; AK004813; BAB23584.1; -.
DR   HSSP; P49799; 1AGR.
DR   MGD; MGI:1918979; 1200016K18Rik.
DR   InterPro; IPR000634; dehydrtse_ser_thr.
DR   InterPro; IPR003109; GoLoco.
DR   InterPro; IPR003116; RBD.
DR   InterPro; IPR000342; RGS.
DR   Pfam; PF02188; GoLoco; 1.
DR   Pfam; PF02196; RBD; 2.
DR   Pfam; PF00615; RGS; 1.
DR   PRINTS; PR01301; RGSPROTEIN.
DR   ProDom; PD001580; RGS; 1.
DR   SMART; SM00390; GoLoco; 1.
DR   SMART; SM00455; RBD; 2.
DR   SMART; SM00315; RGS; 1.
DR   PROSITE; PS00165; DEHYDRATASE_SER_THR; UNKNOWN_1.
DR   PROSITE; PS50132; RGS; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   742 AA;  80828 MW;  ACAFE5225ECBE74D CRC64;


  Query Match             74.0%;  Score 37;  DB 11;  Length 742;
  Best Local Similarity   66.7%;  Pred. No. 1.6e+02;
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Qy       1 YSSPGSPGT 9
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Db     651 HSTPGPPGT 659


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Job time: 341 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 21, 2002, 11:18:07 ; Search time 51.55 Seconds
(without alignments)
19.392 Million cell updates/sec

Title: US-09-734-281-2
Perfect score: 50
Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	9	14	AAR36557	Peptide sequence f
2	50	100.0	12	14	AAR38235	Alzheimer paired h
3	50	100.0	12	14	AAR37554	Phosphorylated tau
4	50	100.0	12	18	AAW34857	Human tau protein
5	50	100.0	12	21	AAY81390	Human phosphorylat
6	50	100.0	14	21	AAB21959	Phosphorylated tau
7	50	100.0	34	15	AAR61330	Peptide phosphoryl
8	50	100.0	34	18	AAW34875	Human tau protein
9	50	100.0	67	15	AAR59837	Sequence of human
10	50	100.0	78	22	AAB85640	Tau peptide region
11	50	100.0	106	17	AAR92516	Microtubule-associ
12	50	100.0	112	16	AAR76937	PHF-tau (143-254)
13	50	100.0	351	21	AAY15200	Human Tau protein.
14	50	100.0	352	10	AAP91294	Paired helical fil
15	50	100.0	352	14	AAR32708	Human tau-protein.
16	50	100.0	352	19	AAY20248	Human microtubule
17	50	100.0	390	17	AAW05283	Truncated human ta
18	50	100.0	441	15	AAR58810	Human tau protein.
19	50	100.0	441	17	AAW05282	Human tau protein.
20	50	100.0	441	18	AAW34856	Human tau protein.
21	50	100.0	441	21	AAY81386	Human paired helic
22	43	86.0	13	13	AAR28237	Phosphopeptide as
23	43	86.0	13	18	AAW34860	Human tau protein
24	43	86.0	13	18	AAW34858	Human tau protein
25	40	80.0	263	18	AAW29455	Oerskovia xanthine
26	40	80.0	435	18	AAW29456	Oerskovia xanthine
27	39	78.0	7	14	AAR38233	Alzheimer paired h
28	39	78.0	7	14	AAR37552	Phosphorylated tau
29	39	78.0	263	22	AAU17141	Novel signal trans
30	39	78.0	376	22	AAM80057	Human protein SEQ
31	39	78.0	424	21	AAB41838	Human ORFX ORF1602
32	39	78.0	424	22	AAM79073	Human protein SEQ
33	39	78.0	424	22	AAB27227	Human EXMAD-5 SEQ
34	38	76.0	98	22	AAO05662	Human polypeptide
35	37	74.0	284	22	ABG27348	Novel human diagno
36	37	74.0	335	13	AAR25063	Soluble human IL-5
37	37	74.0	335	14	AAR33699	shIL-5R-alpha. Sy
38	37	74.0	350	22	AAM93217	Human polypeptide,
39	37	74.0	351	22	AAM52310	Chicken zyxine fra
40	37	74.0	353	13	AAR28314	AHSV protein. Afr
41	37	74.0	395	22	AAM39380	Human polypeptide
42	37	74.0	396	13	AAR22216	Sequence of human
43	37	74.0	396	13	AAR22220	Sequence of secret
44	37	74.0	418	17	AAR98562	Human neurotensin
45	37	74.0	418	22	ABB56371	Non-endogenous hum
46	37	74.0	420	13	AAR22215	Sequence of human
47	37	74.0	420	13	AAR22219	Sequence of secret
48	37	74.0	420	19	AAW82842	Human interleukin-
49	37	74.0	421	13	AAR25064	Human IL-5 recepto
50	37	74.0	464	22	AAM93631	Human polypeptide,
51	37	74.0	494	22	AAM41166	Human polypeptide
52	37	74.0	539	21	AAY87747	Human brain proteo
53	37	74.0	542	22	ABG12316	Novel human diagno
54	37	74.0	542	22	AAM52304	Chicken zyxine. G
55	37	74.0	545	18	AAW28867	Human brain Neurog

ALIGNMENTS

RESULT 1
AAR36557
ID AAR36557 standard; peptide; 9 AA.
XX
AC AAR36557;
XX
DT 10-AUG-1993 (first entry)
XX
DE Peptide sequence for abnormally phosphorylated tau protein.
XX
KW Alzheimer's disease; Down's syndrome; Pick's disease; monoclonal;
KW antibody; detection; SSPE; antigen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 3
FT /note= "may be phoshorylated"
FT Misc-difference 6
FT /note= "may be phosphorylated"
XX
PN WO9308302-A.
XX
PD 29-APR-1993.

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XX
PF   17-OCT-1992;   92WO-EP02392.
XX
PR   25-OCT-1991;   91EP-0402871.
XX
PA   (INNO-) INNOGENETICS NV SA.
XX
PI   Mandelkow E,  Mercken M,  Van DE VOORDE A,  Vandermeeren M;
PI   Vanmechelen E;
XX
DR   WPI; 1993-152493/18.
XX
PT   Monoclonal antibodies binding abnormal micro-tubule-associated
PT   tau-protein - for diagnosing neurological disorders e.g.
PT   Alzheimer's disease, Downs syndrome, Picks disease, etc.
XX
PS   Claim 8; Page 36; 47pp; English.
XX
CC   The peptide is able to form an immunogenic complex with a
CC   monoclonal antibody contg. a phosphorylated epitope of an antigen
CC   belonging to human abnormally phosphorylated tau protein which can be
CC   obtd. from a brain homogenate isolated from the cerebral cortex of a
CC   patient having Alzheimer's disease.  The monoclonal antibody is able
CC   to specifically detect only abnormally phosphorylated tau protein and
CC   not react with normal tau protein, and thus may be used in the detection
CC   or diagnosis of neurological diseases, e.g. Alzheimer's disease, Down's
CC   syndrome, Pick's disease or SSPE.
CC   See also AAR36556.
XX
SQ   Sequence   9 AA;

  Query Match             100.0%;  Score 50;  DB 14;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db       1 ysspgspgt 9


RESULT   2
AAR38235
ID   AAR38235 standard; peptide; 12 AA.
XX
AC   AAR38235;
XX
DT   08-OCT-1993  (first entry)
XX
DE   Alzheimer paired helical filament tau protein epitope 197-208.
XX
KW   Alzheimer tau protein; phosphorylation-dependent; PHF;
KW   neuronal microtubule; mitogen activated protein kinase; MAP kinase.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site    3..4
FT                    /label= Phosphorylation_motif
FT   Modified-site    6..7
FT                    /label= Phosphorylation_motif
FT   Modified-site    9..10
FT                    /label= Phosphorylation_motif
XX
PN   WO9311231-A.
XX
PD   10-JUN-1993.
XX
PF   07-DEC-1992;   92WO-EP02829.
XX
PR   06-DEC-1991;   91EP-0120974.
PR   16-NOV-1992;   92EP-0119551.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Biernat J,  Drewes G,  Lichtenberg-Kraag B,  Mandelkow E;
PI   Steiner B;
XX
DR   WPI; 1993-197050/24.
XX
PT   Tau protein epitope(s), specific antibodies and protein kinase(s)
PT   - used in the prevention, diagnosis and treatment of Alzheimer's
PT   disease
XX
PS   Claim 5; Page 89; 148pp; English.
XX
CC   This is one of 26 preferred epitopes which occur in a phosphorylated
CC   state in tau protein from Alzheimer paired helical filaments. The
CC   epitopes all include phosphorylatable serine residues in Ser-Pro
CC   motifs, Ile-Gly-Ser motifs or Cys-Gly-Ser motifs and/or
CC   phosphorylatable threonine residues in Thr-Pro motifs. The pattern
CC   of tau protein phosphorylation differs between Alzheimer's and
CC   non-Alzheimer's individuals. Knowledge of the phosphorylated
CC   epitopes and antibodies which recognise them may be useful in
CC   diagnosis, treatment and prevention of Alzheimer's Disease. The
CC   protein kinases present in mammalian brain which phosphorylate the
CC   different epitopes are also claimed but no sequences are given.
XX
SQ   Sequence   12 AA;

  Query Match             100.0%;  Score 50;  DB 14;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db       1 ysspgspgt 9


RESULT   3
AAR37554
ID   AAR37554 standard; peptide; 12 AA.
XX
AC   AAR37554;
XX
DT   07-OCT-1993  (first entry)
XX
DE   Phosphorylated tau protein epitope.
XX
KW   Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
KW   treatment; formation; inhibition; inhibitor.
XX
OS   Homo sapiens.
XX
PN   EP544942-A.
XX
PD   09-JUN-1993.
XX
PF   06-DEC-1991;   91EP-0120974.
XX
PR   06-DEC-1991;   91EP-0120974.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Biernat J,  Drewes G,  Lichtenberg-Kraag B,  Mandelkow EM,  Steiner B;
XX
DR   WPI; 1993-183841/23.
XX
PT   Phosphorylated tau protein epitope associated with Alzheimer's
PT   disease - is used as protein kinase inhibitor for treatment and
PT   diagnosis
XX
PS   Claim 4; Page 16; 34pp; English.
XX
CC   The sequence is that of an epitope of tau protein which specifically
```

```
CC   occurs in a phosphorylated state in tau protein from Alzheimer's
CC   paired helical fragments. It may be used as part of a method for the
CC   in vitro diagnosis and/or monitoring of Alzheimer disease. It may
CC   also be used in an in vitro model for the study of the generation of
CC   the Alzheimer state of proteins and the testing of substances which
CC   prevent the conversion of normal to Alzheimer tau protein. The
CC   epitope occurs at residues 197-208 of human tau protein.
XX
SQ   Sequence   12 AA;


  Query Match             100.0%;  Score 50;  DB 14;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          |||||||||
Db      1 ysspgspgt 9


RESULT   4
AAW34857
ID   AAW34857 standard; peptide; 12 AA.
XX
AC   AAW34857;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Human tau protein fragment.
XX
KW   Antibody; phosphorylated tau protein; paired helical filament;
KW   detection; Alzheimer's disease; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   6
FT                   /note= "phosphoserine"
XX
PN   WO9734145-A1.
XX
PD   18-SEP-1997.
XX
PF   13-MAR-1997;   97WO-JP00804.
XX
PR   13-MAR-1996;   96JP-0056090.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
PI   Imahori K,  Ishiguro K,  Park J,  Sato K,  Uchida T;
XX
DR   WPI; 1997-470978/43.
XX
PT   Antibody prepared using a partial peptide containing part of
PT   phosphorylated tau protein - used for detecting Alzheimer's disease
XX
PS   Example; Page 28; 48pp; Japanese.
XX
CC   An antibody, prepared using a partial peptide containing the
CC   phosphorylated residue of the phosphorylated tau protein, e.g. the
CC   present sequence, in a paired helical filament, can be used to
CC   detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC   protein in brain extracts or tissue fragments.
XX
SQ   Sequence   12 AA;


  Query Match             100.0%;  Score 50;  DB 18;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          |||||||||
Db      4 ysspgspgt 12


RESULT   5
AAY81390
ID   AAY81390 standard; protein; 12 AA.
XX
AC   AAY81390;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Human phosphorylated tau protein derived peptide fragment, PS199.
XX
KW   Phosphorylated tau protein; human; paired helical filament; fragment;
KW   polyclonal antibody; Alzheimer's disease; cerebrospinal fluid; CSF;
KW   diagnosis; detection.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   6
FT                   /note= "Phosphorylated"
XX
PN   JP2000034300-A.
XX
PD   02-FEB-2000.
XX
PF   17-JUL-1998;   98JP-0204040.
XX
PR   17-JUL-1998;   98JP-0204040.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
DR   WPI; 2000-285529/25.
XX
PT   Anti-phosphated tau protein antibody - for the detection of Alzheimer
PT   disease
XX
PS   Claim 4; Page 4; 12pp; Japanese.
XX
CC   The invention relates to an antibody against a phosphorylated tau
CC   protein (AAY81386), which is a component of the paired helical filament
CC   found in the plaques associated with Alzheimer's disease. A
CC   phosphorylated tau protein fragment selected from peptides
CC   AAY81387-Y81390 is conjugated to keyhole limpet haemocyanin (KLH), and
CC   used to raise polyclonal antibodies in a rabbit. The antibodies of the
CC   invention are specific for phosphorylated tau protein and may be used to
CC   detect phosphorylated tau protein in the cerebrospinal fluid (CSF) of a
CC   patient suspected of having Alzheimer's disease. Use of the antibodies of
CC   the invention provides specific diagnosis of Alzheimer's disease.
CC   Sequences AAY81387-Y81390 represent phosphorylated peptides derived from
CC   tau protein used to raise anti-phosphorylated tau antibodies. The
CC   N-terminal residue is not part of the full-length tau protein, but
CC   facilitates KLH conjugation.
XX
SQ   Sequence   12 AA;


  Query Match             100.0%;  Score 50;  DB 21;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          |||||||||
Db      4 ysspgspgt 12


RESULT   6
AAB21959
ID   AAB21959 standard; Peptide; 14 AA.
XX
AC   AAB21959;
```

```
XX
DT   02-JAN-2001  (first entry)
XX
DE   Phosphorylated tau peptide #3.
XX
KW   WW-domain; protein-protein interaction; cell growth regulation;
KW   protein degradation regulation; Alzheimer's; Dementia pugilistica;
KW   Down's syndrome; Parkinson's disease; Pick's; neurodegenerative;
KW   microtubule assembly; hyperplasia; neoplasia; malignancy;
KW   psoriasis; retinosis; atherosclerosis; leukaemia; lymphoma; papiloma;
KW   pulmonary fibrosis; rhematoid arthritis; multiple sclerosis;
KW   muscular dystrophy; tau.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                   /note= "Phosphorylated residue"
XX
PN   WO200048621-A2.
XX
PD   24-AUG-2000.
XX
PF   18-FEB-2000; 2000WO-US04278.
XX
PR   18-FEB-1999;   99US-0252404.
XX
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI   Lu KP,  Zhou XZ;
XX
DR   WPI; 2000-594014/56.
XX
PT   Mediating protein-protein interactions, useful for regulating cell
PT   growth and for treating neurodegenerative disorders, comprises
PT   modulating binding of WW domain containing polypeptide with
PT   phosphorylated ligand -
XX
PS   Example 10; Page 45; 82pp; English.
XX
CC   The present invention relates to a method for mediating protein-protein
CC   interaction, which comprises modulating the binding of a WW-domain
CC   containing peptide with a phosphorylated ligand. WW-domains are highly
CC   conserved regions of approximately 40 amino acid residues with two
CC   invariant tryptophans (W) in a triple stranded beta-sheet. When a
CC   WW-domain containing peptide is phosphorylated at serine or threonine
CC   residues, dephosphorylation of ligands bound to the peptide is inhibited.
CC   WW-domain peptides may be useful for mediating protein-protein
CC   interaction, regulating cell growth, regulating protein degradation,
CC   restoring the function of tau to bind microtubules and promote or restore
CC   microtubule assembly in neurodegenerative diseases e.g. Alzheimer's,
CC   Dementia pugilistica, Down's syndrome, Parkinson's disease, Pick's
CC   disease, multiple sclerosis, muscular dystrophy, Corticobasal
CC   degeneration, Frontotemporal dementias, Myotonic dystrophy, Niemann-Pick
CC   disease, prion disease with tangles, progressive supranuclear palsy and
CC   subacute sclerosing panencephalistis. In addition, inhibitors or
CC   stimulators of interactions between WW-domains and ligands of the present
CC   invention can be used to treat hyperplastic and neoplastic disorders e.g.
CC   all forms of malignancies, psoriasis, retinosis, atherosclerosis
CC   resulting from plaque formation, leukaemias, benign tumour growth,
CC   lymphomas, papilomas, pulmonary fibrosis and rhematoid arthritis. The
CC   present sequence is a phosphorylated tau peptide. Tau is a WW-domain
CC   containing peptide ligand. This peptide was used to investigate the
CC   interactions between Tau and the WW-domain of Pin1 peptide. It was found
CC   that the Pin1 WW-domain mediates specific interactions between Pin1 and
CC   tau.
XX
SQ   Sequence   14 AA;

  Query Match             100.0%;  Score 50;  DB 21;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db       2 ysspgspgt 10


RESULT   7
AAR61330
ID   AAR61330 standard; Protein; 34 AA.
XX
AC   AAR61330;
XX
DT   24-APR-1995  (first entry)
XX
DE   Peptide phosphorylated by human tau-protein kinase.
XX
KW   Tau-protein kinase I enzyme; TPK-I; Phosphorylated peptide.
XX
OS   Synthetic.
XX
PN   EP616032-A.
XX
PD   21-SEP-1994.
XX
PF   01-MAR-1994;   94EP-0103057.
XX
PR   02-MAR-1993;   93JP-0041160.
PR   22-MAR-1993;   93JP-0085143.
PR   02-AUG-1993;   93JP-0191246.
XX
PA   (TAKA/) TAKASHIMA A.
PA   (MITU ) MITSUBISHI KASEI CORP.
XX
PI   Hoshino T,  Imahori K,  Saito K,  Sato S,  Shiratsuchi A;
PI   Takashima A;
XX
DR   WPI; 1994-287181/36.
XX
PT   Newly isolated tau-protein kinase I enzyme - with specificity for
PT   tau-protein providing means for prevention and treatment of
PT   Alzheimer's disease
XX
PS   Example 4; Page 25; 30pp; English.
XX
CC   AAR61330 is a peptide which has been phosphorylated by human
CC   tau-protein kinase (AAR61326).
XX
SQ   Sequence   34 AA;

  Query Match             100.0%;  Score 50;  DB 15;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db       7 ysspgspgt 15


RESULT   8
AAW34875
ID   AAW34875 standard; peptide; 34 AA.
XX
AC   AAW34875;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Human tau protein fragment.
XX
KW   Antibody; phosphorylated tau protein; paired helical filament;
KW   detection; Alzheimer's disease; human.
XX
OS   Homo sapiens.
```

XX
PN WO9734145-A1.
XX
PD 18-SEP-1997.
XX
PF 13-MAR-1997; 97WO-JP00804.
XX
PR 13-MAR-1996; 96JP-0056090.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
PI Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
XX
DR WPI; 1997-470978/43.
XX
PT Antibody prepared using a partial peptide containing part of
PT phosphorylated tau protein - used for detecting Alzheimer's disease
XX
PS Example; Pages 36-37; 48pp; Japanese.
XX
CC An antibody, prepared using a partial peptide containing the
CC phosphorylated residue of the phosphorylated tau protein, e.g. the
CC present sequence, in a paired helical filament, can be used to
CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC protein in brain extracts or tissue fragments.
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 50; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 7 yssPgspgt 15

RESULT 9
AAR59837
ID AAR59837 standard; peptide; 67 AA.
XX
AC AAR59837;
XX
DT 04-MAR-1995 (first entry)
XX
DE Sequence of human microtubule-associated protein tau.
XX
KW Tau protein; brain; cerebral cortex; hybridoma ECACC 92100853;
KW Alzheimer's disease; monoclonal antibody; paried helical filament.
XX
OS Homo sapiens.
XX
PN WO9413795-A.
XX
PD 23-JUN-1994.
XX
PF 10-DEC-1993; 93WO-EP03499.
XX
PR 14-DEC-1992; 92EP-0403403.
XX
PA (INNO-) INNOGENETICS NV SA.
XX
PI Mercken M, Van De Voorde A, Vandermeeren M, Vanmechelen E;
XX
DR WPI; 1994-234211/28.
XX
PT Monoclonal antibody reactive with tau protein - used to develop
PT prods. for detection of brain diseases involving tau or paired
PT helical filaments esp. Alzheimer's disease
XX
PS Claim 6; Page 38; 52pp; English.
XX
CC Paired helical filament (PHF) tau was partially purified from
CC postmortem tissue, consisting mostly of grey matter from the frontal
CC and temporal cortex obtd. from Anzheimer patients. The tissue (5-10g)
CC was homogenised with 10 vols of cold buffer (10mM Tris, 1mM EGTA,
CC 0.8M NaCl, 10% sucrose, pH 7.4). After centrifugation for 20 mins at
CC 4 degrees C, the supernatant was adjusted to 1% (wt/vol) N-
CC laurosylsarcosine and 1% (vol/vol) 2-mercaptoethanol and incubated
CC while rotating on a mixer for 2.5 hrs at 37 degrees C. The mixt. was
CC centrifuged at 108,000 g for 35 mins at 20 degrees C. The PHF-tau
CC contg. pellet was washed with PBS and resuspended in 1ml of the same
CC buffer. Hybridomas which produced MAbs reactive with tau protein
CC were obtd. from the spleen cells of Balb/C mice primed s.c. with
CC partially purified PHF. A MAb which forms an immunological complex
CC with a human tau protein of sequence in AAR59837 is secreted by the
CC hybridoma deposited at ECACC on Oct. 8 1992 under No. 92100853.
XX
SQ Sequence 67 AA;

Query Match 100.0%; Score 50; DB 15; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 43 yssPgspgt 51

RESULT 10
AAB85640
ID AAB85640 standard; peptide; 78 AA.
XX
AC AAB85640;
XX
DT 29-OCT-2001 (first entry)
XX
DE Tau peptide region (residues 155-232).
XX
KW Tauopathy; phospho-tau (181); neurological marker; monoclonal antibody;
KW HT7; AT270; nootropic; neuroprotective; cerobroprotective; epitope.
XX
OS Homo sapiens.
XX
PN WO200155725-A2.
XX
PD 02-AUG-2001.
XX
PF 18-JAN-2001; 2001WO-EP00560.
XX
PR 24-JAN-2000; 2000EP-0870008.
PR 27-JAN-2000; 2000US-0178391.
PR 22-NOV-2000; 2000EP-0870280.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Vanmechelen E, Vanderstichele H;
XX
DR WPI; 2001-476242/51.
XX
PT Determining the ratio of phospho-tau / total tau is useful for
PT diagnosing a tauopathy i.e. Alzheimer's disease or Pick's disease,
PT versus a non tauopathy -
XX
PS Example 1; Fig 1; 71pp; English.
XX
CC The invention provides a method of diagnosis of tauopathies in an
CC individual that comprises determining the ratio of phospho-tau (181)/
CC total tau. Tau and phospho tau are useful as neurological markers for the
CC manufacture of a diagnostic kit for the diagnosis of a tauopathy and/or
CC the differential diagnosis of a tauopathy versus a non tauopathy. A
CC phospho-peptide liable to form an immunological complex with monoclonal
CC antibody HT7 and MAb AT270 comprising at least the minimal epitope of HT7
CC or AT270 is useful to measure phospho-tau levels and diagnose a tauopathy

```
CC   and/or for the differential diagnosis of a tauopathy versus a non
CC   tauopathy. The kit is useful for the diagnosis of Alzheimer's disease,
CC   Pick's disease, sporadic Frontotemporal dementia and/or Frontotemporal
CC   dementia with Parkinsonism linked to chromosome 17, Creutzfeldt Jacob
CC   disease, stroke and/or neurotoxicity in patients with leukemia. The
CC   phosphopeptide kits and methods are useful for therapeutic monitoring and
CC   for determining the effectiveness of a treatment. The present sequence
CC   represents a tau peptide fragment.
XX
SQ   Sequence   78 AA;

  Query Match             100.0%;  Score 50;  DB 22;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db      43 yysspgspgt 51


RESULT  11
AAR92516
ID   AAR92516 standard; peptide; 106 AA.
XX
AC   AAR92516;
XX
DT   20-SEP-1996  (first entry)
XX
DE   Microtubule-associated tau protein epitope corresp. to pos. 146-251.
XX
KW   Epitope; microtubule-associated protein; tau; phosphorylation; subclass;
KW   paired helical fibre; neurofibrillary tangle; dementia; neurological;
KW   Alzheimer's disease; monoclonal antibody; brain; pathology.
XX
OS   Synthetic.
XX
PN   WO9604309-A1.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;   95WO-EP03032.
XX
PR   29-JUL-1994;   94EP-0870131.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Van DE VOORDE A,  Vanmechelen E;
XX
DR   WPI; 1996-129338/13.
XX
PT   Monoclonal antibodies specific for phosphorylated tau - for improved
PT   detection and diagnosis of e.g. Alzheimer's Disease
XX
PS   Claim 2; Page 32; 42pp; English.
XX
CC   This is the amino acid of an epitope derived from the microtubule-
CC   associated tau protein.  The phosphorylated subclass of tau protein
CC   from which this epitope originates, forms a major part of the paired
CC   helical fibres which make up neurofibrillary tangles seen in patients
CC   suffering from dementia e.g. Alzheimer's disease.  The epitope is esp.
CC   isolated from patients who have recently died from Alzheimer's disease.
CC   It is used to generate monoclonal antibodies for the in vitro detection
CC   or diagnosis of brain/neurological diseases such a Alzheimer's disease
CC   or other diseases where neurofibrillary tangles are a pathological
CC   symptom.
XX
SQ   Sequence   106 AA;

  Query Match             100.0%;  Score 50;  DB 17;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db      52 yysspgspgt 60


RESULT  12
AAR76937
ID   AAR76937 standard; Peptide; 112 AA.
XX
AC   AAR76937;
XX
DT   04-DEC-1995  (first entry)
XX
DE   PHF-tau (143-254) peptide.
XX
KW   PHF-tau; paried helical filament tau protein; monoclonal antibody;
KW   MAb; phosphorylation; neurological disease; Alzheimer disease;
KW   cerebrospinal fluid.
XX
OS   Homo sapiens.
XX
PN   WO9517429-A.
XX
PD   29-JUN-1995.
XX
PF   14-DEC-1994;   94WO-EP04146.
XX
PR   21-DEC-1993;   93EP-0403133.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Van De Voorde A,  Vandermeeren M,  Vanmechelen E;
XX
DR   WPI; 1995-240616/31.
XX
PT   Novel monoclonal antibodies specific for abnormally phosphorylated
PT   paired helical filament tau protein (PHF-Tau) - useful for post
PT   mortem or in vitro detection of neurological diseases eg. Alzheimer's
PT   disease
XX
PS   Claim 1; Page 44; 57pp; English.
XX
CC   Novel MAbs AT180 and AT270 (ECACC 92122204, 93070774) form
CC   immunological complexes with a phosphorylated epitope, given in
CC   AAR76937, of abnormally phosphorylated tau protein (PHF-tau).  The
CC   MAbs are used to specifically detect PHF-tau in cerebrospinal fluid.
XX
SQ   Sequence   112 AA;

  Query Match             100.0%;  Score 50;  DB 16;  Length 112;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db      55 yysspgspgt 63


RESULT  13
AAY15200
ID   AAY15200 standard; Protein; 351 AA.
XX
AC   AAY15200;
XX
DT   28-FEB-2000  (first entry)
XX
DE   Human Tau protein.
XX
KW   Human Tau gene; neurofibrillary tangle formation; abnormal tau filament;
KW   brain; mutation; phosphorylation; isoform ratio; diagnosis; tauopathy;
KW   treatment; neurodegenerative disorder; Fronto-Temporal Dementia;
```

KW Familial Multiple System Tauopathy with presenile Dementia; MSTD;
KW Pick's Disease; Progressive Supranuclear Palsy; PSP; Alzheimer's Disease;
KW Corticobasal Degeneration; CD; Prion Protein Cerebral Amyloid Angiopathy;
KW cognitive disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1..351
FT /label= Tau_protein
FT /note= "Microtubule related protein"
XX
PN WO9962548-A1.
XX
PD 09-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US12036.
XX
PR 01-JUN-1998; 98US-0087557.
XX
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
PI Ghetti B, Spillantini MG, Murrell JR, Goedert M, Farlow MR;
PI Klug A;
XX
DR WPI; 2000-086858/07.
DR N-PSDB; AAZ29262.
XX
PT Diagnosing a tauopathy, especially a Fronto-Temporal Dementia -
XX
PS Disclosure; Page 85; 90pp; English.
XX
CC The present amino acid sequence is a form of human Tau protein.
CC There are six tau isoforms, expressed in the normal adult brain with a
CC slight preponderance of those with 3 repeats over those with 4 repeats.
CC Mutations in the tau gene affects phosphorylation and leads to formation
CC of neurofibrillary tangles and alters the tau isoform ratio. The
CC increased ratio of 4:3 repeat and abnormal tau filaments is closely
CC related to neurodegenerative disorders. This sequence can be used for
CC diagnosis and treatment of tauopathies, like Fronto-Temporal Dementia,
CC Familial Multiple System Tauopathy with presenile Dementia (MSTD),
CC Pick's Disease, Progressive Supranuclear Palsy (PSP), Corticobasal
CC Degeneration (CD) or Alzheimer's Disease. A composition that decreases
CC the ratio of 4:3 repeat tau isomers, along with an agent for treatment
CC of a cognitive disorder, is useful for treating a tauopathy. It may also
CC be useful in diagnosis of Prion Protein Cerebral Amyloid Angiopathy and
CC other prion protein associated disease characterized by abnormal tau
CC filament formation.
XX
SQ Sequence 351 AA;

Query Match 100.0%; Score 50; DB 21; Length 351;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 139 ysspgspgt 147

RESULT 14
AAP91294
ID AAP91294 standard; protein; 352 AA.
XX
AC AAP91294;
XX
DT 18-DEC-1989 (first entry)
XX
DE Paired helical filament (PHF) core protein.
XX
KW Paired helical filament (PHF) core protein; Alzheimer's disease;
KW neurofibrillary tangles.
XX
OS Homo sapiens.
XX
PN WO8903993-A.
XX
PD 05-MAY-1989.
XX
PF 19-OCT-1988; 88WO-GB00867.
XX
PR 19-OCT-1987; 87GB-0024412.
XX
PA (MEDI) MEDICAL RESEARCH COUNCIL.
XX
PI Wischik CM, Milstein C, Klug A;
XX
DR WPI; 1989-150854/20.
XX
PT Paired helical filament core protein - used for providing reagents
PT sensitive to neurofibrillary tangles used for diagnosing Alzheimer's
PT disease.
XX
PS Disclosure; fig 1; 29pp; English.
XX
CC Paired helical filament core protein was sequenced from DNA obtained
CC from brain tissue contg. Alzheimer neurofibrillary tangles. The protein
CC can be used to make MAb's to the PHF core or nucleotide probes, used to
CC diagnose Alzheimer's disease. The protein sequence QIVYKP (AAs 218-223)
CC was used to design the probes.
CC See also AAN91707.
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 50; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 139 ysspgspgt 147

RESULT 15
AAR32708
ID AAR32708 standard; Protein; 352 AA.
XX
AC AAR32708;
XX
DT 15-JUN-1993 (first entry)
XX
DE Human tau-protein.
XX
KW Alzheimer's disease; diagnosis; subtyping; monitoring; assay.
XX
OS Homo sapiens.
XX
PN WO9303369-A.
XX
PD 18-FEB-1993.
XX
PF 03-AUG-1992; 92WO-US06382.
XX
PR 01-AUG-1991; 91US-0738778.
XX
PA (VOOR/) VOORHEIS P H.
XX
PI Voorheis PH;
XX
DR WPI; 1993-076670/09.
DR N-PSDB; AAQ37305.
XX
PT Method for diagnosing, subtyping and monitoring Alzheimer's
PT disease - by assaying a sample of body fluid for the presence of a

PT tau-peptide using an anti-tau antibody
XX
PS Disclosure; Fig 1; 43pp; English.
XX
CC The sequence is that one form of human tau protein (from Goedert
CC et al., PNAS USA 85: 4051-4055) which was used for the prodn.
CC of anti-tau peptide antibodies. These are used as part of a method
CC for diagnosing, subtyping or monitoring Alzheimer's disease by
CC assaying a sample of body fluid for the presence of a tau-peptide
CC using an anti-tau antibody or the presence of an anti-tau-peptide
CC autoantibody. The methods can be used for confirming a clinical
CC diagnosis of Alzheimer's disease and in following the course of the
CC disease and treatment.
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 50; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 139 ysspgspgt 147

RESULT 16
AAY20248
ID AAY20248 standard; Protein; 352 AA.
XX
AC AAY20248;
XX
DT 22-JUL-1999 (first entry)
XX
DE Human microtubule associated protein Tau wild type fragment.
XX
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.
XX
OS Homo sapiens.
XX
PN WO9845322-A2.
XX
PD 15-OCT-1998.
XX
PF 02-APR-1998; 98WO-IB00705.
XX
PR 10-APR-1997; 97US-0043163.
XX
PA (UYUT-) RIJKSUNIV UTRECHT.
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
XX
DR WPI; 1998-609901/51.
DR N-PSDB; AAX75754.
XX
PT Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also
PT for treatment and prevention with specific ribozymes or wild-type
PT RNA
XX
PS Disclosure; Figure 3; 258pp; English.
XX
CC This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC and many others listed) or susceptibility to these disorders. The method
CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the
CC used of neuronal system RNA molecules, specifically proteins including
CC beta-amyloid precursor protein (beta-APP), the microtubule associated
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC protein-C (HMGP-C) and neuroendocrine specific protein A.
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 50; DB 19; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 139 ysspgspgt 147

RESULT 17
AAW05283
ID AAW05283 standard; Protein; 390 AA.
XX
AC AAW05283;
XX
DT 20-DEC-1996 (first entry)
XX
DE Truncated human tau protein.
XX
KW Tau protein; inhibition; modulation; prophylaxis; treatment;
KW Alzheimer's disease; motor neurone disease; Lewy body disease;
KW progressive supranuclear palsy; Pick's disease.
XX
OS Homo sapiens.
XX
PN WO9630766-A1.
XX
PD 03-OCT-1996.
XX
PF 25-MAR-1996; 96WO-EP01307.
XX
PR 27-MAR-1995; 95GB-0006197.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
XX
DR WPI; 1996-455570/45.
XX
PT Assay for inhibitors of tau-tau interaction - used for identifying
PT cpds., partic. phenothiazine cpds., for treating pathological
PT tau-tau or neuro:filament aggregation
XX
PS Claim 11; ; 97pp; English.
XX
CC Detecting an agent which modulates or inhibits tau-tau protein
CC association comprises contacting two tau proteins, distinct from
CC each other yet capable of binding to the other and where one of the
CC tau proteins is labelled, in the presence of the agent suspected of
CC being capable of modulating or inhibiting tau-tau interaction.

```
CC   Agents identified as being modulators or inhibitors of tau-tau
CC   interaction may be used for the prophylaxis and treatment of
CC   Alzheimer's disease, motor neurone disease, Lewy body disease,
CC   Pick's disease or progressive supranuclear palsy. This sequence of
CC   the human tau protein is truncated at amino acid residue 390.  The
CC   full length protein is given in AAW05282.
XX
SQ   Sequence   390 AA;


  Query Match           100.0%;  Score 50;  DB 17;  Length 390;
  Best Local Similarity  100.0%;  Pred. No. 4.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          |||||||||
Db    197 yssPgspgt 205


RESULT  18
AAR58810
ID   AAR58810 standard; protein; 441 AA.
XX
AC   AAR58810;
XX
DT   27-MAR-1995  (first entry)
XX
DE   Human tau protein.
XX
KW   Tau; cerebrospinal fluid; immunoassay; antibody; detection;
KW   diagnosis; central nervous system; CNS; cytopathies; cytopathy;
KW   Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO9418560-A.
XX
PD   18-AUG-1994.
XX
PF   10-FEB-1994;   94WO-JP00196.
XX
PR   12-FEB-1993;   93JP-0046133.
XX
PA   (TEIJ ) TEIJIN LTD.
XX
PI   Eguchi H,  Hosoda K,  Kobayashi S,  Kubota T,  Mori H;
PI   Nakamoto T;
XX
DR   WPI; 1994-279910/34.
XX
PT   Sandwich immunoassay of tau protein in cerebrospinal fluid - for
PT   diagnosis of Alzheimer's disease and other CNS cytopathies
XX
PS   Claim 1; Page 16-18; 36pp; Japanese.
XX
CC   Detection of the human tau protein (or fragments of it) in samples
CC   of cerebrospinal fluid enables the diagnosis of central nervous
CC   system cytopathies such as Alzheimer's disease.  Detection is
CC   performed using labelled antibodies which recognise sites within the
CC   region defined by the amino acid residues 251-441.  The antibodies
CC   are preferably polyclonal.
XX
SQ   Sequence   441 AA;


  Query Match           100.0%;  Score 50;  DB 15;  Length 441;
  Best Local Similarity  100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          |||||||||
Db    197 yssPgspgt 205


RESULT  19
AAW05282
ID   AAW05282 standard; Protein; 441 AA.
XX
AC   AAW05282;
XX
DT   20-DEC-1996  (first entry)
XX
DE   Human tau protein.
XX
KW   Tau protein; inhibition; modulation; prophylaxis; treatment;
KW   Alzheimer's disease; motor neurone disease; Lewy body disease;
KW   progressive supranuclear palsy; Pick's disease.
XX
OS   Homo sapiens.
XX
PN   WO9630766-A1.
XX
PD   03-OCT-1996.
XX
PF   25-MAR-1996;   96WO-EP01307.
XX
PR   27-MAR-1995;   95GB-0006197.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Edwards PC,  Harrington CR,  Klug A,  Roth M,  Wischik CM;
XX
DR   WPI; 1996-455570/45.
DR   N-PSDB; AAT39591.
XX
PT   Assay for inhibitors of tau-tau interaction - used for identifying
PT   cpds., partic. phenothiazine cpds., for treating pathological
PT   tau-tau or neuro:filament aggregation
XX
PS   Example 2; Page 53-54; 97pp; English.
XX
CC   Detecting an agent which modulates or inhibits tau-tau protein
CC   association comprises contacting two tau proteins, distinct from
CC   each other yet capable of binding to the other and where one of the
CC   tau proteins is labelled, in the presence of the agent suspected of
CC   being capable of modulating or inhibiting tau-tau interaction.
CC   Agents identified as being modulators or inhibitors of tau-tau
CC   interaction may be used for the prophylaxis and treatment of
CC   Alzheimer's disease, motor neurone disease, Lewy body disease,
CC   Pick's disease or progressive supranuclear palsy.
XX
SQ   Sequence   441 AA;


  Query Match           100.0%;  Score 50;  DB 17;  Length 441;
  Best Local Similarity  100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          |||||||||
Db    197 yssPgspgt 205


RESULT  20
AAW34856
ID   AAW34856 standard; protein; 441 AA.
XX
AC   AAW34856;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Human tau protein.
XX
KW   Antibody; phosphorylated tau protein; paired helical filament;
KW   detection; Alzheimer's disease; human.
XX
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```
OS   Homo sapiens.
XX
PN   WO9734145-A1.
XX
PD   18-SEP-1997.
XX
PF   13-MAR-1997;   97WO-JP00804.
XX
PR   13-MAR-1996;   96JP-0056090.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
PI   Imahori K,  Ishiguro K,  Park J,  Sato K,  Uchida T;
XX
DR   WPI; 1997-470978/43.
XX
PT   Antibody prepared using a partial peptide containing part of
PT   phosphorylated tau protein - used for detecting Alzheimer's disease
XX
PS   Claim 2; Pages 25-27; 48pp; Japanese.
XX
CC   An antibody, prepared using a partial peptide containing the
CC   phosphorylated residue of the phosphorylated tau protein, e.g. the
CC   present sequence, in a paired helical filament, can be used to
CC   detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC   protein in brain extracts or tissue fragments.
XX
SQ   Sequence   441 AA;

  Query Match             100.0%;  Score 50;  DB 18;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     197 ysspgspgt 205


RESULT  21
AAY81386
ID   AAY81386 standard; protein; 441 AA.
XX
AC   AAY81386;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Human paired helical filament phosphorylated tau protein.
XX
KW   Phosphorylated tau protein; human; paired helical filament;
KW   polyclonal antibody; Alzheimer's disease; cerebrospinal fluid; CSF;
KW   diagnosis; detection.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   199
FT                   /note= "Phosphorylated"
FT   Modified-site   231
FT                   /note= "Phosphorylated"
FT   Modified-site   235
FT                   /note= "Phosphorylated"
FT
XX
PN   JP2000034300-A.
XX
PD   02-FEB-2000.
XX
PF   17-JUL-1998;   98JP-0204040.
XX
PR   17-JUL-1998;   98JP-0204040.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
DR   WPI; 2000-285529/25.
XX
PT   Anti-phosphated tau protein antibody - for the detection of Alzheimer
PT   disease
XX
PS   Claim 1; Page 8-9; 12pp; Japanese.
XX
CC   The invention relates to an antibody against a phosphorylated tau
CC   protein (AAY81386), which is a component of the paired helical filament
CC   found in the plaques associated with Alzheimer's disease. A
CC   phosphorylated tau protein fragment selected from peptides
CC   AAY81387-Y81390 is conjugated to keyhole limpet haemocyanin (KLH), and
CC   used to raise polyclonal antibodies in a rabbit. The antibodies of the
CC   invention are specific for phosphorylated tau protein and may be used to
CC   detect phosphorylated tau protein in the cerebrospinal fluid (CSF) of a
CC   patient suspected of having Alzheimer's disease. Use of the antibodies of
CC   the invention provides specific diagnosis of Alzheimer's disease. The
CC   present sequence represents phosphorylated tau protein.
XX
SQ   Sequence   441 AA;

  Query Match             100.0%;  Score 50;  DB 21;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     197 ysspgspgt 205


RESULT  22
AAR28237
ID   AAR28237 standard; peptide; 13 AA.
XX
AC   AAR28237;
XX
DT   18-MAR-1993  (first entry)
XX
DE   Phosphopeptide as Alzheimers's disease detection antigen.
XX
KW   AD; antigen; antibody; paired helical filament; PHF; brain.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   6
FT                   /note= "at least one of Ser6 and Thr9 is modified
FT                    by PO(OH)"
FT   Modified-site   9
FT                   /note= "at least one of Ser6 and Thr9 is modified
FT                    by PO(OH)"
FT   Modified-site   13
FT                   /note= "the C-terminal is amidated"
FT
XX
PN   JP04270299-A.
XX
PD   25-SEP-1992.
XX
PF   25-FEB-1991;   91JP-0146476.
XX
PR   25-FEB-1991;   91JP-0146476.
XX
PA   (MITU ) MITSUBISHI KASEI CORP.
XX
DR   WPI; 1992-369427/45.
XX
PT   New phospho:peptide(s) - useful as antigen for detection of
PT   Alzheimer's disease
XX
PS   Claim 1; Page 2; 4pp; Japanese.
XX
CC   The C-terminal of the peptide is amidated.
```

```
CC   The phosphopeptide is useful as antigen for preparing antibody
CC   against paired helical filaments (PHF) present in brain of patients
CC   with Alzheimer's disease.
XX
SQ   Sequence   13 AA;


  Query Match             86.0%;  Score 43;  DB 13;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 SSPGSPGT 9
          ||||||||
Db      2 sspgspgt 9


RESULT  23
AAW34860
ID   AAW34860 standard; peptide; 13 AA.
XX
AC   AAW34860;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Human tau protein fragment.
XX
KW   Antibody; phosphorylated tau protein; paired helical filament;
KW   detection; Alzheimer's disease; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   3
FT                   /note= "phosphoserine"
FT   Modified-site   6
FT                   /note= "phosphoserine"
XX
PN   WO9734145-A1.
XX
PD   18-SEP-1997.
XX
PF   13-MAR-1997;   97WO-JP00804.
XX
PR   13-MAR-1996;   96JP-0056090.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
PI   Imahori K,  Ishiguro K,  Park J,  Sato K,  Uchida T;
XX
DR   WPI; 1997-470978/43.
XX
PT   Antibody prepared using a partial peptide containing part of
PT   phosphorylated tau protein - used for detecting Alzheimer's disease
XX
PS   Example; Page 29; 48pp; Japanese.
XX
CC   An antibody, prepared using a partial peptide containing the
CC   phosphorylated residue of the phosphorylated tau protein, e.g. the
CC   present sequence, in a paired helical filament, can be used to
CC   detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC   protein in brain extracts or tissue fragments.
XX
SQ   Sequence   13 AA;


  Query Match             86.0%;  Score 43;  DB 18;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 SSPGSPGT 9
          ||||||||
Db      2 sspgspgt 9


RESULT  24
AAW34858
ID   AAW34858 standard; peptide; 13 AA.
XX
AC   AAW34858;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Human tau protein fragment.
XX
KW   Antibody; phosphorylated tau protein; paired helical filament;
KW   detection; Alzheimer's disease; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   6
FT                   /note= "phosphoserine"
XX
PN   WO9734145-A1.
XX
PD   18-SEP-1997.
XX
PF   13-MAR-1997;   97WO-JP00804.
XX
PR   13-MAR-1996;   96JP-0056090.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
PI   Imahori K,  Ishiguro K,  Park J,  Sato K,  Uchida T;
XX
DR   WPI; 1997-470978/43.
XX
PT   Antibody prepared using a partial peptide containing part of
PT   phosphorylated tau protein - used for detecting Alzheimer's disease
XX
PS   Example; Page 28; 48pp; Japanese.
XX
CC   An antibody, prepared using a partial peptide containing the
CC   phosphorylated residue of the phosphorylated tau protein, e.g. the
CC   present sequence, in a paired helical filament, can be used to
CC   detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC   protein in brain extracts or tissue fragments.
XX
SQ   Sequence   13 AA;


  Query Match             86.0%;  Score 43;  DB 18;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 SSPGSPGT 9
          ||||||||
Db      2 sspgspgt 9


RESULT  25
AAW29455
ID   AAW29455 standard; Protein; 263 AA.
XX
AC   AAW29455;
XX
DT   14-APR-1998  (first entry)
XX
DE   Oerskovia xanthineolytica mature beta-1,3-glucanase.
XX
KW   Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation;
KW   fungal cell wall; intracellular product; purification; protoplast.
XX
OS   Oerskovia xanthineolytica LLG109 (DSM 10297).
XX
FH   Key             Location/Qualifiers
```

```
FT   CDS             23..955
FT                   /*tag=  a
FT   sig_peptide     23..120
FT                   /*tag=  b
FT   mat_peptide     164..952
FT                   /*tag=  c
XX
PN   WO9739114-A1.
XX
PD   23-OCT-1997.
XX
PF   14-APR-1997;    97WO-DK00160.
XX
PR   23-AUG-1996;    96DK-0000885.
PR   12-APR-1996;    96DK-0000427.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Diers I,  Ferrer P,  Halkier T,  Hedegaard L;
XX
DR   WPI; 1997-526451/48.
DR   N-PSDB; AAT89155.
XX
PT   New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia
PT   xanthineolytica, used particularly for the lysis of microbial cells
PT   for obtaining desirable products
XX
PS   Example 2; Page 35-36; 64pp; English.
XX
CC   This polypeptide comprises a novel Oerskovia xanthineolytica (OX)
CC   enzyme that exhibits beta-1,3-glucanase (BG) activity.  Its amino
CC   acid sequence was deduced from an isolated genomic DNA sequence
CC   (see AAT89155).  Claimed DNA constructs that encode the novel BG (see
CC   also AAW29456 for corrected sequence), a mannose binding domain (see
CC   AAW29458) or a full-length enzyme, i.e. BG with mannose binding
CC   domain (see AAW29456), can be used to produce recombinant BG
CC   polypeptides, with or without a mannose binding domain, in fungal
CC   or bacterial host cells.  BG polypeptides are used for the
CC   degradation or modification of beta-glucan containing material,
CC   especially for the gentle lysis of microbial cell walls, thereby
CC   enabling recovery of desirable intracellular products with a
CC   reduced amount of contaminants.  They can also be used for the
CC   production of e.g. pigments, colourants, flavourants, yeast
CC   extracts, pharmaceuticals, food or feed compositions, and to
CC   prepare protoplasts for use in fusion, transformation and cloning
CC   studies.
XX
SQ   Sequence   263 AA;

  Query Match             80.0%;  Score 40;  DB 18;  Length 263;
  Best Local Similarity   87.5%;  Pred. No. 1e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||:|||
Db     244 sspgnpgt 251


RESULT  26
AAW29456
ID   AAW29456 standard; Protein; 435 AA.
XX
AC   AAW29456;
XX
DT   14-APR-1998  (first entry)
XX
DE   Oerskovia xanthineolytica beta-1,3-glucanase.
XX
KW   Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation;
KW   fungal cell wall; intracellular product; purification; protoplast.
XX
OS   Oerskovia xanthineolytica LLG109 (DSM 10297).
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..52
FT                   /label= Sig_peptide
FT   Protein         53..435
FT                   /label= Mat_protein
FT   Domain          304..435
FT                   /label= Mannose-binding_domain
XX
PN   WO9739114-A1.
XX
PD   23-OCT-1997.
XX
PF   14-APR-1997;    97WO-DK00160.
XX
PR   23-AUG-1996;    96DK-0000885.
PR   12-APR-1996;    96DK-0000427.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Diers I,  Ferrer P,  Halkier T,  Hedegaard L;
XX
DR   WPI; 1997-526451/48.
DR   N-PSDB; AAT89156.
XX
PT   New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia
PT   xanthineolytica, used particularly for the lysis of microbial cells
PT   for obtaining desirable products
XX
PS   Example 2; Page 39-40; 64pp; English.
XX
CC   This sequence comprises the polypeptide precursor of a novel
CC   Oerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase
CC   (BG) activity and which includes a mannose binding domain (MBD).
CC   Its amino acid sequence was deduced from an isolated genomic DNA
CC   sequence (see AAT89156).  Claimed DNA constructs that encode the
CC   novel BG lacking a MBD (see AAW29455 and AAW29457), a MDB (see
CC   AAW29458), or the full-length enzyme can be used to produce recombinant
CC   BG polypeptides, with or without a mannose binding domain, in fungal
CC   or bacterial host cells.  BG polypeptides are used for the
CC   degradation or modification of beta-glucan containing material,
CC   especially for the gentle lysis of microbial cell walls, thereby
CC   enabling recovery of desirable intracellular products with a
CC   reduced amount of contaminants.  They can also be used for the
CC   production of e.g. pigments, colourants, flavourants, yeast
CC   extracts, pharmaceuticals, food or feed compositions, and to
CC   prepare protoplasts for use in fusion, transformation and cloning
CC   studies.
XX
SQ   Sequence   435 AA;

  Query Match             80.0%;  Score 40;  DB 18;  Length 435;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||:|||
Db     297 sspgnpgt 304


RESULT  27
AAR38233
ID   AAR38233 standard; peptide; 7 AA.
XX
AC   AAR38233;
XX
DT   08-OCT-1993  (first entry)
XX
DE   Alzheimer paired helical filament tau protein epitope 197-203.
XX
KW   Alzheimer tau protein; phosphorylation-dependent; PHF;
KW   neuronal microtubule; mitogen activated protein kinase; MAP kinase.
```

XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 3..4
FT /label= Phosphorylation_motif
FT Modified-site 6..7
FT /label= Phosphorylation_motif
XX
PN WO9311231-A.
XX
PD 10-JUN-1993.
XX
PF 07-DEC-1992; 92WO-EP02829.
XX
PR 06-DEC-1991; 91EP-0120974.
PR 16-NOV-1992; 92EP-0119551.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow E;
PI Steiner B;
XX
DR WPI; 1993-197050/24.
XX
PT Tau protein epitope(s), specific antibodies and protein kinase(s)
PT - used in the prevention, diagnosis and treatment of Alzheimer's
PT disease
XX
PS Claim 5; Page 89; 148pp; English.
XX
CC This is one of 26 preferred epitopes which occur in a phosphorylated
CC state in tau protein from Alzheimer paired helical filaments. The
CC epitopes all include phosphorylatable serine residues in Ser-Pro
CC motifs, Ile-Gly-Ser motifs or Cys-Gly-Ser motifs and/or
CC phosphorylatable threonine residues in Thr-Pro motifs. The pattern
CC of tau protein phosphorylation differs between Alzheimer's and
CC non-Alzheimer's individuals. Knowledge of the phosphorylated
CC epitopes and antibodies which recognise them may be useful in
CC diagnosis, treatment and prevention of Alzheimer's Disease. The
CC protein kinases present in mammalian brain which phosphorylate the
CC different epitopes are also claimed but no sequences are given.
XX
SQ Sequence 7 AA;

Query Match 78.0%; Score 39; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSP 7
|||||||
Db 1 yssPgsp 7

RESULT 28
AAR37552
ID AAR37552 standard; peptide; 7 AA.
XX
AC AAR37552;
XX
DT 07-OCT-1993 (first entry)
XX
DE Phosphorylated tau protein epitope.
XX
KW Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
KW treatment; formation; inhibition; inhibitor.
XX
OS Homo sapiens.
XX
PN EP544942-A.
XX
PD 09-JUN-1993.
XX
PF 06-DEC-1991; 91EP-0120974.
XX
PR 06-DEC-1991; 91EP-0120974.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow EM, Steiner B;
XX
DR WPI; 1993-183841/23.
XX
PT Phosphorylated tau protein epitope associated with Alzheimer's
PT disease - is used as protein kinase inhibitor for treatment and
PT diagnosis
XX
PS Claim 4; Page 16; 34pp; English.
XX
CC The sequence is that of an epitope of tau protein which specifically
CC occurs in a phosphorylated state in tau protein from Alzheimer's
CC paired helical fragments. It may be used as part of a method for the
CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may
CC also be used in an in vitro model for the study of the generation of
CC the Alzheimer state of proteins and the testing of substances which
CC prevent the conversion of normal to Alzheimer tau protein. The
CC epitope occurs at residues 197-203 of human tau protein.
XX
SQ Sequence 7 AA;

Query Match 78.0%; Score 39; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSP 7
|||||||
Db 1 yssPgsp 7

RESULT 29
AAU17141
ID AAU17141 standard; Protein; 263 AA.
XX
AC AAU17141;
XX
DT 07-NOV-2001 (first entry)
XX
DE Novel signal transduction pathway protein, Seq ID 706.
XX
KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
KW immune system disorder; rheumatoid arthritis; inflammatory condition;
KW organ transplant rejection; infection; hepatitis C; blood disorder;
KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW reproductive system; gastrointestinal; liver disorder; AIDS;
KW acquired immune deficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200154733-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01312.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465460/50.
DR N-PSDB; AAS27058.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders -
XX
PS Claim 1; SEQ ID No 706; 880pp; English.
XX
CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for

```
CC   diagnosing, preventing and treating diseases including immune system
CC   disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC   disorders (e.g rheumatoid arthritis), inflammatory conditions, organ
CC   transplant rejections and graft versus host disease, infectious diseases
CC   (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC   other blood-related disorders (sickle cell anaemia), myeloproliferative
CC   disorders, primary haematopoietic disorders, hyperproliferative
CC   disorders (e.g. Gaucher's disease and cancer), neurodegenerative
CC   disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
CC   abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
CC   disorders (e.g. glomerulonephritis), cardiovascular disorders
CC   (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
CC   wound healing, epithelial cell proliferation, endocrine disorders (e.g.
CC   Addison's disease), reproductive system disorders, gastrointestinal
CC   disorder (inflammatory disorders), liver disorders (cirrhosis),
CC   as stimulators of B-cell responsiveness to pathogens, activators of
CC   T-cells, to induce higher affinity antibodies, and as a means to induce
CC   tumour proliferation in pathologies e.g. acquired immune deficiency
CC   syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction
CC   pathway protein, amino acid sequences of the invention.
XX

  Query Match             78.0%;  Score 39;  DB 22;  Length 263;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db     180 spgspgt 186


RESULT  30
AAM80057
ID   AAM80057 standard; Protein; 376 AA.
XX
AC   AAM80057;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human protein SEQ ID NO 3703.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US04098.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
PR   20-JUN-2000; 2000US-0598075.
PR   19-JUL-2000; 2000US-0620325.
PR   01-SEP-2000; 2000US-0654936.
PR   15-SEP-2000; 2000US-0663561.
PR   20-OCT-2000; 2000US-0693325.
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   N-PSDB; AAK53190.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 20; Page 415; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence   376 AA;

  Query Match             78.0%;  Score 39;  DB 22;  Length 376;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db     358 spgspgt 364


RESULT  31
AAB41838
ID   AAB41838 standard; Protein; 424 AA.
XX
AC   AAB41838;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human ORFX ORF1602 polypeptide sequence SEQ ID NO:3204.
XX
KW   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW   vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW   anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW   immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW   hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW   antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW   antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW   neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW   cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW   cholesterol ester storage; systemic lupus erythematosus; infection;
KW   severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW   allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW   bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW   thrombosis; contraceptive.
XX
OS   Homo sapiens.
XX
PN   WO200058473-A2.
XX
PD   05-OCT-2000.
XX
PF   31-MAR-2000; 2000WO-US08621.
XX
PR   31-MAR-1999;   99US-0127607.
PR   02-APR-1999;   99US-0127636.
PR   05-APR-1999;   99US-0127728.
PR   30-MAR-2000; 2000US-0540763.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
```

DR WPI; 2000-602362/57.
DR N-PSDB; AAC76047.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
PS Claim 11; Page 2417-2418; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ Sequence 424 AA;

Query Match 78.0%; Score 39; DB 21; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SPGSPGT 9
|||||||
Db 341 spgspgt 347

RESULT 32
AAM79073
ID AAM79073 standard; Protein; 424 AA.
XX
AC AAM79073;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1735.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK52206.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 4070-4071; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 424 AA;

Query Match 78.0%; Score 39; DB 22; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SPGSPGT 9
|||||||
Db 341 spgspgt 347

RESULT 33
AAB27227
ID AAB27227 standard; Protein; 424 AA.
XX
AC AAB27227;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human EXMAD-5 SEQ ID NO: 5.
XX
KW Extracellular matrix and adhesion-associated protein; EXMAD; cancer;
KW inflammation; reproductive disorder; cardiovascular disorder;
KW immune disorder; musculoskeletal disorder; developmental disorder;
KW gastrointestinal disorder; cell proliferation disorder.
XX
OS Homo sapiens.
XX
PN WO200068380-A2.
XX
PD 16-NOV-2000.
XX
PF 10-MAY-2000; 2000WO-US12811.
XX
PR 11-MAY-1999; 99US-0133643.
PR 23-AUG-1999; 99US-0150409.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Hillman JL, Tang YT, Lal P, Yue H, Baughn MR, Lu DAM;
PI Azimzai Y;

XX
DR WPI; 2001-007395/01.
DR N-PSDB; AAC66894.
XX
PT Isolated polynucleotide encoding extracellular matrix or
PT adhesion-associated protein (EXMAD) useful for diagnosing, treating, or
PT preventing disorders associated with expression of EXMAD such as
PT proliferative, immune and genetic disorders -
XX
PS Claim 1; Page 92-93; 129pp; English.
XX
CC The present invention provides the protein and coding sequences for 25
CC novel extracellular matrix and adhesion-associated proteins (EXMADs).
CC These are designated EXMAD-1, EXMAD-2, EXMAD-3, EXMAD-4, EXMAD-5,
CC EXMAD-6, EXMAD-7, EXMAD-8, EXMAD-9, EXMAD-10, EXMAD-11, EXMAD-12,
CC EXMAD-13, EXMAD-14, EXMAD-15, EXMAD-16, EXMAD-17, EXMAD-18, EXMAD-19,
CC EXMAD-20, EXMAD-21, EXMAD-22, EXMAD-23, EXMAD-24 and EXMAD-25. They are
CC useful in the prevention and treatment of cancers, cell proliferation,
CC cardiovascular, reproductive, immune, musculoskeletal, developmental and
CC gastrointestinal disorders and inflammation.
XX
SQ Sequence 424 AA;

Query Match 78.0%; Score 39; DB 22; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SPGSPGT 9
|||||||
Db 341 spgspgt 347

RESULT 34
AAO05662
ID AAO05662 standard; Protein; 98 AA.
XX
AC AAO05662;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 19554.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI85593.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 19554; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 98 AA;

Query Match 76.0%; Score 38; DB 22; Length 98;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPG 8
|||||||
Db 79 sspgspg 85

RESULT 35
ABG27348
ID ABG27348 standard; Protein; 284 AA.
XX
AC ABG27348;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #27339.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS91535.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 57707; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as

```
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   284 AA;

  Query Match             74.0%;  Score 37;  DB 22;  Length 284;
  Best Local Similarity   75.0%;  Pred. No. 3.2e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           : ||||||
Db      56 fgspgspg 63


RESULT  36
AAR25063
ID   AAR25063 standard; Protein; 335 AA.
XX
AC   AAR25063;
XX
DT   10-DEC-1992  (first entry)
XX
DE   Soluble human IL-5 receptor alpha chain.
XX
KW   Soluble interleukin-5; chronic asthma; eosinophilia;
KW   screening antagonists; ss.
XX
OS   Homo sapiens.
XX
PN   EP492214-A.
XX
PD   01-JUL-1992.
XX
PF   06-DEC-1991;   91EP-0120951.
XX
PR   27-DEC-1990;   90EP-0811030.
PR   30-APR-1991;   91EP-0810327.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Devos R,  Fiers W,  Plaetinck G,  Tavernier J,  Van Der Hayden J;
XX
DR   WPI; 1992-218502/27.
DR   N-PSDB; AAQ25789.
XX
PT   Recombinant alpha chain of human interleukin-5 receptor - and DNA
PT   encoding it, for treatment of interleukin-5 mediated disorders
PT   such as chronic asthma
XX
PS   Claim 7; Fig 1; 15pp; English.
XX
CC   This amino acid sequence was deduced from the nucleotide sequence,
CC   isolated as detailed in AAQ25789. Recombinant IL-5 alpha chain can be
CC   used as an IL-5 antagonist in chronic asthma or other disease
CC   states with demonstrated esosinophilia. It may also be used either
CC   alone or with the beta chain of the whole IL-5 receptor as a tool
CC   for screening for IL-5 antagonists. See also AAQ25790-2, AAQ30767,8
CC   AAR25064.
XX
SQ   Sequence   335 AA;

  Query Match             74.0%;  Score 37;  DB 13;  Length 335;
  Best Local Similarity   66.7%;  Pred. No. 3.7e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 happgspgt 127


RESULT  37
AAR33699
ID   AAR33699 standard; Protein; 335 AA.
XX
AC   AAR33699;
XX
DT   09-JUL-1993  (first entry)
XX
DE   shIL-5R-alpha.
XX
KW   Probe; murine; interleukin-5; IL-5; receptor; IL-5R; IL-5R-alpha; IgG;
KW   chain; human; hIL-5R; constant domain; heavy; light; immunoglobulin;
KW   IgA; IgM; IgE; chimeric protein; antagonist; asthma; half-life.
XX
OS   Synthetic.
XX
PN   EP533006-A.
XX
PD   24-MAR-1993.
XX
PF   05-SEP-1992;   92EP-0115246.
XX
PR   18-SEP-1991;   91EP-0810738.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Devos R,  Fiers W,  Tavernier J;
XX
DR   WPI; 1993-095341/12.
DR   N-PSDB; AAQ38440.
XX
PT   Deoxyribonucleic acid sequence for chimeric polypeptide prodn. -
PT   comprises parts coding fragment of alpha and/or beta chain of
PT   human interleukin-5 receptor and heavy or light chain of
PT   immunoglobulin, for chronic asthma treatment
XX
PS   Disclosure; Fig 1; 17pp; English.
XX
CC   The sequence given reppresents soluble human interleukin-5 (IL-5)
CC   receptor (IL-5R)-alpha chain.  This sequence was used in the
CC   construction of a chimeric human IL-5R-alpha-IgG1 molecule.  Chimeric
CC   proteins such as this can be used as IL-5 antagonists in the treatment
CC   of diseases, esp. chronic asthma.  The chimeric proteins have an
CC   increased half-life in vivo compared to hIL-5R.  See also AAQ38433-40.
XX
SQ   Sequence   335 AA;

  Query Match             74.0%;  Score 37;  DB 14;  Length 335;
  Best Local Similarity   66.7%;  Pred. No. 3.7e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 happgspgt 127


RESULT  38
AAM93217
ID   AAM93217 standard; Protein; 350 AA.
XX
AC   AAM93217;
XX
DT   06-NOV-2001  (first entry)
```

XX
DE Human polypeptide, SEQ ID NO: 2622.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
DR N-PSDB; AAK94126.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Claim 8; SEQ ID NO 2622; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a polypeptide
CC encoded by a full length human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 350 AA;

Query Match 74.0%; Score 37; DB 22; Length 350;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
::||| |||
Db 249 ftspgypgt 257

RESULT 39
AAM52310
ID AAM52310 standard; Protein; 351 AA.
XX
AC AAM52310;
XX
DT 18-JAN-2002 (first entry)
XX
DE Chicken zyxine fragment.
XX
KW Actin polymerisation; Ena/VASP; vasodilator-stimulated phosphoprotein;
KW metastatic cancer; parasitic infection; cytotoxic; Chicken; zyxine.
XX
OS Gallus gallus.
XX
PN WO200171356-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-FR00843.
XX
PR 22-MAR-2000; 2000FR-0003637.
XX
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
XX
PI Fradelizi J, Friederich E, Golsteyn RM, Louvard D, Noireaux V;
PI Sykes C;
XX
DR WPI; 2001-639148/73.
DR N-PSDB; AAI71780.
XX
PT Identifying modulators of actin polymerization, potentially useful for
PT treating tumor metastasis and parasitic infection, using proteins that
PT contain Ena/VASp binding sites -
XX
PS Claim 16; Pages 77-78; 109pp; French.
XX
CC The present invention relates to a method for identifying modulators of
CC actin polymerisation. The method involves using proteins that contain at
CC least one binding motif for proteins of the Ena/VASP
CC (vasodilator-stimulated phosphoprotein) family in the preparation of
CC reagents for identification/screening of molecules that modulate
CC formation of the actin cytoskeleton. The proteins used in the method
CC (i.e. the proteins with binding motif(s) for Ena/VASP proteins) do not
CC bind to the Arp2/3 protein complex. The modulators identified by the
CC method are potentially useful for treating disorders of actin
CC polymerisation, e.g. metastatic cancer or parasitic infection; and as
CC cytotoxic agents. The present sequence one such protein with binding
CC motif(s) for Ena/VASP proteins, which was used in the method of the
CC present invention.
XX
SQ Sequence 351 AA;

Query Match 74.0%; Score 37; DB 22; Length 351;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
:|||:|||
Db 2 aspgtpgt 9

RESULT 40
AAR28314
ID AAR28314 standard; Protein; 353 AA.
XX
AC AAR28314;
XX
DT 24-MAR-1993 (first entry)
XX
DE AHSV protein.
XX
KW African horse sickness virus; diagnosis; S7.
XX
OS African horse sickness virus serotype 7.
XX
PN EP515235-A.
XX
PD 25-NOV-1992.
XX
PF 26-MAY-1992; 92EP-0304734.
XX
PR 23-MAY-1991; 91GB-0011111.
PR 14-JUN-1991; 91GB-0012875.
XX
PA (NAIN-) INST NACIONAL INVESTIGACIONS AGRARIAS.
PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.
XX
PI Roy P, Sanchez-Vizcaino Rodrique, JM;

XX
DR WPI; 1992-391791/48.
DR N-PSDB; AAQ30130.
XX
PT DNA coding for African horse sickness virus protein - used for
PT diagnosis, and producing polypeptide(s) for use in diagnosis and
PT vaccines
XX
PS Claim 9; Fig 1; 29pp; English.
XX
CC African horse sickness virus serotype 7 clones were identified by
CC colony hybridisation and Northern blot analysis. A full length clone
CC contained fragments at the 5' and 3' ends of the sequence which are
CC characteristic of orbivirus RNA segments. The DNA fragment may be
CC inserted into an expression system and used in assays for detecting
CC AHSV RNA and as primers in amplification processes.
XX
SQ Sequence 353 AA;

Query Match 74.0%; Score 37; DB 13; Length 353;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
|:||:|||
Db 204 sapgapgt 211

Search completed: May 21, 2002, 11:18:08
Job time: 478 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 21, 2002, 11:19:10 ; Search time 26.77 Seconds
(without alignments)
32.305 Million cell updates/sec

Title: US-09-734-281-2
Perfect score: 50
Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	316	1	QRHUT2	microtubule-associ
2	50	100.0	341	2	B28820	microtubule-associ
3	50	100.0	364	2	A28820	microtubule-associ
4	50	100.0	374	2	S46264	microtubule-associ
5	50	100.0	402	1	QRBOT2	microtubule-associ
6	50	100.0	432	2	JS0306	microtubule-associ
7	50	100.0	441	1	QRHUT1	microtubule-associ
8	50	100.0	448	1	QRBOT1	microtubule-associ
9	50	100.0	686	2	A38235	microtubule-associ
10	50	100.0	733	2	A45301	microtubule-associ
11	39	78.0	150	2	T35638	microtubule-associ
12	39	78.0	272	2	T36770	hypothetical prote
13	39	78.0	2232	2	T34434	probable expressio
14	38	76.0	710	2	S72497	hypothetical prote
15	38	76.0	756	1	A55943	oligopeptide trans
16	38	76.0	1345	2	T29090	1-phosphatidylinos
17	38	76.0	3122	2	T17202	surface layer-asso
18	37	74.0	168	2	B88066	DNA-directed DNA p
19	37	74.0	302	2	T40490	protein R52.4 [imp
20	37	74.0	335	2	A40267	probable 26s prote
21	37	74.0	353	1	JQ1946	interleukin-5 rece
22	37	74.0	372	2	AE3191	core protein VP7 -
23	37	74.0	393	2	S16844	conserved hypothet
24	37	74.0	415	1	W2WLEP	titin - rabbit (fr
25	37	74.0	418	2	S29506	E2 protein - Europ
26	37	74.0	420	2	S21052	neurotensin recept
27	37	74.0	515	2	H75589	interleukin-5 rece
28	37	74.0	542	2	A44358	aldehyde dehydroge
29	37	74.0	847	1	A53800	zyxin - chicken
30	37	74.0	963	2	T19140	mixed-lineage prot
31	37	74.0	1387	2	JC5502	hypothetical prote
32	37	74.0	1986	2	S28353	G-protein signalin
33	37	74.0	3623	2	T09456	probable polyketid
34	37	74.0	6805	2	S20901	intrinsic factor-B
35	37	74.0	26926	1	I38344	titin - rabbit (fr
36	36	72.0	119	2	T17003	titin, cardiac mus
37	36	72.0	305	2	S41860	dormancy-associate
38	36	72.0	323	2	A55983	gene Nkx-1.1 prote
39	36	72.0	329	2	T32783	microtubule-associ
40	36	72.0	351	2	A75621	hypothetical prote
41	36	72.0	381	2	S51375	TorS-related prote
42	36	72.0	425	2	F97437	microtubule-associ
43	36	72.0	425	2	AI2655	phosphoribosylamin
44	36	72.0	438	2	C86271	phosphoribosylamin
45	36	72.0	472	2	I67793	F21F23.21 protein
46	36	72.0	501	2	D64453	microtubule-associ
47	36	72.0	506	2	H83396	biotin carboxylase
48	36	72.0	511	2	S10527	probable aldehyde
49	36	72.0	603	2	S51461	endoglucanase B pr
50	36	72.0	680	2	S31216	BUD8 protein - yea
51	36	72.0	729	2	E70803	collagen alpha 1(X
52	36	72.0	914	2	S18942	hypothetical prote
53	36	72.0	1321	2	T00382	hypothetical prote
54	36	72.0	1824	1	QRHUMT	hypothetical prote
55	36	72.0	1825	2	S13507	microtubule-associ

ALIGNMENTS

RESULT 1
QRHUT2
microtubule-associated protein tau, fetal (clone p18) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 02-Sep-1997
C;Accession: PN0001
R;Lee, G.; Neve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A;Title: The microtubule binding domain of tau protein.
A;Reference number: JN0009; MUID:90180482
A;Accession: PN0001
A;Molecule type: mRNA
A;Residues: 1-316 <LEE>
A;Note: this sequence differs from a previously reported fetal tau protein sequence o
C;Genetics:
A;Gene: GDB:MAPT; MTBT1
A;Cross-references: GDB:119434; OMIM:157140
A;Map position: 17q21-17q21
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule bindi
F;158-188/Domain: MAP2/tau repeat homology <MT1>
F;189-219/Domain: MAP2/tau repeat homology <MT2>
F;220-251/Domain: MAP2/tau repeat homology <MT3>

Query Match 100.0%; Score 50; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 YSSPGSPGT 9
           |||||||||
Db     103 YSSPGSPGT 111
```

RESULT 2
B28820
microtubule-associated protein tau type 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: B28820
R;Lee, G.; Cowan, N.; Kirschner, M.
Science 239, 285-288, 1988

A;Title: The primary structure and heterogeneity of tau protein from mouse brain.
A;Reference number: A94298; MUID:88099510
A;Accession: B28820
A;Molecule type: mRNA
A;Residues: 1-341 <LEE>
A;Cross-references: GB:M18775; NID:g201114; PIDN:AAA40165.1; PID:g201115
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; tandem repeat
F;183-213/Domain: MAP2/tau repeat homology <MT1>
F;214-244/Domain: MAP2/tau repeat homology <MT2>
F;245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match 100.0%; Score 50; DB 2; Length 341;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 128 YSSPGSPGT 136

RESULT 3
A28820
microtubule-associated protein tau type 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: A28820
R;Lee, G.; Cowan, N.; Kirschner, M.
Science 239, 285-288, 1988
A;Title: The primary structure and heterogeneity of tau protein from mouse brain.
A;Reference number: A94298; MUID:88099510
A;Accession: A28820
A;Molecule type: mRNA
A;Residues: 1-364 <LEE>
A;Cross-references: GB:M18776; NID:g201116; PIDN:AAA40166.1; PID:g201117
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; tandem repeat
F;183-213/Domain: MAP2/tau repeat homology <MT1>
F;214-244/Domain: MAP2/tau repeat homology <MT2>
F;245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match 100.0%; Score 50; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 128 YSSPGSPGT 136

RESULT 4
S46264
microtubule-associated protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 13-Aug-1999
C;Accession: S46264
R;Sadot, E.; Marx, R.; Barg, J.; Behar, L.; Ginzburg, I.
J. Mol. Biol. 241, 325-331, 1994
A;Title: Complete sequence of 3'-untranslated region of tau from rat central nervous sys
A;Reference number: S46264; MUID:94334997
A;Accession: S46264
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <SAD>
A;Cross-references: EMBL:X79321; NID:g517393; PIDN:CAA55889.1; PID:g517394
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
F;185-215/Domain: MAP2/tau repeat homology <MT1>
F;216-246/Domain: MAP2/tau repeat homology <MT2>
F;247-277/Domain: MAP2/tau repeat homology <MT3>
F;278-309/Domain: MAP2/tau repeat homology <MT4>

Query Match 100.0%; Score 50; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 130 YSSPGSPGT 138

RESULT 5
QRBOT2
microtubule-associated protein tau, form 3 - bovine
N;Contains: microtubule-associated protein tau, form 4; microtubule-associated prote
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 31-Mar-1996
C;Accession: B31939; A48885; A28173
R;Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.
Mol. Cell. Biol. 9, 1381-1388, 1989
A;Title: Tau consists of a set of proteins with repeated C-terminal microtubule-bind
A;Reference number: A31939; MUID:89261765
A;Accession: B31939
A;Molecule type: mRNA
A;Residues: 1-402 <HIM>
A;Cross-references: GB:M26157; GB:M26158
R;Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.
J. Biol. Chem. 268, 23512-23518, 1993
A;Title: Brain proline-directed protein kinase phosphorylates tau on sites that are
A;Reference number: A48885; MUID:94043150
A;Accession: A48885
A;Molecule type: protein
A;Residues: 'X',157-162,'X',164-165,'X',167-170;192-195,'X',197-201,'X';358-364,'X',
A;Experimental source: brain
A;Note: sequence modified after extraction from NCBI backbone
R;Aizawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
J. Biol. Chem. 263, 7703-7707, 1988
A;Title: Microtubule-binding domain of Tau proteins.
A;Reference number: A28173; MUID:88227970
A;Accession: A28173
A;Molecule type: protein
A;Residues: 159-172,'X',174-177 <AIZ>
A;Experimental source: brain.
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
F;1-402/Product: microtubule-associated protein tau, form 3 #status predicted <BT4>
F;1-234,297-402/Product: microtubule-associated protein tau, form 5 #status predicte
F;101-402/Product: microtubule-associated protein tau, form 4 #status predicted <BT
F;159-177/Region: microtubule binding #status experimental
F;213-243/Domain: MAP2/tau repeat homology <MT1>
F;244-274/Domain: MAP2/tau repeat homology <MT2>
F;275-305/Domain: MAP2/tau repeat homology <MT3>
F;306-337/Domain: MAP2/tau repeat homology <MT4>
F;156,163,196,202,365/Binding site: phosphate (Ser) (covalent) (by proline-directed
F;166/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status

Query Match 100.0%; Score 50; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 158 YSSPGSPGT 166

RESULT 6
JS0306
microtubule-associated protein tau - rat
C;Species: Rattus norvegicus (Norway. rat)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Dec-1993
C;Accession: JS0306; A33574
R;Kosik, K.S.; Orecchio, L.D.; Bakalis, S.; Neve, R.L.
Neuron 2, 1389-1397, 1989

A;Title: Developmentally regulated expression of specific tau sequences.
A;Reference number: JS0306; MUID:90180457
A;Accession: JS0306
A;Molecule type: mRNA
A;Residues: 1-432 <KOS>
A;Note: the sequence shown is from adult rat brain
A;Note: the partial sequence from fetal rat brain is lacking residues 266-296; the fetal
R;Kanai, Y.; Takemura, R.; Oshima, T.; Mori, H.; Ihara, Y.; Yanagisawa, M.; Masaki, T.;
J. Cell Biol. 109, 1173-1184, 1989
A;Title: Expression of multiple tau isoforms and microtubule bundle formation in fibrobl
A;Reference number: A33574; MUID:89359509
A;Accession: A33574
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-432 <KAN>
A;Note: a variant lacking residues 63-91 was also found
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; Alzheimer's disease; calmodulin binding; microtubule b
F;243-273/Domain: MAP2/tau repeat homology <MT1>
F;274-304/Domain: MAP2/tau repeat homology <MT2>
F;305-335/Domain: MAP2/tau repeat homology <MT3>
F;336-367/Domain: MAP2/tau repeat homology <MT4>
F;282-313/Disulfide bonds: #status experimental
F;347/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 100.0%; Score 50; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 188 YSSPGSPGT 196

RESULT 7
QRHUT1
microtubule-associated protein tau, long splice form - human
N;Alternate names: microtubule-binding protein tau; neurofibrillary tangle protein paire
N;Contains: microtubule-associated protein tau type II; microtubule-associated protein t
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 03-May-1996 #text_change 22-Jun-1999
C;Accession: JS0370; A30217; JN0009; S03796; S26665; S26666; S26662; S17302; A43444; A27
R;Goedert, M.; Spillantini, M.G.; Jakes, R.; Rutherford, D.; Crowther, R.A.
Neuron 3, 519-526, 1989
A;Title: Multiple isoforms of human microtubule-associated protein tau: sequences and lo
A;Reference number: JS0370; MUID:90380393
A;Accession: JS0370
A;Molecule type: mRNA
A;Residues: 1-441 <GOE>
A;Note: six isoforms are found; the clone htau40 sequence is shown. Residues 45-73, 74-1
the clone htau24 sequence lacks inserts 1 and 2; the clone htau37 sequence lacks insert
R;Goedert, M.; Wischik, C.M.; Crowther, R.A.; Walker, J.E.; Klug, A.
Proc. Natl. Acad. Sci. U.S.A. 85, 4051-4055, 1988
A;Title: Cloning and sequencing of the cDNA encoding a core protein of the paired helica
A;Reference number: A30217; MUID:88234557
A;Accession: A30217
A;Molecule type: mRNA
A;Residues: 1-44,103-274,306-441 <GO2>
A;Cross-references: GB:J03778; NID:g338684; PIDN:AAA60615.1; PID:g338685
R;Lee, G.; Neve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A;Title: The microtubule binding domain of tau protein.
A;Reference number: JN0009; MUID:90180482
A;Accession: JN0009
A;Molecule type: mRNA
A;Residues: 1-44,103-274,306-441 <LEE>
R;Goedert, M.; Spillantini, M.G.; Potier, M.C.; Ulrich, J.; Crowther, R.A.
EMBO J. 8, 393-399, 1989
A;Title: Cloning and sequencing of the cDNA encoding an isoform of microtubule-associate
A;Reference number: S03796; MUID:89251564
A;Accession: S03796
A;Molecule type: mRNA
A;Residues: 1-44,103-441 <GO3>
A;Cross-references: EMBL:X14474; NID:g36724; PIDN:CAA32636.1; PID:g36725
R;Andreadis, A.; Brown, W.M.; Kosik, K.S.
Biochemistry 31, 10626-10633, 1992
A;Title: Structure and novel exons of the human tau gene.
A;Reference number: S26662; MUID:93041757
A;Accession: S26665
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 144-185 <AND>
A;Cross-references: EMBL:X61372; NID:g36718; PID:g36719
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
A;Accession: S26666
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 187-274 <AN2>
A;Cross-references: EMBL:X61374; NID:g36722; PID:g36723
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
A;Accession: S26662
A;Molecule type: DNA
A;Residues: 371-441 <ANW>
A;Cross-references: EMBL:X61373
R;Jakes, R.; Novak, M.; Davison, M.; Wischik, C.M.
EMBO J. 10, 2725-2729, 1991
A;Title: Identification of 3- and 4-repeat tau isoforms within the PHF in Alzheimer'
A;Reference number: S17302; MUID:92007714
A;Accession: S17302
A;Status: preliminary
A;Molecule type: protein
A;Residues: 268-274,306-395 <JAK>
R;Hasegawa, M.; Morishima-Kawashima, M.; Takio, K.; Suzuki, M.; Titani, K.; Ihara, Y
J. Biol. Chem. 267, 17047-17054, 1992
A;Title: Protein sequence and mass spectrometric analyses of tau in the Alzheimer's d
A;Reference number: A43444; MUID:92381012
A;Accession: A43444
A;Molecule type: protein
A;Residues: 2-73;103-130;151-180;191-254;260-269;275-290;299-317;322-340;344-347;354-
A;Experimental source: Alzheimer's disease brain
A;Note: sequence extracted from NCBI backbone (NCBIP:112039)
C;Comment: This heterogeneous protein, which is found predominantly in cells of the n
o the core protein of the paired helical filament of Alzheimer's disease.
C;Genetics:
A;Gene: GDB:MAPT
A;Cross-references: GDB:119434; OMIM:157140
A;Map position: 17q21-17q21
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule bindi
F;1-441/Product: microtubule-associated protein tau, long splice form #status predict
F;1-274,306-441/Product: microtubule-associated protein tau (clone htau39) #status pr
F;1-73,103-441/Product: microtubule-associated protein tau (clone htau34) #status pre
F;1-73,103-274,306-441/Product: microtubule-associated protein tau (clone htau37) #st
F;1-44,103-274,306-441/Product: microtubule-associated protein tau, fetal #status pre
F;1-44,103-441/Product: microtubule-associated protein tau type II #status predicted
F;252-282/Domain: MAP2/tau repeat homology <MT1>
F;283-313/Domain: MAP2/tau repeat homology <MT2>
F;314-344/Domain: MAP2/tau repeat homology <MT3>
F;345-376/Domain: MAP2/tau repeat homology <MT4>

Query Match 100.0%; Score 50; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 197 YSSPGSPGT 205

RESULT 8
QRBOT1
microtubule-associated protein tau, form 1 - bovine
N;Contains: microtubule-associated protein tau, form 2

```
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: A31939; A33914; S04005; A48885; A28173; B33734
R;Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.
Mol. Cell. Biol. 9, 1381-1388, 1989
A;Title: Tau consists of a set of proteins with repeated C-terminal microtubule-binding
A;Reference number: A31939; MUID:89261765
A;Accession: A31939
A;Molecule type: mRNA
A;Residues: 1-448 <HIM>
A;Cross-references: GB:M26157; NID:g514913; PIDN:AAA30770.1; PID:g514914
R;Iqbal, K.; Grundke-Iqbal, I.; Smith, A.J.; George, L.; Tung, Y.C.; Zaidi, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 5646-5650, 1989
A;Title: Identification and localization of a tau-peptide to paired helical filaments of
A;Reference number: A33914; MUID:89315854
A;Accession: A33914
A;Molecule type: protein
A;Residues: 28,'A',30-38,'IG',41,'AP',44,'LK' <IQB>
A;Experimental source: brain
A;Note: 40-Pro was also found
R;Iqbal, K.; Smith, A.J.; Zaidi, T.; Grundke-Iqbal, I.
FEBS Lett. 248, 87-91, 1989
A;Title: Microtubule-associated protein tau. Identification of a novel peptide from bovi
A;Reference number: S04005; MUID:89252057
A;Accession: S04005
A;Molecule type: protein
A;Residues: 28,'A',30-38,'IG',41,'AP',44,'LK' <IQ2>
A;Experimental source: brain
A;Note: 40-Pro was also found
R;Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.
J. Biol. Chem. 268, 23512-23518, 1993
A;Title: Brain proline-directed protein kinase phosphorylates tau on sites that are abnc
A;Reference number: A48885; MUID:94043150
A;Accession: A48885
A;Molecule type: protein
A;Residues: 'X',203-208,'X',210-211,'X',213-216;238-241,'X',243-247,'X';404-410,'X',412-
A;Experimental source: brain
A;Note: sequence modified after extraction from NCBI backbone
R;Aizawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
J. Biol. Chem. 263, 7703-7707, 1988
A;Title: Microtubule-binding domain of Tau proteins.
A;Reference number: A28173; MUID:88227970
A;Accession: A28173
A;Molecule type: protein
A;Residues: 205-218,'X',220-223 <AIZ>
A;Experimental source: brain
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
F;1-448/Product: microtubule-associated protein tau, form 1 #status predicted <BT43>
F;1-174,193-448/Product: microtubule-associated protein tau, form 2 #status predicted <E
F;205-223/Region: microtubule binding #status experimental
F;259-289/Domain: MAP2/tau repeat homology <MT1>
F;290-320/Domain: MAP2/tau repeat homology <MT2>
F;321-351/Domain: MAP2/tau repeat homology <MT3>
F;352-383/Domain: MAP2/tau repeat homology <MT4>
F;202,209,242,248,411/Binding site: phosphate (Ser) (covalent) (by proline-directed kina
F;212/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status expe

  Query Match             100.0%;  Score 50;  DB 1;  Length 448;
  Best Local Similarity   100.0%;  Pred. No. 0.84;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     204 YSSPGSPGT 212


RESULT   9
A38235
microtubule-associated protein, 110K tau - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Aug-1999
C;Accession: A38235
R;Goedert, M.; Spillantini, M.G.; Crowther, R.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 1983-1987, 1992
A;Title: Cloning of a big tau microtubule-associated protein characteristic of the p
A;Reference number: A38235; MUID:92179305
A;Accession: A38235
A;Molecule type: mRNA
A;Residues: 1-686 <GOE>
A;Cross-references: GB:M84156; NID:g207157; PIDN:AAA42204.1; PID:g207158
A;Note: sequence extracted from NCBI backbone (NCBIN:87358, NCBIP:87359)
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; microtubule binding; tandem repeat
F;497-527/Domain: MAP2/tau repeat homology <MT1>
F;528-558/Domain: MAP2/tau repeat homology <MT2>
F;559-589/Domain: MAP2/tau repeat homology <MT3>
F;590-621/Domain: MAP2/tau repeat homology <MT4>

  Query Match             100.0%;  Score 50;  DB 2;  Length 686;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     442 YSSPGSPGT 450


RESULT  10
A45301
microtubule-associated protein tau - mouse
N;Alternate names: microtubule binding protein tau
C;Species: Mus musculus (house mouse)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 13-Aug-1999
C;Accession: A45301; S31658
R;Couchie, D.; Mavilia, C.; Georgieff, I.S.; Liem, R.K.; Shelanski, M.L.; Nunez, J.
Proc. Natl. Acad. Sci. U.S.A. 89, 4378-4381, 1992
A;Title: Primary structure of high molecular weight tau present in the peripheral n
A;Reference number: A45301; MUID:92262443
A;Accession: A45301
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-733 <COU>
A;Note: this sequence is inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:102045, NCBIP:102046)
R;Kenner, L.; Forstner, M.; Hutter, H.; Hoefler, G.; Kurzbauer, R.; Zatloukal, K.;
submitted to the EMBL Data Library, May 1992
A;Description: First observation of mRNA for a tau-protein from murine liver and ki
A;Reference number: S31658
A;Accession: S31658
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'T',529-651 <KEN>
A;Cross-references: EMBL:Z12133; NID:g54263; PIDN:CAA78121.1; PID:g388534
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: microtubule binding; tandem repeat
F;544-574/Domain: MAP2/tau repeat homology <MT1>
F;575-605/Domain: MAP2/tau repeat homology <MT2>
F;606-636/Domain: MAP2/tau repeat homology <MT3>
F;637-668/Domain: MAP2/tau repeat homology <MT4>

  Query Match             100.0%;  Score 50;  DB 2;  Length 733;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     489 YSSPGSPGT 497


RESULT  11
T35638
hypothetical protein SC6G9.42c - Streptomyces coelicolor
```

```
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35638
R;Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21584
A;Accession: T35638
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-150 <SEE>
A;Cross-references: EMBL:AL079356; PIDN:CAB45633.1; GSPDB:GN00070; SCOEDB:SC6G9.42c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC6G9.42c


  Query Match             78.0%;  Score 39;  DB 2;  Length 150;
  Best Local Similarity   87.5%;  Pred. No. 18;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            |||| |||
Db       3 SSPGKPGT 10


RESULT  12
T36770
probable expression regulator - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36770
R;Saunders, D.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21613
A;Accession: T36770
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-272 <SAU>
A;Cross-references: EMBL:AL096849; PIDN:CAB50963.1; GSPDB:GN00070; SCOEDB:SCI11.37c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCI11.37c


  Query Match             78.0%;  Score 39;  DB 2;  Length 272;
  Best Local Similarity   66.7%;  Pred. No. 32;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            |: ||:|||
Db     170 YAPPGAPGT 178


RESULT  13
T34434
hypothetical protein K06A9.1a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T34434
R;Geisel, C.; Gattung, S.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid K06A9.
A;Reference number: Z21525
A;Accession: T34434
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2232 <GEI>
A;Cross-references: EMBL:U80846; PIDN:AAC70890.1; GSPDB:GN00028; CESP:K06A9.1a
A;Experimental source: strain Bristol N2; clone K06A9
C;Genetics:
A;Gene: CESP:K06A9.1a
A;Map position: X
A;Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 2075/


  Query Match             78.0%;  Score 39;  DB 2;  Length 2232;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
            |||||||
Db     886 SPGSPGT 892


RESULT  14
S72497
oligopeptide transport protein PepT1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C;Accession: S72497; S68161
R;Miyamoto, K.I.
submitted to the EMBL Data Library, June 1995
A;Reference number: S72497
A;Accession: S72497
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-710 <MIY>
A;Cross-references: EMBL:D50664; NID:g1384098; PIDN:BAA09318.1; PID:g1212746
R;Miyamoto, K.; Shiraga, T.; Morita, K.; Yamamoto, H.; Haga, H.; Taketani, Y.; Tamai
Biochim. Biophys. Acta 1305, 34-38, 1996
A;Title: Sequence, tissue distribution and developmental changes in rat intestinal o
A;Reference number: S68161; MUID:96180982
A;Accession: S68161
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-258,'E',260-278,'MV',281-710 <MI2>
A;Cross-references: GB:D50664
C;Genetics:
A;Gene: PepT1
C;Superfamily: peptide transport protein PEPT1
C;Keywords: oligopeptide transport; transmembrane protein; transport protein


  Query Match             76.0%;  Score 38;  DB 2;  Length 710;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
            |||||||
Db     441 SSPGSPG 447


RESULT  15
A55943
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-1 [vali
N;Alternate names: phosphoinositidase C; phospholipase C-delta-1; triphosphoinositide
C;Species: Homo sapiens (man)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: A55943
R;Cheng, H.F.; Jiang, M.J.; Chen, C.L.; Liu, S.M.; Wong, L.P.; Lomasney, J.W.; King,
J. Biol. Chem. 270, 5495-5505, 1995
A;Title: Cloning and identification of amino acid residues of human phospholipase Cde
A;Reference number: A55943; MUID:95197554
A;Accession: A55943
A;Molecule type: mRNA
A;Residues: 1-756 <CHE>
A;Cross-references: GB:U09117; NID:g483919; PIDN:AAA73567.1; PID:g483920
A;Experimental source: aortic smooth muscle
C;Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-tripho
C;Genetics:
A;Gene: GDB:PLCD1
A;Cross-references: GDB:6075994
C;Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-p
phosphodiesterase domain Y homology; calmodulin repeat homology; pleckstrin repeat ho
C;Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; si
F;19-128/Domain: pleckstrin repeat homology <PLK>
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F;140-172/Domain: calmodulin repeat homology <EF1>
F;176-208/Domain: calmodulin repeat homology <EF2>
F;298-440/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
F;491-612/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
F;614-724/Domain: protein kinase C C2 region homology <KC2>


  Query Match             76.0%;  Score 38;  DB 1;  Length 756;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
            :||||:||
Db     507 FSSPGTPG 514


RESULT  16
T29090
surface layer-associated STABLE proteinase - Staphylothermus marinus
N;Alternate names: hyperthermostable proteinase
C;Species: Staphylothermus marinus
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T29090
R;Mayr, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J.
Curr. Biol. 6, 739-749, 1996
A;Title: A hyperthermostable protease of the subtilisin family bound to the surface laye
A;Reference number: Z20559; MUID:96385442
A;Accession: T29090
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1345 <MAY>
A;Cross-references: EMBL:U57968; NID:g1374755; PID:g1374756; PIDN:AAB02323.1
A;Experimental source: strain F1
C;Function:
A;Description: probably serves an exodigestive function related to the organism's energy
A;Note: stoichiometric S-layer component


  Query Match             76.0%;  Score 38;  DB 2;  Length 1345;
  Best Local Similarity   77.8%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            ||| |:|||
Db     596 YSSNGAPGT 604


RESULT  17
T17202
DNA-directed DNA polymerase (EC 2.7.7.7) zeta chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17202
R;Van Sloun, P.P.H.; Romeijn, R.J.; Eeken, J.C.J.
Mutat. Res. 433, 109-116, 1999
A;Title: Molecular cloning, expression and chromosomal localisation of the mouse Rev31 g
A;Reference number: Z18720; MUID:99202265
A;Accession: T17202
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3122 <VAN>
A;Cross-references: EMBL:AF083464; NID:g4079830; PID:g4079831; PIDN:AAC98785.1
A;Experimental source: strain 129/Ola; testis
C;Genetics:
A;Map position: 10
C;Keywords: nucleotidyltransferase


  Query Match             76.0%;  Score 38;  DB 2;  Length 3122;
  Best Local Similarity   87.5%;  Pred. No. 5.4e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
            |||| |||
Db    2108 YSSPDSPG 2115


RESULT  18
B88066
protein R52.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: B88066
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bi
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A;Accession: B88066
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-168 <STO>
A;Cross-references: GB:chr_II; PIDN:AB71062.1; PID:g2429536; GSPDB:GN00020; CESP:R52
C;Genetics:
A;Gene: R52.4
A;Map position: 2


  Query Match             74.0%;  Score 37;  DB 2;  Length 168;
  Best Local Similarity   75.0%;  Pred. No. 43;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            ::||||||
Db      40 TTPGSPGT 47


RESULT  19
T40490
probable 26s proteasome regulatory subunit - fission yeast (Schizosaccharomyces pom
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: T40490
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft,
submitted to the EMBL Data Library, February 1998
A;Reference number: Z21910
A;Accession: T40490
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-302 <WOO>
A;Cross-references: EMBL:AL021730; PIDN:CAA16829.1; GSPDB:GN00067; SPDB:SPBC4C3.07
A;Experimental source: strain 972h-; cosmid c4C3
C;Genetics:
A;Gene: SPDB:SPBC4C3.07
A;Map position: 2
C;Superfamily: mov-34 protein


  Query Match             74.0%;  Score 37;  DB 2;  Length 302;
  Best Local Similarity   66.7%;  Pred. No. 77;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            |:||  |||
Db     123 YASPAEPGT 131


RESULT  20
A40267
interleukin-5 receptor alpha chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
C;Accession: A40267
R;Tavernier, J.; Devos, R.; Cornelis, S.; Tuypens, T.; Van der Heyden, J.; Fiers,
Cell 66, 1175-1184, 1991
```

```
A;Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-speci
A;Reference number: A40267; MUID:92005669
A;Accession: A40267
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-335 <TAV>
A;Cross-references: GB:M75914; NID:g186387; PIDN:AAA36110.1; PID:g186388
C;Keywords: cytokine receptor; transmembrane protein


  Query Match             74.0%;  Score 37;  DB 2;  Length 335;
  Best Local Similarity   66.7%;  Pred. No. 85;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          :: ||||||
Db    119 HAPPGSPGT 127


RESULT  21
JQ1946
core protein VP7 - African horse sickness virus (serotype 4, strain Spane)
C;Species: African horse sickness virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jun-2000
C;Accession: JQ1946
R;Roy, P.; Hirasawa, T.; Fernandez, M.; Blinov, V.M.; Sanchez-Vixcain Rodrique, J.M.
J. Gen. Virol. 72, 1237-1241, 1991
A;Title: The complete sequence of the group-specific antigen, VP7, of African horsesickn
A;Reference number: JQ1946; MUID:91259049
A;Accession: JQ1946
A;Molecule type: genomic RNA
A;Residues: 1-353 <ROY>
A;Cross-references: GB:D12533; NID:g221010; PIDN:BAA02096.1; PID:g221011
C;Genetics:
A;Map position: segment 7
C;Superfamily: bluetongue virus core protein VP7
C;Keywords: core protein


  Query Match             74.0%;  Score 37;  DB 1;  Length 353;
  Best Local Similarity   75.0%;  Pred. No. 90;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 SSPGSPGT 9
          |:||:|||
Db    204 SAPGAPGT 211


RESULT  22
AE3191
conserved hypothetical protein Atu5258 [imported] - Agrobacterium tumefaciens (strain C5
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AE3191
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AE3191
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-372 <KUR>
A;Cross-references: GB:AE008687; PIDN:AAL45947.1; PID:g17743697; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu5258
A;Genome: plasmid


  Query Match             74.0%;  Score 37;  DB 2;  Length 372;
  Best Local Similarity   66.7%;  Pred. No. 94;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          |  |||||:
Db    146 YHQPGSPGS 154


RESULT  23
S16844
titin - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Jun-1999
C;Accession: S16844
R;Fritz, J.D.; Greaser, M.L.; Wolff, J.A.
Nucleic Acids Res. 19, 3747, 1991
A;Title: A novel 3' extension technique using random primers in RNA-PCR.
A;Reference number: S16844; MUID:91305130
A;Accession: S16844
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-393 <FRI>
A;Cross-references: EMBL:X59596; NID:g1722; PIDN:CAA42165.1; PID:g1723
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1991
C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology;


  Query Match             74.0%;  Score 37;  DB 2;  Length 393;
  Best Local Similarity   66.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          |  || |||
Db     55 YKEPGPPGT 63


RESULT  24
W2WLEP
E2 protein - European elk papillomavirus
C;Species: European elk papillomavirus
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-May-2000
C;Accession: D29499; D94457; D94506
R;Ahola, H.; Bergman, P.; Stroem, A.C.; Moreno-Lopez, J.; Pettersson, U.
Gene 50, 195-205, 1986
A;Title: Organization and expression of the transforming region from the European elk
A;Reference number: A91567; MUID:87219878
A;Accession: D29499
A;Molecule type: DNA
A;Residues: 1-415 <AHO>
A;Cross-references: GB:M15953; NID:g333025; PIDN:AAA66854.1; PID:g484020
R;Eriksson, A.
unpublished results 1987, cited by GenBank
A;Reference number: A94457
A;Accession: D94457
A;Molecule type: DNA
A;Residues: 1-415 <ERI>
A;Cross-references: GB:M15953; NID:g333025; PIDN:AAA66854.1; PID:g484020
R;Pettersson, U.
submitted to GenBank, August 1987
A;Reference number: A94506
A;Accession: D94506
A;Molecule type: DNA
A;Residues: 1-415 <PET>
A;Cross-references: GB:M15953; NID:g333025; PIDN:AAA66854.1; PID:g484020
C;Superfamily: papillomavirus E2 protein
C;Keywords: early protein


  Query Match             74.0%;  Score 37;  DB 1;  Length 415;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       1 YSSPGSPGT 9
             ||:| |||:
Db     268 YSAPSSPGS 276


RESULT  25
S29506
neurotensin receptor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000
C;Accession: S29506
R;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Dumont, X.; Kaghad, M.; Gully, D.; le F
FEBS Lett. 317, 139-142, 1993
A;Title: Cloning and expression of a complementary DNA encoding a high affinity human ne
A;Reference number: S29506; MUID:93154505
A;Accession: S29506
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-418 <VIT>
A;Cross-references: EMBL:X70070; NID:g35020; PIDN:CAA49675.1; PID:g35021
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein


  Query Match             74.0%;  Score 37;  DB 2;  Length 418;
  Best Local Similarity   75.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           |:||:|||
Db       6 SAPGTPGT 13


RESULT  26
S21052
interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored is
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C;Accession: S21052; S21050; S21053; A46175; S78106; S78107
R;Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression of the human interleukin 5 receptor.
A;Reference number: S21050; MUID:92121815
A;Accession: S21052
A;Molecule type: DNA
A;Residues: 1-420 <MUR>
A;Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844
A;Experimental source: clone lambda h5R.12
A;Accession: S21050
A;Molecule type: DNA
A;Residues: 1-395,'I' <MU2>
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
A;Experimental source: clone lambda h5R.27
A;Accession: S21053
A;Molecule type: mRNA
A;Residues: 1-332,'K' <MU3>
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
A;Experimental source: clone lambda h5R.25
R;Tavernier, J.; Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A;Title: Molecular basis of the membrane-anchored and two soluble isoforms of the human
A;Reference number: A46175; MUID:92357767
A;Accession: A46175
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 333-420 <TAV>
A;Experimental source: HL-60 cells and eosinophils
A;Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
R;Murata, Y.
submitted to the EMBL Data Library, July 1991
A;Reference number: S78106
A;Accession: S78106
A;Molecule type: DNA
A;Residues: 1-128,'I',130-395,'I' <MUW>
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
R;Murata, Y.
submitted to the EMBL Data Library, September 1991
A;Reference number: S78107
A;Accession: S78107
A;Molecule type: mRNA
A;Residues: 1-128,'I',130-332,'K' <MU4>
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane pro
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>
F;345-365/Domain: transmembrane #status predicted <TMM>
F;35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predict


  Query Match             74.0%;  Score 37;  DB 2;  Length 420;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
             :: ||||||
Db     119 HAPPGSPGT 127


RESULT  27
H75589
aldehyde dehydrogenase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: H75589
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
A;Reference number: A75250; MUID:20036896
A;Accession: H75589
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-515 <WHI>
A;Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12436.1; PID:g6
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRA0348
A;Map position: 2
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology


  Query Match             74.0%;  Score 37;  DB 2;  Length 515;
  Best Local Similarity   55.6%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
             |::||:||:
Db      13 YANPGTPGS 21


RESULT  28
A44358
zyxin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Jun-1993 #sequence_revision 06-Feb-1995 #text_change 21-Jul-2000
C;Accession: A44358; S30506
R;Sadler, I.; Crawford, A.W.; Michelsen, J.W.; Beckerle, M.C.
J. Cell Biol. 119, 1573-1587, 1992
A;Title: Zyxin and cCRP: two interactive LIM domain proteins associated with the cy
A;Reference number: A44358; MUID:93107157
A;Accession: A44358
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-542 <SAD>
A;Cross-references: EMBL:X69190; NID:g63897; PIDN:CAA48936.1; PID:g63898
```

A;Note: sequence extracted from NCBI backbone (NCBIN:121172, NCBIP:121174)
A;Note: this sequence may be one segment of several
C;Superfamily: LIM metal-binding repeat homology
F;352-404/Domain: LIM metal-binding repeat homology <LIM1>
F;412-463/Domain: LIM metal-binding repeat homology <LIM2>
F;472-533/Domain: LIM metal-binding repeat homology <LIM3>

Query Match 74.0%; Score 37; DB 2; Length 542;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
:|||:|||
Db 2 ASPGTPGT 9

RESULT 29
A53800
mixed-lineage protein kinase (EC 2.7.1.-) 3 - human
N;Alternate names: protein kinase PTK1; protein kinase SPRK
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A53800; I58395
R;Gallo, K.A.; Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J.
J. Biol. Chem. 269, 15092-15100, 1994
A;Title: Identification and characterization of SPRK, a novel src-homology 3 domain-cont
A;Reference number: A53800; MUID:94253068
A;Accession: A53800
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-847 <GAL>
A;Cross-references: GB:U07747; NID:g464027; PIDN:AAA19647.1; PID:g464028
R;Ing, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassam, N.J.
Oncogene 9, 1745-1750, 1994
A;Title: MLK-3: identification of a widely-expressed protein kinase bearing an SH3 domai
A;Reference number: I58395; MUID:94239754
A;Accession: I58395
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-847 <RES>
A;Cross-references: GB:L32976; NID:g488295; PIDN:AAA59859.1; PID:g488296
C;Genetics:
A;Gene: GDB:MLK3; PTK1; SPRK
A;Cross-references: GDB:134755; OMIM:600050
A;Map position: 11q13.1-11q13.3
C;Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
C;Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein k
F;48-100/Domain: SH3 homology <SH32>
F;115-383/Domain: protein kinase homology <KIN>
F;123-131/Region: protein kinase ATP-binding motif
F;403-424/Region: leucine zipper motif
F;438-459/Region: leucine zipper motif
F;468-482/Region: basic

Query Match 74.0%; Score 37; DB 1; Length 847;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
|:||:|||
Db 748 SAPGTPGT 755

RESULT 30
T19140
hypothetical protein C09G5.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19140
R;Palmer, S.
submitted to the EMBL Data Library, November 1994
A;Reference number: Z19080
A;Accession: T19140
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-963 <WIL>
A;Cross-references: EMBL:Z46791; PIDN:CAA86755.1; GSPDB:GN00020; CESP:C09G5.6
A;Experimental source: clone C09G5
C;Genetics:
A;Gene: CESP:C09G5.6
A;Map position: 2
A;Introns: 48/3; 862/3; 898/1

Query Match 74.0%; Score 37; DB 2; Length 963;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
|:||:|||
Db 559 SAPGAPGT 566

RESULT 31
JC5502
G-protein signaling regulator 12 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C;Accession: JC5502
R;Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, D.P.
Biochem. Biophys. Res. Commun. 233, 770-777, 1997
A;Title: Molecular cloning and expression analysis of rat Rgs12 and Rgs14.
A;Reference number: JC5502; MUID:97312490
A;Accession: JC5502
A;Molecule type: mRNA
A;Residues: 1-1387 <SNO>
A;Cross-references: GB:U92280; NID:g2088557; PIDN:AAC53176.1; PID:g2088558
C;Comment: This protein funcitons as GTPase activating protein. It interacts with ras
F;18-80/Domain: rhophilin-like #status predicted <RHO>
F;712-761/Domain: GH1 #status predicted <GH1>
F;765-800/Domain: GH2 #status predicted <GH2>
F;804-828/Domain: GH3 #status predicted <GH3>
F;1204-1220/Region: conserved #status predicted
F;1266-1295/Region: coiled heptad repeat (S-P-X-S-A)

Query Match 74.0%; Score 37; DB 2; Length 1387;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
:|:|| |||
Db 1296 HSTPGPPGT 1304

RESULT 32
S28353
probable polyketide synthase - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-May-2000
C;Accession: S28353
R;Mayorga, M.E.; Timberlake, W.E.
Mol. Gen. Genet. 235, 205-212, 1992
A;Title: The developmentally regulated Aspergillus nidulans wA gene encodes a polypep
A;Reference number: S28353; MUID:93101122
A;Accession: S28353
A;Molecule type: DNA
A;Residues: 1-1986 <MAY>
A;Cross-references: EMBL:X65866; NID:g5508; PID:g5509
C;Genetics:
A;Gene: wA
A;Introns: 96/2; 193/3; 1336/3; 1588/3
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acyl carrier pro
C;Keywords: carrier protein

F;397-805/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F;911-1199/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1648-1718/Domain: acyl carrier protein homology <ACP>
F;1766-1840/Domain: acyl carrier protein homology <ACP1>

Query Match 74.0%; Score 37; DB 2; Length 1986;
Best Local Similarity 87.5%; Pred. No. 5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
||| ||||
Db 1749 SSPASPGT 1756

RESULT 33
T09456
intrinsic factor-B12 receptor Cubilin precursor - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09456
R;Kozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
ion.
A;Reference number: Z16677; MUID:98241400
A;Accession: T09456
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3623 <KOZ>
A;Cross-references: EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3929529
C;Genetics:
A;Map position: 10p12
C;Superfamily: unassigned EGF-related proteins; EGF homology
C;Keywords: receptor; vitamin B12 uptake
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F;436-467/Domain: EGF homology <EGF>

Query Match 74.0%; Score 37; DB 2; Length 3623;
Best Local Similarity 66.7%; Pred. No. 9.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
::||| |||
Db 3522 FTSPGYPGT 3530

RESULT 34
S20901
titin - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C;Accession: S20901; I46520
R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.
EMBO J. 11, 1711-1716, 1992
A;Title: Towards a molecular understanding of titin.
A;Reference number: S20897; MUID:92258380
A;Accession: S20901
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-6805 <LAB>
A;Cross-references: EMBL:X64696
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R;Labeit, S.; Barlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Hsieh, C.L.; Francke, U.;
Nature 345, 273-276, 1990
A;Title: A regular pattern of two types of 100-residue motif in the sequence of titin.
A;Reference number: I46520; MUID:90238553
A;Accession: I46520
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 4235-5250 <LA2>
A;Cross-references: EMBL:X17329; NID:g1756; PIDN:CAA35207.1; PID:g930251
C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology;
C;Keywords: muscle

Query Match 74.0%; Score 37; DB 2; Length 6805;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
| || |||
Db 5282 YKEPGPPGT 5290

RESULT 35
I38344
titin, cardiac muscle [validated] - human
N;Alternate names: connectin
N;Contains: serine/threonine-specific protein kinase (EC 2.7.1.-)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Sep-2000
C;Accession: I38344; I38345; S20898; S20897; S20899; S63665; S37393
R;Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Reference number: A57430; MUID:96026330
A;Accession: I38344
A;Status: nucleic acid sequence not shown; translation not shown; translated from GI
A;Molecule type: mRNA
A;Residues: 1-26926 <LAB1>
A;Cross-references: EMBL:X90568; NID:g1017424; PID:g1017425
R;Musco, G.; Tziatzios, C.; Schuck, P.; Pastore, A.
Biochemistry 34, 553-561, 1995
A;Title: Dissecting titin into its structural motifs: identification of an alpha-he
A;Reference number: I38345; MUID:95119041
A;Accession: I38345
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1977-2014 <MUS>
A;Cross-references: EMBL:X83270; NID:g602579; PIDN:CAA58243.1; PID:g602580
A;Note: conformation and properties are reported for a synthetic peptide correspond
R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.
EMBO J. 11, 1711-1716, 1992
A;Title: Towards a molecular understanding of titin.
A;Reference number: S20897; MUID:92258380
A;Accession: S20898
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 13597-14200,'I',14202-14696 <LAB2>
A;Cross-references: EMBL:X64698; NID:g37192; PIDN:CAA45939.1; PID:g37193
A;Accession: S20897
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 16330-16382,'S',16384-16756,'F',16758-16860 <LAB3>
A;Cross-references: EMBL:X64699; NID:g37190; PIDN:CAA45940.1; PID:g37191
A;Accession: S20899
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 'P',22278-22431,'R',22433-22448,'G',22450-22453,'Q',22455-22480,'TR',2
A;Cross-references: EMBL:X64697; NID:g37190; PIDN:CAA45938.1; PID:g37195
R;Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labeit, S.
J. Mol. Biol. 256, 556-563, 1996
A;Title: Genomic organization of M line titin and its tissue-specific expression i
A;Reference number: S63665; MUID:96177761
A;Accession: S63665
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 26729-26825 <KOL>
A;Cross-references: EMBL:X92412; NID:g1236761
R;Gautel, M.; Leonard, K.; Labeit, S.
EMBO J. 12, 3827-3834, 1993
A;Title: Phosphorylation of KSP motifs in the C-terminal region of titin in differ
A;Reference number: S37393; MUID:94008990

A;Accession: S37393
A;Molecule type: mRNA
A;Residues: 26831-26926 <GAU>
R;Improta, S.; Politou, A.S.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, February 1996
A;Reference number: A66736; PDB:1TIT
A;Contents: annotation; conformation by (1)H-NMR, residues 5253-5341
R;Pfuhl, M.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A66201; PDB:1NCT
A;Contents: annotation; conformation by (1)H-NMR, residues 'S',26059-26155
C;Genetics:
A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q32
C;Function:
A;Description: structural protein forming filaments in striated muscle
C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; prc
C;Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; glycc
structural protein
F;24752-25008/Domain: protein kinase homology <KIN>
F;84,177,905,2276,2378,2459,2481,2563,2669,2763,2896,3088,3179,3384,3432,3628,3772,4068,
98,11066,11488,11515,11635,11949,12170,12478,12526,12645,12875,13001,13036,13295,13540,1
tatus predicted
F;16780,16976,17579,17602,17667,17681,17845,17899,18121,18188,18209,18336,18670,18680,18
,21900,21935,22295,22495,22627,22897,23024,23318,23883,24012,24177,24290,24447,24642,248
F;26171,26178,26184,26190/Binding site: phosphate (Ser) (covalent) #status experimental

  Query Match 74.0%; Score 37; DB 1; Length 26926;
  Best Local Similarity 66.7%; Pred. No. 6.7e+03;
  Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
 | || |||
Db 16923 YKEPGPPGT 16931

RESULT 36
T17003
dormancy-associated protein [similarity] - apple tree
C;Species: Malus domestica (apple tree)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T17003
R;Lee, S.A.; Gardner, R.C.; Lay-Yee, M.
Plant Physiol. 103, 1017, 1993
A;Title: An apple gene highly expressed in fruit.
A;Reference number: Z18646; MUID:94294548
A;Accession: T17003
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-119 <LEE>
A;Cross-references: EMBL:L15194; NID:g439878; PIDN:AAA71994.1; PID:g439879
A;Experimental source: cultivar Golden delicious; fruit cortical

  Query Match 72.0%; Score 36; DB 2; Length 119;
  Best Local Similarity 85.7%; Pred. No. 44;
  Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SPGSPGT 9
 |||:|||
Db 51 SPGTPGT 57

RESULT 37
S41860
gene Nkx-1.1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C;Accession: S41860
R;Schubert, F.R.; Gruss, P.
submitted to the EMBL Data Library, October 1993
A;Description: Expression of the novel Murine homeobox gene Nkx-1.1 in the developin
A;Reference number: S41860
A;Accession: S41860
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <SCH>
A;Cross-references: EMBL:X75384; NID:g453171; PIDN:CAA53153.1; PID:g453172
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;157-213/Domain: homeobox homology <HOX>

  Query Match 72.0%; Score 36; DB 2; Length 305;
  Best Local Similarity 75.0%; Pred. No. 1.1e+02;
  Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSPGSPGT 9
 :||||||:
Db 134 ASPGSPGS 141

RESULT 38
A55983
microtubule-associated protein MAP2 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 23-Aug-1997
C;Accession: A55983; A41011; A33734
R;Coffey, R.L.; Joly, J.C.; Cain, B.D.; Purich, D.L.
Biochemistry 33, 13199-13207, 1994
A;Title: Exploring the microtubule-binding region of bovine microtubule-associated pr
A;Reference number: A55983; MUID:95034751
A;Accession: A55983
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-323 <COF>
A;Cross-references: GB:S74025
R;Dingus, J.; Obar, R.A.; Hyams, J.S.; Goedert, M.; Vallee, R.B.
J. Biol. Chem. 266, 18854-18860, 1991
A;Title: Use of a heat-stable microtubule-associated protein class-specific antibody
A;Reference number: A41011; MUID:92011652
A;Accession: A41011
A;Molecule type: protein
A;Residues: 227-258 <DIN>
R;Joly, J.C.; Flynn, G.; Purich, D.L.
J. Cell Biol. 109, 2289-2294, 1989
A;Title: The microtubule-binding fragment of microtubule-associated protein-2: locati
A;Reference number: A33734; MUID:90037224
A;Accession: A33734
A;Status: preliminary
A;Molecule type: protein
A;Residues: 121-139 <JOL>
C;Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
C;Keywords: microtubule binding; tandem repeat
F;165-195/Domain: MAP2/tau repeat homology <MT1>
F;227-258/Domain: MAP2/tau repeat homology <MT2>

  Query Match 72.0%; Score 36; DB 2; Length 323;
  Best Local Similarity 72.7%; Pred. No. 1.2e+02;
  Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy 1 YSS--PGSPGT 9
 ||| ||:|||
Db 105 YSSRTPGTPGT 115

RESULT 39
T32783
hypothetical protein C50D2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C;Accession: T32783
R;Sammons, L.; Wohldmann, P.; Bauer, C.

submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid C50D2.
A;Reference number: Z21224
A;Accession: T32783
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-329 <SAM>
A;Cross-references: EMBL:AF040642; PIDN:AAB94952.1; GSPDB:GN00020; CESP:C50D2.4
A;Experimental source: strain Bristol N2; clone C50D2
C;Genetics:
A;Gene: CESP:C50D2.4
A;Map position: 2
A;Introns: 27/1; 59/3; 76/3; 237/1
C;Superfamily: unassigned collagens

Query Match 72.0%; Score 36; DB 2; Length 329;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SPGSPGT 9
||| :|||
Db 160 SPGNPGT 166

RESULT 40
A75621
TorS-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: A75621
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
A;Accession: A75621
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-351 <WHI>
A;Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12581.1; PID:g6460877; TIGR:DRB00
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRB0027
A;Map position: megaplasmid
A;Genome: plasmid
A;Note: plasmid MP1

Query Match 72.0%; Score 36; DB 2; Length 351;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|| : |:|||
Db 95 YSTAGTPGT 103

Search completed: May 21, 2002, 11:19:11
Job time: 206 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 21, 2002, 11:24:11 ; Search time 13.48 Seconds
(without alignments)
25.851 Million cell updates/sec

Title: US-09-734-281-2
Perfect score: 50
Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	382	1	TAU_PAPHA	Q9myx8 papio hamad
2	50	100.0	402	1	TAU_CAPHI	O02828 capra hircu
3	50	100.0	447	1	TAU_BOVIN	P29172 bos taurus
4	50	100.0	458	1	TAU_MACMU	P57786 macaca mula
5	50	100.0	732	1	TAU_MOUSE	P10637 mus musculu
6	50	100.0	751	1	TAU_RAT	P19332 rattus norv
7	50	100.0	757	1	TAU_HUMAN	P10636 homo sapien
8	39	78.0	639	1	P2B1_CRYNE	O42773 cryptococcu
9	38	76.0	710	1	PET1_RAT	P51574 rattus norv
10	38	76.0	756	1	PID1_HUMAN	P51178 homo sapien
11	38	76.0	3122	1	DPOZ_MOUSE	Q61493 mus musculu
12	37	74.0	164	1	CDN1_FELCA	O19002 felis silve
13	37	74.0	387	1	TIZ2_MOUSE	Q9eqn3 mus musculu
14	37	74.0	395	1	TIZ2_HUMAN	Q9y3q8 homo sapien
15	37	74.0	415	1	VE2_PAPVE	P11329 european el
16	37	74.0	418	1	NTR1_HUMAN	P30989 homo sapien
17	37	74.0	420	1	IL5R_HUMAN	Q01344 homo sapien
18	37	74.0	515	1	DHAL_DEIRA	Q9ryg9 deinococcus
19	37	74.0	542	1	ZYX_CHICK	Q04584 gallus gall
20	37	74.0	963	1	YQ36_CAEEL	Q09457 caenorhabdi
21	37	74.0	1387	1	RGSC_RAT	O08774 rattus norv
22	37	74.0	1986	1	WA_EMENI	Q03149 emericella
23	36	72.0	305	1	SAX1_MOUSE	P42580 mus musculu
24	36	72.0	501	1	PYCA_METJA	Q58626 methanococc
25	36	72.0	511	1	GUNB_PSEFL	P18126 pseudomonas
26	36	72.0	603	1	BUD8_YEAST	P41698 saccharomyc
27	36	72.0	680	1	CA1A_MOUSE	Q05306 mus musculu
28	36	72.0	1171	1	TRI2_STRCO	Q9rkb9 streptomyce
29	36	72.0	1827	1	MAP2_HUMAN	P11137 homo sapien
30	36	72.0	1828	1	MAP2_MOUSE	P20357 mus musculu
31	36	72.0	1861	1	MAP2_RAT	P15146 rattus norv
32	35	70.0	159	1	CDN1_MOUSE	P39689 mus musculu
33	35	70.0	386	1	UR2R_RAT	P49684 rattus norv
34	35	70.0	415	1	IL5R_MOUSE	P21183 mus musculu
35	35	70.0	495	1	HXKG_ASPNG	Q92407 aspergillus
36	35	70.0	573	1	AMH2_HUMAN	Q16671 homo sapien
37	35	70.0	828	1	MRKC_KLEPN	P21647 klebsiella
38	35	70.0	903	1	VGLB_HSV1F	P06436 herpes simp
39	35	70.0	904	1	VGLB_HSV11	P10211 herpes simp
40	35	70.0	904	1	VGLB_HSV1P	P08665 herpes simp
41	35	70.0	956	1	RRPO_SBMV	P21405 southern be
42	35	70.0	1464	1	CA13_MOUSE	P08121 mus musculu
43	35	70.0	1690	1	CA44_HUMAN	P53420 homo sapien
44	35	70.0	1835	1	CCAI_RAT	Q9z0y8 rattus norv
45	34	68.0	114	1	ET3_RABIT	P19998 oryctolagus
46	34	68.0	238	1	ET3_HUMAN	P14138 homo sapien
47	34	68.0	239	1	CALD_MELGA	P13505 meleagris g
48	34	68.0	239	1	MABA_MOUSE	P39039 mus musculu
49	34	68.0	249	1	PSPA_PIG	P49874 sus scrofa
50	34	68.0	298	1	34KD_MYCPA	Q04959 mycobacteri
51	34	68.0	467	1	RPB1_CRIGR	P11414 cricetulus
52	34	68.0	492	1	DYJ2_HUMAN	O43237 homo sapien
53	34	68.0	508	1	CILA_KLEPN	P45413 klebsiella
54	34	68.0	520	1	MRCO_HUMAN	Q9uew3 homo sapien
55	34	68.0	547	1	CD19_MOUSE	P25918 mus musculu

ALIGNMENTS

```
RESULT   1
TAU_PAPHA
ID   TAU_PAPHA      STANDARD;      PRT;   382 AA.
AC   Q9MYX8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR TAU.
OS   Papio hamadryas (Hamadryas baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Papio.
OX   NCBI_TaxID=9557;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Frontal cortex;
RA   Wang X.L., Wang J., Schultz C., Hubbard G.B.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC       BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC       POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC       TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC       TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC       CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS (BY
CC       SIMILARITY).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
CC   -!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC       CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC       MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC       MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF281310; AAF97596.1; -.
DR   InterPro; IPR002955; Tau_protein.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 4.
DR   PRINTS; PR01261; TAUPROTEIN.
DR   PROSITE; PS00229; TAU_MAP; 4.
KW   Microtubules; Cytoskeleton; Repeat; Acetylation; Phosphorylation.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   REPEAT      185    215       TAU/MAP MOTIF 1.
FT   REPEAT      216    246       TAU/MAP MOTIF 2.
FT   REPEAT      247    277       TAU/MAP MOTIF 3.
FT   REPEAT      278    309       TAU/MAP MOTIF 4.
FT   MOD_RES       1.     1       ACETYLATION (BY SIMILARITY).
FT   DISULFID    232    263       BY SIMILARITY.
SQ   SEQUENCE   382 AA;  39879 MW;  D2D15A53AA00E8E7 CRC64;


  Query Match             100.0%;  Score 50;  DB 1;  Length 382;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     138 YSSPGSPGT 146


RESULT   2
TAU_CAPHI
ID   TAU_CAPHI      STANDARD;      PRT;   402 AA.
AC   O02828;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR TAU.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC   TISSUE=Brain cortex;
RX   MEDLINE=97012131; PubMed=8858947;
RA   Nelson P.T., Stefansson K., Gulcher J., Saper C.B.;
RT   "Molecular evolution of tau protein: implications for Alzheimer's
RT   disease.";
RL   J. Neurochem. 67:1622-1632(1996).
CC   -!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC       BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC       POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC       TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC       TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
CC       ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
CC       ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC       CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; TAU-A (SHOWN HERE) AND
CC       TAU-B; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER FROM EACH
CC       OTHER BY THE PRESENCE OR ABSENCE OF TWO EXONS. ONE OF THESE
CC       OPTIONAL EXONS CONTAINS THE ADDITIONAL TAU/MAP REPEAT.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
CC   -!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
CC       CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC       CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC       MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC       MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S83347; AAB50785.1; -.
DR   InterPro; IPR002955; Tau_protein.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 4.
DR   PRINTS; PR01261; TAUPROTEIN.
DR   PROSITE; PS00229; TAU_MAP; 4.
KW   Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
KW   Phosphorylation.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   REPEAT      205    235       TAU/MAP MOTIF 1.
FT   REPEAT      236    266       TAU/MAP MOTIF 2.
FT   REPEAT      267    297       TAU/MAP MOTIF 3.
FT   REPEAT      298    329       TAU/MAP MOTIF 4.
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   DISULFID    252    283       BY SIMILARITY.
FT   VARSPLIC     33     61       MISSING (IN ISOFORM TAU-B).
FT   VARSPLIC    236    266       MISSING (IN ISOFORM TAU-B).
SQ   SEQUENCE   402 AA;  41716 MW;  3E623B684E9F8AEF CRC64;


  Query Match             100.0%;  Score 50;  DB 1;  Length 402;
  Best Local Similarity   100.0%;  Pred. No. 0.32;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     158 YSSPGSPGT 166


RESULT   3
TAU_BOVIN
ID   TAU_BOVIN      STANDARD;      PRT;   447 AA.
AC   P29172; P29173; Q28185; Q28186; Q28187; Q28188; Q28189; Q28190;
DT   01-DEC-1992 (Rel. 24, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR TAU.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-A; TAU-B; TAU-G AND TAU-H).
RC   TISSUE=Brain;
RX   MEDLINE=89261765; PubMed=2498649;
RA   Himmler A., Drechsel D., Kirschner M.W., Martin D.W. Jr.;
RT   "Tau consists of a set of proteins with repeated C-terminal
RT   microtubule-binding domains and variable N-terminal domains.";
RL   Mol. Cell. Biol. 9:1381-1388(1989).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-A TO TAU-F AND TAU-I TO TAU-T).
RC   TISSUE=Brain;
RX   MEDLINE=89261766; PubMed=2498650;
RA   Himmler A.;
RT   "Structure of the bovine tau gene: alternatively spliced transcripts
RT   generate a protein family.";
RL   Mol. Cell. Biol. 9:1389-1396(1989).
RN   [3]
RP   GLYCOSYLATION.
RX   MEDLINE=97067111; PubMed=8910513;
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RA   Arnold C.S., Johnson G.V.W., Cole R.N., Dong D.L.-Y., Lee M.,
RA   Hart G.W.;
RT   "The microtubule-associated protein tau is extensively modified with
RT   O-linked N-acetylglucosamine.";
RL   J. Biol. Chem. 271:28741-28744(1996).
CC   -!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC       BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC       POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC       TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC       TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
CC       ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
CC       ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC       CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 20 ISOFORMS; TAU-A/PBT43I12 (SHOWN
CC       HERE), TAU-B/PBT43-12, TAU-C, TAU-D, TAU-E, TAU-F, TAU-G/PBT4,
CC       TAU-H/PBT7, TAU-I, TAU-J, TAU-K, TAU-L, TAU-M, TAU-N, TAU-O, TAU-
CC       P, TAU-Q, TAU-R, TAU-S AND TAU-T; ARE PRODUCED BY ALTERNATIVE
CC       SPLICING. THEY DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE
CC       OF UP TO 6 OF THE 14 EXONS. ONE OF THESE OPTIONAL EXONS CONTAINS
CC       THE ADDITIONAL TAU/MAP REPEAT. TAU-A CDNA HAS BEEN CONSTRUCTED
CC       FROM TWO OVERLAPPING CDNAS BY THE AUTHORS OF REF.1. TAU-G AND TAU-
CC       H SEQUENCES BEGIN WITH EXON 6 OR A PART OF IT (EXON 6 IS MISSING
CC       IN ISOFORMS THAT BEGIN WITH EXON 1). 3 DIFFERENT C-TERMINI ARE
CC       OBTAINED EITHER BY THE RETENTION OR THE SPLICING OF INTRON 13/14
CC       (2 DIFFERENT 5' SPLICE DONORS).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
CC   -!- INDUCTION: DURING NEURITE OUTGROWTH.
CC   -!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
CC       CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC       CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC       MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC       MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC   -!- PTM: O-LINKED N-ACETYLGLUCOSAMINATION AT MORE THAN 4 SITES PER
CC       PROTEIN. SITE-SPECIFIC OR STOICHIOMETRIC CHANGES IN GLYCOSYLATION
CC       MAY MODULATE TAU FUNCTION AND ALSO PLAY A ROLE IN PHF'S FORMATION.
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L34953; AAA51609.1; -.
DR   EMBL; L34940; AAA51609.1; JOINED.
DR   EMBL; L34941; AAA51609.1; JOINED.
DR   EMBL; L34942; AAA51609.1; JOINED.
DR   EMBL; L34943; AAA51609.1; JOINED.
DR   EMBL; L34944; AAA51609.1; JOINED.
DR   EMBL; L34946; AAA51609.1; JOINED.
DR   EMBL; L34947; AAA51609.1; JOINED.
DR   EMBL; L34948; AAA51609.1; JOINED.
DR   EMBL; L34949; AAA51609.1; JOINED.
DR   EMBL; L34950; AAA51609.1; JOINED.
DR   EMBL; L34951; AAA51609.1; JOINED.
DR   EMBL; L34952; AAA51609.1; JOINED.
DR   EMBL; M26157; AAA30770.1; -.
DR   EMBL; M26158; AAA30771.1; -.
DR   EMBL; M26178; AAA51601.1; ALT_SEQ.
DR   EMBL; L34940; AAA51601.1; JOINED.
DR   EMBL; L34941; AAA51601.1; JOINED.
DR   EMBL; L34942; AAA51601.1; JOINED.
DR   EMBL; L34943; AAA51601.1; JOINED.
DR   EMBL; L34944; AAA51601.1; JOINED.
DR   EMBL; L34946; AAA51601.1; JOINED.
DR   EMBL; L34947; AAA51601.1; JOINED.
DR   EMBL; L34948; AAA51601.1; JOINED.
DR   EMBL; L34949; AAA51601.1; JOINED.
DR   EMBL; L34950; AAA51601.1; JOINED.
DR   EMBL; L34951; AAA51601.1; JOINED.
DR   EMBL; M26178; AAA51602.1; ALT_SEQ.
DR   EMBL; L34940; AAA51602.1; JOINED.
DR   EMBL; L34941; AAA51602.1; JOINED.
DR   EMBL; L34943; AAA51602.1; JOINED.
DR   EMBL; L34944; AAA51602.1; JOINED.
DR   EMBL; L34946; AAA51602.1; JOINED.
DR   EMBL; L34948; AAA51602.1; JOINED.
DR   EMBL; L34949; AAA51602.1; JOINED.
DR   EMBL; L34950; AAA51602.1; JOINED.
DR   EMBL; L34951; AAA51602.1; JOINED.
DR   EMBL; M26178; AAA51603.1; ALT_SEQ.
DR   EMBL; L34940; AAA51603.1; JOINED.
DR   EMBL; L34941; AAA51603.1; JOINED.
DR   EMBL; L34943; AAA51603.1; JOINED.
DR   EMBL; L34944; AAA51603.1; JOINED.
DR   EMBL; L34946; AAA51603.1; JOINED.
DR   EMBL; L34948; AAA51603.1; JOINED.
DR   EMBL; L34950; AAA51603.1; JOINED.
DR   EMBL; L34951; AAA51603.1; JOINED.
DR   EMBL; M26178; AAA51604.1; ALT_SEQ.
DR   EMBL; L34940; AAA51604.1; JOINED.
DR   EMBL; L34941; AAA51604.1; JOINED.
DR   EMBL; L34944; AAA51604.1; JOINED.
DR   EMBL; L34946; AAA51604.1; JOINED.
DR   EMBL; L34947; AAA51604.1; JOINED.
DR   EMBL; L34948; AAA51604.1; JOINED.
DR   EMBL; L34949; AAA51604.1; JOINED.
DR   EMBL; L34950; AAA51604.1; JOINED.
DR   EMBL; L34951; AAA51604.1; JOINED.
DR   EMBL; M26178; AAA51605.1; ALT_SEQ.
DR   EMBL; L34940; AAA51605.1; JOINED.
DR   EMBL; L34941; AAA51605.1; JOINED.
DR   EMBL; L34944; AAA51605.1; JOINED.
DR   EMBL; L34946; AAA51605.1; JOINED.
DR   EMBL; L34948; AAA51605.1; JOINED.
DR   EMBL; L34949; AAA51605.1; JOINED.
DR   EMBL; L34950; AAA51605.1; JOINED.
DR   EMBL; L34951; AAA51605.1; JOINED.
DR   EMBL; M26178; AAA51606.1; ALT_SEQ.
DR   EMBL; L34940; AAA51606.1; JOINED.
DR   EMBL; L34941; AAA51606.1; JOINED.
DR   EMBL; L34944; AAA51606.1; JOINED.
DR   EMBL; L34946; AAA51606.1; JOINED.
DR   EMBL; L34948; AAA51606.1; JOINED.
DR   EMBL; L34950; AAA51606.1; JOINED.
DR   EMBL; L34951; AAA51606.1; JOINED.
DR   PIR; A31939; QRBOT1.
DR   InterPro; IPR002955; Tau_protein.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 4.
DR   PRINTS; PR01261; TAUPROTEIN.
DR   PROSITE; PS00229; TAU_MAP; 4.
KW   Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
KW   Phosphorylation; Glycoprotein.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   REPEAT      250    280       TAU/MAP MOTIF 1.
FT   REPEAT      281    311       TAU/MAP MOTIF 2.
FT   REPEAT      312    342       TAU/MAP MOTIF 3.
FT   REPEAT      343    374       TAU/MAP MOTIF 4.
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   DISULFID    297    328       BY SIMILARITY.
FT   VARSPLIC      1    130       AEPRQEFDVMEDHAQGDYTLQDQEGDMDPGLKESPLQTPAD
FT                                DGSEEPGSETSDAKSTPTAEDATAPLVDEGAPGEQAAAQAP
FT                                AEIPEGTAAEEAGIGDTSNLEDQAAGHVTQARMVSKGKDGT
FT                                GPDDKKT -> PLNHYLPYLFLVSVLFQFVPFSHVLTFILI
FT                                LFMFMFKPSTPSSAKTLKNRPCLSPKRPTPGSSDPLIKPSS
FT                                PAVCPEPSSSPKHVSSVTPRTGNSGAKEMKV (IN
FT                                ISOFORM TAU-G).
FT   VARSPLIC      1    130       AEPRQEFDVMEDHAQGDYTLQDQEGDMDPGLKESPLQTPAD
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FT                                   DGSEEPGSETSDAKSTPTAEDATAPLVDEGAPGEQAAAQAP
FT                                   AEIPEGTAAEEAGIGDTSNLEDQAAGHVTQARMVSKGKDGT
FT                                   GPDDKKT -> KV (IN ISOFORM TAU-H).
FT   VARSPLIC      62     90        MISSING (IN ISOFORM TAU-D, ISOFORM TAU-E,
FT                                   ISOFORM TAU-F, ISOFORM TAU-J, ISOFORM
FT                                   TAU-K, ISOFORM TAU-L, ISOFORM TAU-M,
FT                                   ISOFORM TAU-N, ISOFORM TAU-P, ISOFORM
FT                                   TAU-Q, ISOFORM TAU-R, ISOFORM TAU-S AND
FT                                   ISOFORM TAU-T).
FT   VARSPLIC      91    112        MISSING (IN ISOFORM TAU-L, ISOFORM TAU-M,
FT                                   ISOFORM TAU-N, ISOFORM TAU-R, ISOFORM
FT                                   TAU-S AND ISOFORM TAU-T).
FT   VARSPLIC     174    191        MISSING (IN ISOFORM TAU-B, ISOFORM TAU-C,
FT                                   ISOFORM TAU-E, ISOFORM TAU-F, ISOFORM
FT                                   TAU-G, ISOFORM TAU-H, ISOFORM TAU-J,
FT                                   ISOFORM TAU-K, ISOFORM TAU-M, ISOFORM
FT                                   TAU-N, ISOFORM TAU-P, ISOFORM TAU-Q,
FT                                   ISOFORM TAU-S AND ISOFORM TAU-T).
FT   VARSPLIC     281    311        MISSING (IN ISOFORM TAU-C, ISOFORM TAU-F,
FT                                   ISOFORM TAU-K, ISOFORM TAU-N, ISOFORM
FT                                   TAU-Q AND ISOFORM TAU-T).
FT   VARSPLIC     438    447        VSASLAKQGL -> PCVCPHHACVSAVRSLVTACPLTTSCC

  Query Match             100.0%;  Score 50;  DB 1;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 0.36;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     203 YSSPGSPGT 211


RESULT   4
TAU_MACMU
ID   TAU_MACMU      STANDARD;      PRT;   458 AA.
AC   P57786;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR TAU.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D).
RC   TISSUE=Brain;
RX   MEDLINE=97012131; PubMed=8858947;
RA   Nelson P.T., Stefansson K., Gulcher J., Saper C.B.;
RT   "Molecular evolution of tau protein: implications for Alzheimer's
RT   disease.";
RL   J. Neurochem. 67:1622-1632(1996).
CC   -!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC       BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC       POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC       TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC       TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
CC       ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
CC       ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC       CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; TAU A (SHOWN HERE),
CC       TAU-B, TAU-C AND TAU-D; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY
CC       DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE OF UP TO 4
CC       EXONS. ONE OF THESE OPTIONAL EXONS CONTAINS THE ADDITIONAL TAU/MAP
CC       REPEAT. THE SEQUENCE SHOWN HERE IS THAT OF THE COMPLETE ISOFORM
CC       NOT YET CHARACTERIZED.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS.
CC   -!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
CC       CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC       CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC       MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC       MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
DR   InterPro; IPR002955; Tau_protein.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 4.
DR   PRINTS; PR01261; TAUPROTEIN.
DR   PROSITE; PS00229; TAU_MAP; 4.
KW   Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
KW   Phosphorylation.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   REPEAT      261    291       TAU/MAP MOTIF 1.
FT   REPEAT      292    322       TAU/MAP MOTIF 2.
FT   REPEAT      323    353       TAU/MAP MOTIF 3.
FT   REPEAT      354    385       TAU/MAP MOTIF 4.
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   DISULFID    308    339       BY SIMILARITY.
FT   VARSPLIC     44    101       MISSING (IN ISOFORM TAU-B AND ISOFORM
FT                                 TAU-C).
FT   VARSPLIC    185    202       MISSING (IN ISOFORM TAU-C AND ISOFORM
FT                                 TAU-D).
FT   VARSPLIC    292    322       MISSING (IN ISOFORM TAU-B).
SQ   SEQUENCE   458 AA;  47841 MW;  68BE63DBA30665A8 CRC64;

  Query Match             100.0%;  Score 50;  DB 1;  Length 458;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     214 YSSPGSPGT 222


RESULT   5
TAU_MOUSE
ID   TAU_MOUSE      STANDARD;      PRT;   732 AA.
AC   P10637; P10638; Q60684; Q60685; Q60686; Q62286;
DT   01-JUL-1989 (Rel. 11, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR MTAPT OR TAU.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM PNS-TAU).
RC   TISSUE=Neuroblastoma;
RX   MEDLINE=92262443; PubMed=1374898;
RA   Couchie D., Mavilia C., Georgieff I.S., Liem R.K.H., Shelanski M.L.,
RA   Nunez J.;
RT   "Primary structure of high molecular weight tau present in the
RT   peripheral nervous system.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:4378-4381(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-A; TAU-D AND TAU-E).
RC   STRAIN=Him OF1; TISSUE=Liver, Kidney, and Brain;
RX   MEDLINE=95012085; PubMed=7927211;
RA   Kenner L., el-Shabrawi Y., Hutter H., Forstner M., Zatloukal K.,
RA   Hoefler G., Preisegger K.-H., Kurzbauer R., Denk H.;
RT   "Expression of three- and four-repeat tau isoforms in mouse liver.";
RL   Hepatology 20:1086-1089(1994).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-B AND TAU-C).
RC   TISSUE=Brain;
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RX   MEDLINE=88099510; PubMed=3122323;
RA   Lee G., Cowan N.J., Kirschner M.;
RT   "The primary structure and heterogeneity of tau protein from mouse
RT   brain.";
RL   Science 239:285-288(1988).
RN   [4]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM B).
RC   STRAIN=ICR; TISSUE=Brain;
RX   MEDLINE=95182802; PubMed=7877441;
RA   Sawa A., Oyama F., Matsushita M., Ihara Y.;
RT   "Molecular diversity at the carboxyl terminus of human and rat tau.";
RL   Brain Res. Mol. Brain Res. 27:111-117(1994).
RN   [5]
RP   CHARACTERIZATION.
RX   MEDLINE=94005827; PubMed=8402267;
RA   Couchie D., Gache Y., Mavilia C., Guilleminot J., Bridoux A.-M.,
RA   Nivez M.-P., Nunez J.;
RT   "High molecular weight tau proteins and acquisition of neuronal
RT   polarity in peripheral nervous system.";
RL   C. R. Acad. Sci., III, Sci. Vie 316:404-409(1993).
CC   -!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC       BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC       POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC       TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC       TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
CC       ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
CC       ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC       CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; PNS-TAU (SHOWN HERE),
CC       TAU-A, TAU-B, TAU-C, TAU-D AND TAU-E; ARE PRODUCED BY ALTERNATIVE
CC       SPLICING. THEY DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE
CC       OF UP TO 5 OF THE 14 EXONS. ONE OF THESE OPTIONAL EXONS CONTAINS
CC       THE ADDITIONAL TAU/MAP REPEAT. TWO DIFFERENT C-TERMINI ARE
CC       OBTAINED EITHER BY THE RETENTION OR THE SPLICING OF INTRON 13/14.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS AND AT A LOWER LEVEL IN
CC       THE LIVER AND KIDNEY. PNS-TAU IS EXPRESSED IN THE PERIPHERAL
CC       NERVOUS SYSTEM WHILE THE OTHERS ARE EXPRESSED IN THE CENTRAL
CC       NERVOUS SYSTEM.
CC   -!- DEVELOPMENTAL STAGE: SHORTER FORMS OR LOW MOLECULAR WEIGHT TAU
CC       (LMW-TAU) ARE GENERALLY EXPRESSED AT EARLY DEVELOPMENT STAGES AND
CC       LONGER FORMS OR HIGH MOLECULAR WEIGHT TAU (HMW-TAU) IN THE ADULT
CC       BRAIN.
CC   -!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
CC       CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC       CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC       MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC       MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC   -!- DISEASE: MAY BE INVOLVED IN THE PATHOGENESIS OF CYTOPLASMIC
CC       INCLUSIONS (AS MALLORY BODIES) IN LIVERS OF MICE CHRONICALLY
CC       INTOXICATED WITH GRISEOFULVIN OR DDC (3,5-DIETHOXYCARBONYL-2,4-
CC       DIHYDROCOLLIDINE), A MODEL FOR HUMAN ALCOHOLIC HEPATITIS.
CC       ALTERATION OF TAU (ABNORMAL PHOSPHORYLATION AND CROSSLINKING)
CC       COULD CONTRIBUTE TO MALLORY BODIES FORMATION AND DISTURBANCE OF
CC       MICROTUBULE FUNCTION IN ALCOHOLIC LIVER DISEASE.
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U12914; AAA58343.1; -.
DR   EMBL; U12915; AAA58344.1; -.
DR   EMBL; U12916; AAA58345.1; -.
DR   EMBL; Z12133; CAA78121.1; -.
DR   EMBL; M93266; -; NOT_ANNOTATED_CDS.
DR   EMBL; M18775; AAA40165.1; -.
DR   EMBL; M18776; AAA40166.1; -.
DR   EMBL; D30627; BAA18878.1; -.
DR   PIR; A28820; A28820.
DR   PIR; B28820; B28820.
DR   MGD; MGI:97180; Mapt.
DR   InterPro; IPR002955; Tau_protein.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 7.
DR   PRINTS; PR01261; TAUPROTEIN.
DR   PROSITE; PS00229; TAU_MAP; 3.
KW   Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
KW   Phosphorylation.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   REPEAT      535    565       TAU/MAP MOTIF 1.
FT   REPEAT      566    596       TAU/MAP MOTIF 2.
FT   REPEAT      597    627       TAU/MAP MOTIF 3.
FT   REPEAT      628    659       TAU/MAP MOTIF 4.
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   DISULFID    582    613       BY SIMILARITY.
FT   VARSPLIC     33     90       MISSING (IN ISOFORM TAU-B, ISOFORM TAU-C,
FT                                ISOFORM TAU-D AND ISOFORM TAU-E).
FT   VARSPLIC     91    112       MISSING (IN ISOFORM TAU-E).
FT   VARSPLIC    113    349       MISSING (IN ISOFORM TAU-A, ISOFORM TAU-B,
FT                                ISOFORM TAU-C, ISOFORM TAU-D AND ISOFORM
FT                                TAU-E).
FT   VARSPLIC    367    432       MISSING (IN ISOFORM TAU-A, ISOFORM TAU-B,
FT                                ISOFORM TAU-C, ISOFORM TAU-D AND ISOFORM
FT                                TAU-E).
FT   VARSPLIC    566    596       MISSING (IN ISOFORM TAU-B AND ISOFORM
FT                                TAU-C).
FT   VARSPLIC    732    732       L -> KAALLSSQVWNYSHDLATITDLGL (IN
FT                                ISOFORM TAU-B).
FT   CONFLICT      2      2       D -> N (IN REF. 1).
FT   CONFLICT      8      8       D -> N (IN REF. 1).
FT   CONFLICT    527    527       P -> T (IN REF. 2; CAA78121).
FT   CONFLICT    671    671       E -> Q (IN REF. 1).
SQ   SEQUENCE   732 AA;  76112 MW;  BFDF0767E41C7A3A CRC64;


  Query Match             100.0%;  Score 50;  DB 1;  Length 732;
  Best Local Similarity   100.0%;  Pred. No. 0.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     488 YSSPGSPGT 496


RESULT   6
TAU_RAT
ID   TAU_RAT        STANDARD;      PRT;   751 AA.
AC   P19332; Q63567; Q9QW06; Q63677;
DT   01-NOV-1990 (Rel. 16, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE   (Paired helical filament-tau) (PHF-tau).
GN   MAPT OR MTAPT OR TAU.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM TAU-B).
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=92179305; PubMed=1542696;
RA   Goedert M., Spillantini M.G., Crowther R.A.;
RT   "Cloning of a big tau microtubule-associated protein characteristic of
RT   the peripheral nervous system.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:1983-1987(1992).
RN   [2]
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RP   SEQUENCE FROM N.A. (ISOFORM TAU-B).
RC   TISSUE=Dorsal root ganglion;
RX   MEDLINE=94013081; PubMed=8408300;
RA   Georgieff I.S., Liem R.K.H., Couchie D., Mavilia C., Nunez J.,
RA   Shelanski M.L.;
RT   "Expression of high molecular weight tau in the central and peripheral
RT   nervous systems.";
RL   J. Cell Sci. 105:729-737(1993).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM TAU-F).
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=94334997; PubMed=8057376;
RA   Sadot E., Marx R., Barg J., Behar L., Ginzburg I.;
RT   "Complete sequence of 3'-untranslated region of tau from rat central
RT   nervous system. Implications for mRNA heterogeneity.";
RL   J. Mol. Biol. 241:325-331(1994).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-E AND TAU-G).
RC   TISSUE=Brain;
RX   MEDLINE=90180457; PubMed=2560640;
RA   Kosik K.S., Orecchio L.D., Bakalis S., Neve R.L.;
RT   "Developmentally regulated expression of specific tau sequences.";
RL   Neuron 2:1389-1397(1989).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS TAU-E AND TAU-C).
RX   MEDLINE=89359509; PubMed=2504728;
RA   Kanai Y., Takemura R., Oshima T., Mori H., Ihara Y., Yanagisawa M.,
RA   Masaki T., Hirokawa N.;
RT   "Expression of multiple tau isoforms and microtubule bundle formation
RT   in fibroblasts transfected with a single tau cDNA.";
RL   J. Cell Biol. 109:1173-1184(1989).
RN   [6]
RP   SEQUENCE OF 359-460 FROM N.A. (ISOFORM TAU-A), AND SEQUENCE OF 105-112
RP   AND 367-460 FROM N.A. (ISOFORM TAU-D).
RC   TISSUE=Spinal cord;
RX   MEDLINE=95054048; PubMed=7964751;
RA   Mavilia C., Couchie D., Nunez J.;
RT   "Diversity of high-molecular-weight tau proteins in different regions
RT   of the nervous system.";
RL   J. Neurochem. 63:2300-2306(1994).
RN   [7]
RP   SEQUENCE OF 696-751 FROM N.A. (ISOFORMS TAU-A TO TAU-G), AND SEQUENCE
RP   OF 751-774 FROM N.A. (ISOFORM TAU-H).
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=95182802; PubMed=7877441;
RA   Sawa A., Oyama F., Matsushita M., Ihara Y.;
RT   "Molecular diversity at the carboxyl terminus of human and rat tau.";
RL   Brain Res. Mol. Brain Res. 27:111-117(1994).
CC   -!- FUNCTION: PROMOTES MICROTUBULE ASSEMBLY AND STABILITY, AND MIGHT
CC       BE INVOLVED IN THE ESTABLISHMENT AND MAINTENANCE OF NEURONAL
CC       POLARITY. THE C-TERMINUS BINDS AXONAL MICROTUBULES WHILE THE N-
CC       TERMINUS BINDS NEURAL PLASMA MEMBRANE COMPONENTS, SUGGESTING THAT
CC       TAU FUNCTIONS AS A LINKER PROTEIN BETWEEN BOTH. AXONAL POLARITY IS
CC       PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC       DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME. THE SHORT
CC       ISOFORMS ALLOW PLASTICITY OF THE CYTOSKELETON WHEREAS THE LONGER
CC       ISOFORMS MAY PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
CC   -!- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS, IN THE
CC       CYTOSOL AND IN ASSOCIATION WITH PLASMA MEMBRANE COMPONENTS.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 8 ISOFORMS; TAU-A/SC1 (SHOWN HERE),
CC       TAU-B/BIG-TAU/HMW-TAU, TAU-C, TAU-D/SC2, TAU-E, TAU-F, TAU-
CC       G/FETAL-TAU AND TAU-H; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY
CC       DIFFER FROM EACH OTHER BY THE PRESENCE OR ABSENCE OF UP TO 4 OF
CC       THE 14 EXONS. TWO DIFFERENT C-TERMINI ARE OBTAINED EITHER BY THE
CC       RETENTION OR THE SPLICING OF INTRON 13/14.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONS. THE LARGER FORMS (TAU-A
CC       AND TAU-B) ARE PREFERENTIALLY EXPRESSED IN THE PERIPHERAL NERVOUS
CC       SYSTEM WHILE THE OTHERS ARE EXPRESSED IN THE CENTRAL NERVOUS
CC       SYSTEM. LOW AMOUNTS OF THE LARGER FORMS ARE ALSO FOUND IN LIMITED
CC       AREAS OF THE CNS.
CC   -!- DEVELOPMENTAL STAGE: DURING THE IMMEDIATE POSTNATAL PERIOD, THE
CC       DORSAL ROOT GANGLIA EXPRESS ALL ISOFORMS WHEREAS ONLY THE LARGER
CC       FORMS PERSIST IN THE ADULTS.
CC   -!- DOMAIN: THE TAU/MAP REPEAT BINDS TO TUBULIN. TYPE I ISOFORMS
CC       CONTAIN 3 REPEATS WHILE TYPE II ISOFORMS CONTAIN 4 REPEATS.
CC   -!- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC       S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (PDPK: CDC2,
CC       CDK5, GSK3, MAPK) (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN
CC       MITOSIS), AND AT SERINE RESIDUES IN K-X-G-S MOTIFS BY
CC       MAP/MICROTUBULE AFFINITY-REGULATING KINASE (MARK) (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M84156; AAA42204.1; -.
DR   EMBL; X79321; CAA55889.1; -.
DR   EMBL; D30628; -; NOT_ANNOTATED_CDS.
DR   EMBL; D30629; -; NOT_ANNOTATED_CDS.
DR   PIR; JS0306; JS0306.
DR   PIR; A33574; A33574.
DR   InterPro; IPR002955; Tau_protein.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 8.
DR   PRINTS; PR01261; TAUPROTEIN.
DR   PROSITE; PS00229; TAU_MAP; 4.
KW   Microtubules; Cytoskeleton; Repeat; Alternative splicing; Acetylation;
KW   Phosphorylation.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   REPEAT      554    584       TAU/MAP MOTIF 1.
FT   REPEAT      585    615       TAU/MAP MOTIF 2.
FT   REPEAT      616    646       TAU/MAP MOTIF 3.
FT   REPEAT      647    678       TAU/MAP MOTIF 4.
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   DISULFID    601    632       BY SIMILARITY.
FT   VARSPLIC     33     90       MISSING (IN ISOFORM TAU-F).
FT   VARSPLIC     62     90       MISSING (IN ISOFORM TAU-C AND ISOFORM
FT                                TAU-G).
FT   VARSPLIC    113    366       MISSING (IN ISOFORM TAU-C, ISOFORM TAU-D,
FT                                ISOFORM TAU-E, ISOFORM TAU-F AND ISOFORM
FT                                TAU-G).
FT   VARSPLIC    386    451       MISSING (IN ISOFORM TAU-B, ISOFORM TAU-C,
FT                                ISOFORM TAU-E, ISOFORM TAU-F AND ISOFORM
FT                                TAU-G).
FT   VARSPLIC    585    615       MISSING (IN ISOFORM TAU-G).
FT   VARSPLIC    751    751       L -> KPVLLSSEVWNYSHDFGHHTDLGL (IN ISOFORM
FT                                TAU-H).
FT   CONFLICT    254    254       F -> L (IN REF. 2).
FT   CONFLICT    283    283       G -> A (IN REF. 2).
FT   CONFLICT    291    291       H -> D (IN REF. 2).
FT   CONFLICT    617    617       H -> Q (IN REF. 2, 3 AND 4).
FT   CONFLICT    704    704       Y -> H (IN REF. 3).
FT   CONFLICT    733    733       P -> A (IN REF. 2).
SQ   SEQUENCE   751 AA;  78432 MW;  B96B7329444D44B2 CRC64;


  Query Match             100.0%;  Score 50;  DB 1;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 0.62;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     507 YSSPGSPGT 515


RESULT   7
TAU_HUMAN
ID   TAU_HUMAN      STANDARD;      PRT;   757 AA.
AC   P10636; P18518; Q14799; Q15551; Q9UQ96; Q15549; Q15550; Q9UDJ3;
AC   Q9UMH0;
DT   01-JUL-1989 (Rel. 11, Created)
```

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Microtubule-associated protein tau (Neurofibrillary tangle protein)
DE (Paired helical filament-tau) (PHF-tau).
GN MAPT OR MTBT1 OR TAU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS PNS-TAU; TAU-A AND TAU-F).
RA Andreadis A.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM TAU-A).
RC TISSUE=Brain;
RX MEDLINE=88234557; PubMed=3131773;
RA Goedert M., Wischik C., Crowther R., Walker J., Klug A.;
RT "Cloning and sequencing of the cDNA encoding a core protein of the
RT paired helical filament of Alzheimer disease: identification as the
RT microtubule-associated protein tau.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS TAU-B; TAU-C; TAU-E AND TAU-F).
RC TISSUE=Brain;
RX MEDLINE=90380393; PubMed=2484340;
RA Goedert M., Spillantini M.G., Jakes R., Rutherford D., Crowther R.A.;
RT "Multiple isoforms of human microtubule-associated protein tau:
RT sequences and localization in neurofibrillary tangles of Alzheimer's
RT disease.";
RL Neuron 3:519-526(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM TAU-D).
RC TISSUE=Brain;
RX MEDLINE=89251564; PubMed=2498079;
RA Goedert M., Spillantini M.G., Potier M.C., Ulrich J., Crowther R.A.;
RT "Cloning and sequencing of the cDNA encoding an isoform of
RT microtubule-associated protein tau containing four tandem repeats:
RT differential expression of tau protein mRNAs in human brain.";
RL EMBO J. 8:393-399(1989).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS TAU-A AND FETAL-TAU).
RC TISSUE=Fetal brain;
RX MEDLINE=90180482; PubMed=2516729;
RA Lee G., Neve R.L., Kosik K.S.;
RT "The microtubule binding domain of tau protein.";
RL Neuron 2:1615-1624(1989).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM TAU-F), AND ALTERNATIVE SPLICING.
RX MEDLINE=93041757; PubMed=1420178;
RA Andreadis A., Brown W.M., Kosik K.S.;
RT "Structure and novel exons of the human tau gene.";
RL Biochemistry 31:10626-10633(1992).
RN [7]
RP SEQUENCE OF 591-621 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=89193714; PubMed=2495000;
RA Mori H., Hamada Y., Kawaguchi M., Honda T., Kondo J., Ihara Y.;
RT "A distinct form of tau is selectively incorporated into Alzheimer's
RT paired helical filaments.";
RL Biochem. Biophys. Res. Commun. 159:1221-1226(1989).
RN [8]
RP SEQUENCE OF 1-72; 102-380; 467-496; 507-570; 576-582; 591-606;
RP 615-633; 638-656; 660-663; 670-699 AND 702-757.
RC TISSUE=Brain;
RX MEDLINE=92381012; PubMed=1512244;
RA Hasegawa M., Morishima-Kawashima M., Takio K., Suzuki M., Titani K.,
RA Ihara Y.;
RT "Protein sequence and mass spectrometric analyses of tau in the
RT Alzheimer's disease brain.";
RL J. Biol. Chem. 267:17047-17054(1992).
RN [9]
RP SEQUENCE OF 576-583; 607-610; 615-627; 638-647 AND 670-685,
RP PHOSPHORYLATION, AND MUTAGENESIS.
RX MEDLINE=95221434; PubMed=7706316;
RA Drewes G., Trinczek B., Illenberger S., Biernat J., Schmitt-Ulms G.,
RA Meyer H.E., Mandelkow E.-M., Mandelkow E.;
RT "Microtubule-associated protein/microtubule affinity-regulating kinase
RT (p110mark). A novel protein kinase that regulates tau-microtubule
RT interactions and dynamic instability by phosphorylation at the
RT Alzheimer-specific site serine 262.";
RL J. Biol. Chem. 270:7679-7688(1995).
RN [10]
RP REVIEW.
RX MEDLINE=91320377; PubMed=1713721;
RA Goedert M., Crowther R.A., Garner C.C.;
RT "Molecular characterization of microtubule-associated proteins tau and
RT MAP2.";
RL Trends Neurosci. 14:193-199(1991).
RN [11]
RP SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
RX MEDLINE=20283597; PubMed=10747907;
RA Maas T., Eidenmueller J., Brandt R.;
RT "Interaction of tau with the neural membrane cortex is regulated by
RT phosphorylation at sites that are modified in paired helical
RT filaments.";
RL J. Biol. Chem. 275:15733-15740(2000).
RN [12]
RP PHOSPHORYLATION, AND MUTAGENESIS.
RX MEDLINE=98413833; PubMed=9735171;
RA Sengupta A., Kabat J., Novak M., Wu Q., Grundke-Iqbal I., Iqbal K.;
RT "Phosphorylation of tau at both Thr 231 and Ser 262 is required for
RT maximal inhibition of its binding to microtubules.";
RL Arch. Biochem. Biophys. 357:299-309(1998).
RN [13]
RP PHOSPHORYLATION, AND MUTAGENESIS.
RX MEDLINE=98278959; PubMed=9614189;
RA Illenberger S., Zheng-Fischhofer Q., Preuss U., Stamer K., Baumann K.,
RA Trinczek B., Biernat J., Godemann R., Mandelkow E.-M., Mandelkow E.;
RT "The endogenous and cell cycle-dependent phosphorylation of tau
RT protein in living cells: implications for Alzheimer's disease.";
RL Mol. Biol. Cell 9:1495-1512(1998).
RN [14]
RP GLYCATION.
RX MEDLINE=97465580; PubMed=9326300;
RA Nacharaju P., Ko L., Yen S.H.;
RT "Characterization of in vitro glycation sites of tau.";
RL J. Neurochem. 69:1709-1719(1997).
RN [15]
RP REVIEW ON VARIANTS.
RX MEDLINE=20437008; PubMed=10899436;
RA Goedert M., Spillantini M.G.;
RT "Tau mutations in frontotemporal dementia FTDP-17 and their relevance
RT for Alzheimer's disease.";
RL Biochim. Biophys. Acta 1502:110-121(2000).
RN [16]
RP VARIANT FTDP17 M-653, AND VARIANTS N-284; A-288; Y-440 AND P-446.
RX MEDLINE=98291804; PubMed=9629852;
RA Poorkaj P., Bird T.D., Wijsman E., Nemens E., Garruto R.M.,
RA Anderson L., Andreadis A., Wiederholt W.C., Raskind M.,
RA Schellenberg G.D.;
RT "Tau is a candidate gene for chromosome 17 frontotemporal dementia.";
RL Ann. Neurol. 43:815-825(1998).
RN [17]
RP ERRATUM.
RA Poorkaj P., Bird T.D., Wijsman E., Nemens E., Garruto R.M.,
RA Anderson L., Andreadis A., Wiederholt W.C., Raskind M.,
RA Schellenberg G.D.;
RL Ann. Neurol. 44:428-428(1998).
RN [18]
RP VARIANT FTDP17 LEU-617.
RX MEDLINE=98409513; PubMed=9736786;
RA Dumanchin C., Camuzat A., Campion D., Verpillat P., Hannequin D.,
RA Dubois B., Saugier-Veber P., Martin C., Penet C., Charbonnier F.,
RA Agid Y., Frebourg T., Brice A.;
RT "Segregation of a missense mutation in the microtubule-associated

```
RT   protein tau gene with familial frontotemporal dementia and
RT   parkinsonism.";
RL   Hum. Mol. Genet. 7:1825-1829(1998).
RN   [19]
RP   VARIANTS FTDP17 VAL-588; LEU-617 AND TRP-722.
RX   MEDLINE=98303385; PubMed=9641683;
RA   Hutton M., Lendon C.L., Rizzu P., Baker M., Froelich S., Houlden H.,
RA   Pickering-Brown S., Chakraverty S., Isaacs A., Grover A., Hackett J.,
RA   Adamson J., Lincoln S., Dickson D., Davies P., Petersen R.C.,
RA   Stevens M., de Graaff E., Wauters E., van Baren J., Hillebrand M.,
RA   Joosse M., Kwon J.M., Nowotny P., Che L.K., Norton J., Morris J.C.,
RA   Reed L.A., Trojanowski J., Basun H., Lannfelt L., Neystat M., Fahn S.,
RA   Dark F., Tannenberg T., Dodd P.R., Hayward N., Kwok J.B.J.,
RA   Schofield P.R., Andreadis A., Snowden J., Craufurd D., Neary D.,
RA   Owen F., Oostra B.A., Hardy J., Goate A., van Swieten J., Mann D.,
RA   Lynch T., Heutink P.;
RT   "Association of missense and 5'-splice-site mutations in tau with the
RT   inherited dementia FTDP-17.";
RL   Nature 393:702-705(1998).
RN   [20]
RP   VARIANT PPND LYS-595, AND VARIANT FTDP17 LEU-617.
RX   MEDLINE=99007274; PubMed=9789048;
RA   Clark L.N., Poorkaj P., Wszolek Z., Geschwind D.H., Nasreddine Z.S.,
RA   Miller B., Li D., Payami H., Awert F., Markopoulou K., Andreadis A.,
RA   D'Souza I., Lee V.M.-Y., Reed L., Trojanowski J.Q., Zhukareva V.,
RA   Bird T., Schellenberg G., Wilhelmsen K.C.;
RT   "Pathogenic implications of mutations in the tau gene in
RT   pallido-ponto-nigral degeneration and related neurodegenerative
RT   disorders linked to chromosome 17.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:13103-13107(1998).
RN   [21]
RP   VARIANTS FTDP17 VAL-588; LYS-596 DEL; LEU-617 AND TRP-722.
RX   MEDLINE=99138654; PubMed=9973279;
RA   Rizzu P., Van Swieten J.C., Joosse M., Hasegawa M., Stevens M.,
RA   Tibben A., Niermeijer M.F., Hillebrand M., Ravid R., Oostra B.A.,
RA   Goedert M., van Duijn C.M., Heutink P.;
RT   "High prevalence of mutations in the microtubule-associated protein
RT   tau in a population study of frontotemporal dementia in the
RT   Netherlands.";
RL   Am. J. Hum. Genet. 64:414-421(1999).
RN   [22]
RP   VARIANTS FTDP17 LEU-617; MET-653 AND TRP-722.
RX   MEDLINE=99229757; PubMed=10214944;
RA   Nacharaju P., Lewis J., Easson C., Yen S., Hackett J., Hutton M.,
RA   Yen S.H.;
RT   "Accelerated filament formation from tau protein with specific FTDP-17
RT   missense mutations.";
RL   FEBS Lett. 447:195-199(1999).
RN   [23]
RP   VARIANT FTDP17/CBD SER-617.
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Query Match 100.0%; Score 50; DB 1; Length 757;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 YSSPGSPGT 9
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Db     513 YSSPGSPGT 521
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RESULT   8
P2B1_CRYNE
ID   P2B1_CRYNE     STANDARD;      PRT;   639 AA.
AC   O42773;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Serine/threonine protein phosphatase 2B catalytic subunit A1
DE   (EC 3.1.3.16) (Calcineurin A1).
GN   CNA1.
OS   Cryptococcus neoformans (Filobasidiella neoformans).
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=5207;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H99;
RX   MEDLINE=97327538; PubMed=9184205;
RA   Odom A., Muir S., Lim E., Toffaletti D.L., Perfect J., Heitman J.;
RT   "Calcineurin is required for virulence of Cryptococcus neoformans.";
RL   EMBO J. 16:2576-2589(1997).
CC   -!- FUNCTION: CALCIUM-DEPENDENT, CALMODULIN-STIMULATED PROTEIN
CC       PHOSPHATASE. THIS SUBUNIT MAY HAVE A ROLE IN THE CALMODULIN
CC       ACTIVATION OF CALCINEURIN (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
CC       THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC       SENSITIVITY.
CC   -!- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-2B
CC       SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF042082; AAB97372.1; -.
DR   HSSP; P08129; 1FJM.
DR   InterPro; IPR000934; Ser_thr_phosphtse.
DR   Pfam; PF00149; STphosphatase; 1.
DR   PRINTS; PR00114; STPHPHTASE.
DR   SMART; SM00156; PP2Ac; 1.
DR   PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
KW   Hydrolase; Calmodulin-binding; Iron; Manganese.
SQ   SEQUENCE   639 AA;  71499 MW;  4B92EBE361C80579 CRC64;
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Query Match 78.0%; Score 39; DB 1; Length 639;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       3 SPGSPGT 9
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Db     556 SPGSPGT 562
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RESULT   9
PET1_RAT
ID   PET1_RAT       STANDARD;      PRT;   710 AA.
AC   P51574;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Oligopeptide transporter, small intestine isoform (Peptide transporter
DE   1) (Intestinal H+/peptide cotransporter) (Proton-coupled dipeptide
DE   cotransporter).
GN   SLC15A1 OR PEPT1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Small intestine;
RX   MEDLINE=96180982; PubMed=8605246;
RA   Miyamoto K., Shiraga T., Morita K., Yamamoto H., Haga H.,
RA   Taketani Y., Tamai I., Sai Y., Tsuji A., Takeda E.;
RT   "Sequence, tissue distribution and developmental changes in rat
RT   intestinal oligopeptide transporter.";
RL   Biochim. Biophys. Acta 1305:34-38(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
```

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RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney;
RX   MEDLINE=96108664; PubMed=8531138;
RA   Saito H., Okuda M., Terada T., Sasaki S., Inui K.;
RT   "Cloning and characterization of a rat H+/peptide cotransporter
RT   mediating absorption of beta-lactam antibiotics in the intestine and
RT   kidney.";
RL   J. Pharmacol. Exp. Ther. 275:1631-1637(1995).
CC   -!- FUNCTION: PROTON-COUPLED INTAKE OF OLIGOPEPTIDES OF 2 TO 4
CC       AMINO ACIDS WITH A PREFERENCE FOR DIPEPTIDES. MAY CONSTITUTE
CC       A MAJOR ROUTE FOR THE ABSORPTION OF PROTEIN DIGESTION END-
CC       PRODUCTS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE PTR2 FAMILY OF TRANSPORTERS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D50664; BAA09318.1; -.
DR   EMBL; D50306; BAA08844.1; -.
DR   InterPro; IPR000109; PTR2.
DR   Pfam; PF00854; PTR2; 2.
DR   PROSITE; PS01022; PTR2_1; 1.
DR   PROSITE; PS01023; PTR2_2; 1.
KW   Peptide transport; Transport; Transmembrane; Symport; Glycoprotein.
FT   TRANSMEM      1     21       POTENTIAL.
FT   DOMAIN       22     53       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     54     74       POTENTIAL.
FT   DOMAIN       75     82       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     83    103       POTENTIAL.
FT   DOMAIN      104    118       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    119    139       POTENTIAL.
FT   DOMAIN      140    161       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    162    182       POTENTIAL.
FT   DOMAIN      183    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    219       POTENTIAL.
FT   DOMAIN      220    276       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    277    297       POTENTIAL.
FT   DOMAIN      298    327       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    328    348       POTENTIAL.
FT   DOMAIN      349    361       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    362    382       POTENTIAL.
FT   DOMAIN      383    586       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    587    607       POTENTIAL.
FT   DOMAIN      608    621       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    622    642       POTENTIAL.
FT   DOMAIN      643    647       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    648    668       POTENTIAL.
FT   DOMAIN      669    710       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    415    415       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    439    439       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    510    510       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    532    532       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    539    539       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    241    241       R -> G (IN REF. 2).
FT   CONFLICT    259    259       N -> E (IN REF. 2).
FT   CONFLICT    279    280       IM -> MV (IN REF. 2).
SQ   SEQUENCE   710 AA;  78928 MW;  435727A6C76F2D7B CRC64;
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  Query Match          76.0%;  Score 38;  DB 1;  Length 710;
  Best Local Similarity  100.0%;  Pred. No. 52;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
           |||||||
Db     441 SSPGSPG 447
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RESULT  10
PID1_HUMAN
ID   PID1_HUMAN     STANDARD;      PRT;   756 AA.
AC   P51178;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1
DE   (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-III).
GN   PLCD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=95197554; PubMed=7890667;
RA   Cheng H.F., Jiang M.J., Chen C.L., Liu S.M., Wong L.P.,
RA   Lomasney J.W., King K.;
RT   "Cloning and identification of amino acid residues of human
RT   phospholipase C delta 1 essential for catalysis.";
RL   J. Biol. Chem. 270:5495-5505(1995).
CC   -!- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC       DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC       MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC       C ENZYMES.
CC   -!- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC       diacylglycerol.
CC   -!- COFACTOR: REQUIRES CALCIUM.
CC   -!- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC       PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC   -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U09117; AAA73567.1; -.
DR   HSSP; P10688; 1MAI.
DR   MIM; 602142; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR001192; PI_PLC.
DR   InterPro; IPR000909; PI_PLC_X.
DR   InterPro; IPR001711; PI_PLC_Y.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00036; efhand; 2.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00388; PI-PLC-X; 1.
DR   Pfam; PF00387; PI-PLC-Y; 1.
DR   PRINTS; PR00360; C2DOMAIN.
DR   PRINTS; PR00390; PHPHLIPASEC.
DR   ProDom; PD001202; PI_PLC_Y; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00148; PLCXc; 1.
DR   SMART; SM00149; PLCYc; 1.
DR   PROSITE; PS00018; EF_HAND; 2.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR   PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
KW   Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat.
FT   DOMAIN       21    130       PH.
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FT   CA_BIND      153    164       EF-HAND 1 (POTENTIAL).
FT   CA_BIND      189    200       EF-HAND 2 (POTENTIAL).
FT   DOMAIN       296    440       DOMAIN X.
FT   DOMAIN       492    609       DOMAIN Y.
FT   DOMAIN       616    720       C2 DOMAIN.
FT   ACT_SITE     311    311       BY SIMILARITY.
FT   ACT_SITE     356    356       BY SIMILARITY.
SQ   SEQUENCE   756 AA;  85763 MW;  AD9A4251C5EBADFB CRC64;
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  Query Match             76.0%;  Score 38;  DB 1;  Length 756;
  Best Local Similarity   75.0%;  Pred. No. 56;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
            :||||:||
Db     507 FSSPGTPG 514
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RESULT  11
DPOZ_MOUSE
ID   DPOZ_MOUSE     STANDARD;      PRT;  3122 AA.
AC   Q61493; Q9QWX6; Q9JMD6;
DT   30-MAY-2000 (Rel. 39, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   DNA polymerase zeta catalytic subunit (EC 2.7.7.7) (Seizure related
DE   protein 4).
GN   REV3L OR POLZ OR SEZ4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/OLA; TISSUE=Testis;
RX   MEDLINE=99202265; PubMed=10102037;
RA   Van Sloun P.P.H., Romeijn R.J., Eeken J.C.J.;
RT   "Molecular cloning, expression and chromosomal localisation of the
RT   mouse Rev3l gene, encoding the catalytic subunit of polymerase zeta.";
RL   Mutat. Res. 433:109-116(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kajiwara K.;
RT   "Molecular analyses of Sez4 encoding murine homologue of yeast REV3 in
RT   brain neurons.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 2368-3122 FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryonic brain;
RX   MEDLINE=96216731; PubMed=8645260;
RA   Kajiwara K., Nagawawa H., Shimizu-Nishikawa K., Ookura T., Kimura M.,
RA   Sugaya E.;
RT   "Molecular characterization of seizure-related genes isolated by
RT   differential screening.";
RL   Biochem. Biophys. Res. Commun. 219:795-799(1996).
CC   -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC       + {DNA}(N).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF083464; AAC98785.1; -.
DR   EMBL; AB031049; BAA90768.1; -.
DR   EMBL; D78644; BAA11461.1; -.
DR   MGD; MGI:1337131; Rev3l.
DR   InterPro; IPR002064; DNA_pol_B.
DR   Pfam; PF00136; DNA_pol_B; 2.
DR   Pfam; PF03104; DNA_pol_B_exo; 1.
DR   PRINTS; PR00106; DNAPOLB.
DR   SMART; SM00486; POLBc; 1.
DR   PROSITE; PS00116; DNA_POLYMERASE_B; 1.
KW   Transferase; DNA-directed DNA polymerase; DNA replication;
KW   DNA-binding; DNA repair; Nuclear protein; Zinc-finger.
FT   ZN_FING     3034   3049       C4-TYPE (POTENTIAL).
FT   ZN_FING     3078   3096       C4-TYPE (POTENTIAL).
FT   CONFLICT      92     92       G -> A (IN REF. 2).
FT   CONFLICT     294    294       A -> T (IN REF. 2).
FT   CONFLICT     578    578       E -> Q (IN REF. 2).
FT   CONFLICT     609    609       R -> Q (IN REF. 2).
FT   CONFLICT    1278   1278       L -> P (IN REF. 2).
FT   CONFLICT    1298   1298       L -> F (IN REF. 2).
FT   CONFLICT    1416   1416       P -> L (IN REF. 2).
FT   CONFLICT    1848   1848       A -> T (IN REF. 2).
FT   CONFLICT    2368   2368       V -> G (IN REF. 3).
SQ   SEQUENCE   3122 AA;  350654 MW;  A39846CAF7365BA8 CRC64;
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  Query Match             76.0%;  Score 38;  DB 1;  Length 3122;
  Best Local Similarity   87.5%;  Pred. No. 2.5e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
            |||| |||
Db    2108 YSSPDSPG 2115
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RESULT  12
CDN1_FELCA
ID   CDN1_FELCA     STANDARD;      PRT;   164 AA.
AC   O19002;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Cyclin-dependent kinase inhibitor 1 (P21) (CDK-interacting protein 1).
GN   CDKN1A OR CIP1 OR WAF1.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph node;
RX   MEDLINE=98036042; PubMed=9370275;
RA   Okuda M., Minehata K., Setoguchi A., Cho K.-W., Nakamura N.,
RA   Nishigaki K., Watari T., Cevario S., O'Brien S.J., Tsujimoto H.,
RA   Hasegawa A.;
RT   "Cloning and chromosome mapping of the feline genes p21WAF1 and
RT   p27Kip1.";
RL   Gene 198:141-147(1997).
CC   -!- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES
CC       ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO
CC       DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
CC       ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
CC       KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D84650; BAA23168.1; -.
DR   HSSP; P46527; 1JSU.
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DR   InterPro; IPR003175; CDI.
DR   Pfam; PF02234; CDI; 1.
KW   Cell cycle; Nuclear protein; Zinc-finger.
FT   ZN_FING      13     41       C4-TYPE (POTENTIAL).
FT   DOMAIN       141    156      NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ   SEQUENCE   164 AA;  18315 MW;  0F7912A76C78BF38 CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 164;
  Best Local Similarity   75.0%;  Pred. No. 16;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            :|||:|||
Db     129 ASPGAPGT 136


RESULT  13
TIZ2_MOUSE
ID   TIZ2_MOUSE      STANDARD;      PRT;   387 AA.
AC   Q9EQN3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   TSC22-related inducible leucine zipper protein 2.
GN   TILZ2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ershler M.A., Belyavsky A.V., Visser J.W.M.;
RT   "Identification and characterization of a family of leucine zipper
RT   genes related to TSC22.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: TRANSCRIPTIONAL REPRESSOR (BY SIMILARITY).
CC   -!- SUBUNIT: FORMS HOMODIMER OR HETERODIMER. CAN FORM AN HETERODIMER
CC       WITH TSC-22.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: BELONGS TO THE TSC-22/DIP/BUN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF201286; AAG41219.1; -.
DR   InterPro; IPR000580; TSC-22_Dip_Bun.
DR   Pfam; PF01166; TSC22; 1.
DR   ProDom; PD007152; TSC-22_Dip_Bun; 1.
DR   PROSITE; PS01289; TSC22; 1.
KW   Transcription regulation; Repressor; Nuclear protein.
FT   DOMAIN       336    357      LEUCINE-ZIPPER.
SQ   SEQUENCE   387 AA;  39987 MW;  C78BB96B5B2DFB90 CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 387;
  Best Local Similarity   75.0%;  Pred. No. 40;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
            |  |||||
Db      19 YEGPGSPG 26


RESULT  14
TIZ2_HUMAN
ID   TIZ2_HUMAN      STANDARD;      PRT;   395 AA.
AC   Q9Y3Q8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   TSC22-related inducible leucine zipper protein 2 (Tsc-22-like protein
DE   THG-1).
GN   TILZ2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99419018; PubMed=10488076;
RA   Kester H.A., Blanchetot C., den Hertog J., van der Saag P.T.,
RA   van der Burg B.;
RT   "Transforming growth factor-beta-stimulated clone-22 is a member of a
RT   family of leucine zipper proteins that can homo- and heterodimerize
RT   and has transcriptional repressor activity.";
RL   J. Biol. Chem. 274:27439-27447(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cervix;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: TRANSCRIPTIONAL REPRESSOR.
CC   -!- SUBUNIT: FORMS HOMODIMER OR HETERODIMER. CAN FORM AN HETERODIMER
CC       WITH TSC-22.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: BELONGS TO THE TSC-22/DIP/BUN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ133115; CAB43491.1; -.
DR   EMBL; BC001966; AAH01966.1; -.
DR   InterPro; IPR000580; TSC-22_Dip_Bun.
DR   Pfam; PF01166; TSC22; 1.
DR   ProDom; PD007152; TSC-22_Dip_Bun; 1.
DR   PROSITE; PS01289; TSC22; 1.
KW   Transcription regulation; Repressor; Nuclear protein.
FT   DOMAIN       344    365      LEUCINE-ZIPPER.
FT   CONFLICT     355    356      NA -> KR (IN REF. 1).
SQ   SEQUENCE   395 AA;  41026 MW;  DA08B5617C9BB151 CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 395;
  Best Local Similarity   75.0%;  Pred. No. 41;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
            |  |||||
Db      19 YEGPGSPG 26


RESULT  15
VE2_PAPVE
ID   VE2_PAPVE      STANDARD;      PRT;   415 AA.
AC   P11329;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Probable regulatory protein E2.
GN   E2.
OS   European elk papillomavirus (EEPV).
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10565;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87219878; PubMed=3034730;
RA   Ahola H., Bergman P., Stroem A.C., Moreno-Lopez J., Petterson U.;
RT   "Organization and expression of the transforming region from the
RT   European elk papillomavirus (EEPV).";
RL   Gene 50:195-205(1986).
CC   -!- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
CC       IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNNNNNGGT-3') PRESENT
CC       IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
CC       ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
CC       WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
CC       BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
CC       INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
CC       REPLICATION.
CC   -!- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M15953; AAA66854.1; -.
DR   PIR; D29499; W2WLEP.
DR   HSSP; P03122; 2BOP.
DR   InterPro; IPR001866; E2_N.
DR   InterPro; IPR000427; Early2_C.
DR   Pfam; PF00511; E2_C; 1.
DR   Pfam; PF00508; E2_N; 1.
DR   ProDom; PD000672; Early2_C; 1.
DR   ProDom; PD000678; E2_N; 1.
KW   Early protein; Transcription regulation; Activator; DNA-binding;
KW   Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SQ   SEQUENCE   415 AA;  46245 MW;  0B7BF6AEEF0AC80C CRC64;
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  Query Match             74.0%;  Score 37;  DB 1;  Length 415;
  Best Local Similarity   66.7%;  Pred. No. 43;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           ||:| |||:
Db     268 YSAPSSPGS 276
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RESULT  16
NTR1_HUMAN
ID   NTR1_HUMAN     STANDARD;      PRT;   418 AA.
AC   P30989; Q9H4T5; Q9H4H1;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Neurotensin receptor type 1 (NT-R-1) (High-affinity levocabastine-
DE   insensitive neurotensin receptor) (NTRH).
GN   NTSR1 OR NTRR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93154505; PubMed=8381365;
RA   Vita N., Laurent P., Lefort S., Chalon P., Dumont X., Kaghad M.,
RA   Gully D., le Fur G., Ferrara P., Caput D.;
RT   "Cloning and expression of a complementary DNA encoding a high
RT   affinity human neurotensin receptor.";
RL   FEBS Lett. 317:139-142(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaslaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
CC   -!- FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. IT IS
CC       ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC       CALCIUM SECOND MESSENGER SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC       HIGHEST TO TACHYKININS RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X70070; CAA49675.1; -.
DR   EMBL; AL357033; CAC14923.1; -.
DR   EMBL; AL035669; CAC12747.1; -.
DR   PIR; S29506; S29506.
DR   GCRDb; GCR_0577; -.
DR   GCRDb; GCR_2067; -.
DR   MIM; 162651; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003985; NT1_rec.
DR   InterPro; IPR003984; NT_rec.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01479; NEUROTENSINR.
DR   PRINTS; PR01480; NEUROTENSN1R.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Phosphorylation; Lipoprotein; Palmitate.
FT   DOMAIN        1      63       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     64      86       1 (POTENTIAL).
FT   DOMAIN       87      95       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     96     120       2 (POTENTIAL).
FT   DOMAIN      121     142       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    143     164       3 (POTENTIAL).
FT   DOMAIN      165     187       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    188     209       4 (POTENTIAL).
FT   DOMAIN      210     234       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    235     259       5 (POTENTIAL).
FT   DOMAIN      260     303       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    304     325       6 (POTENTIAL).
FT   DOMAIN      326     343       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    344     367       7 (POTENTIAL).
FT   DOMAIN      368     418       CYTOPLASMIC (POTENTIAL).
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FT   CARBOHYD      4      4       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     41     41       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    141    224       BY SIMILARITY.
FT   LIPID       383    383       PALMITATE (POTENTIAL).
FT   CONFLICT    200    200       T -> A (IN REF. 2).
SQ   SEQUENCE   418 AA;  46288 MW;  BBBD1EEC2BE6E390 CRC64;
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Query Match 74.0%; Score 37; DB 1; Length 418;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy       2 SSPGSPGT 9
            |:||:|||
Db       6 SAPGTPGT 13
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RESULT  17
IL5R_HUMAN
ID   IL5R_HUMAN     STANDARD;      PRT;   420 AA.
AC   Q01344;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-5 receptor alpha chain precursor (IL-5R-alpha) (CD125
DE   antigen).
GN   IL5RA OR IL5R.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92372031; PubMed=1505961;
RA   Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT   "Structure and sequence of the human alpha-L-iduronidase gene.";
RL   Genomics 13:1311-1313(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92357767; PubMed=1495999;
RA   Tavernier J., Tuypens T., Plaetinck G., Verhee A., Fiers W.,
RA   Devos R.;
RT   "Molecular basis of the membrane-anchored and two soluble isoforms of
RT   the human interleukin 5 receptor alpha subunit.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
RN   [3]
RP   SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
RX   MEDLINE=92005669; PubMed=1833065;
RA   Tavernier J., Devos R., Cornelis S., Tuypens T., van der Heyden J.,
RA   Fiers W., Plaetinck G.;
RT   "A human high affinity interleukin-5 receptor (IL5R) is composed of
RT   an IL5-specific alpha chain and a beta chain shared with the receptor
RT   for GM-CSF.";
RL   Cell 66:1175-1184(1991).
CC   -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC       BINDS TO IL-5.
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC       CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN
CC       HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY
CC       ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CDw125 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw125.htm".
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M96652; AAA59152.1; -.
DR   EMBL; M96651; AAA59151.1; -.
DR   EMBL; M75914; AAA36110.1; -.
DR   EMBL; A26249; CAA01793.1; -.
DR   EMBL; A24587; CAA01731.1; -.
DR   EMBL; A26251; CAA01794.1; -.
DR   PIR; A40267; A40267.
DR   MIM; 147851; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003532; Hematopo_receptor_S_F2.
DR   PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW   Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    420       INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT   DOMAIN       21    342       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    343    362       POTENTIAL.
FT   DOMAIN      363    420       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     35     35       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    131    131       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    216    216       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    244    244       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    333    335       NDE -> FSR (IN SOLUBLE ISOFORM S1).
FT   VARSPLIC    336    420       MISSING (IN SOLUBLE ISOFORM S1).
FT   VARSPLIC    333    333       N -> K (IN SOLUBLE ISOFORM S2).
FT   VARSPLIC    334    420       MISSING (IN SOLUBLE ISOFORM S2).
SQ   SEQUENCE   420 AA;  47700 MW;  420681FBC6B51700 CRC64;
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Query Match 74.0%; Score 37; DB 1; Length 420;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 YSSPGSPGT 9
            :: ||||||
Db     119 HAPPGSPGT 127
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RESULT  18
DHAL_DEIRA
ID   DHAL_DEIRA     STANDARD;      PRT;   515 AA.
AC   Q9RYG9; O32502;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Aldehyde dehydrogenase (EC 1.2.1.3).
GN   ALDA OR DRA0348.
OS   Deinococcus radiodurans.
OC   Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX   NCBI_TaxID=1299;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R1;
RX   MEDLINE=20036896; PubMed=10567266;
RA   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA   Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA   Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA   Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA   Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA   Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA   Fraser C.M.;
RT   "Genome sequence of the radioresistant bacterium Deinococcus
RT   radiodurans R1.";
RL   Science 286:1571-1577(1999).
RN   [2]
RP   SEQUENCE OF 1-258 FROM N.A.
RC   STRAIN=KD8301;
RA   Narumi I., Du Z., Alatas Z., Kitayama S., Watanabe H.;
RT   "Isolation and characterization of pprA, a novel Deinococcus
RT   radiodurans gene involved in DNA repair.";
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RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
CC   -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE001863; AAF12436.1; -.
DR   EMBL; AB003475; BAA21372.1; -.
DR   HSSP; P05091; 1CW3.
DR   TIGR; DRA0348; -.
DR   InterPro; IPR002086; Aldehyde_dehydr.
DR   Pfam; PF00171; aldedh; 1.
DR   PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
DR   PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
KW   Oxidoreductase; NAD; Complete proteome.
FT   NP_BIND     228    234       NAD (ADP PART) (BY SIMILARITY).
FT   ACT_SITE    272    272       BY SIMILARITY.
FT   ACT_SITE    311    311       BY SIMILARITY.
SQ   SEQUENCE   515 AA;  56409 MW;  D8BB5DDF7D2DBBC0 CRC64;
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  Query Match             74.0%;  Score 37;  DB 1;  Length 515;
  Best Local Similarity   55.6%;  Pred. No. 54;
  Matches    5;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            |::||:||:
Db      13 YANPGTPGS 21
```

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RESULT  19
ZYX_CHICK
ID   ZYX_CHICK      STANDARD;      PRT;   542 AA.
AC   Q04584;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Zyxin.
GN   ZYX.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93107157; PubMed=1469049;
RA   Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.;
RT   "Zyxin and cCRP: two interactive LIM domain proteins associated with
RT   the cytoskeleton.";
RL   J. Cell Biol. 119:1573-1587(1992).
CC   -!- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP
CC       PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT
CC       MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN
CC       CYTOSKELETON NEAR THE ADHESION PLAQUES.
CC   -!- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2
CC       ZINC IONS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X69190; CAA48936.1; -.
DR   PIR; A44358; A44358.
DR   InterPro; IPR001781; LIM.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00412; LIM; 3.
DR   ProDom; PD000094; LIM; 3.
DR   SMART; SM00132; LIM; 3.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR   PROSITE; PS50023; LIM_DOMAIN_2; 3.
KW   Repeat; LIM domain; Metal-binding; Zinc; Cell adhesion.
FT   DOMAIN       83     90       PRO-RICH.
FT   DOMAIN      103    130       PRO-RICH.
FT   DOMAIN      352    411       LIM 1.
FT   DOMAIN      412    471       LIM 2.
FT   DOMAIN      472    538       LIM 3.
FT   VARIANT     463    463       D -> V.
SQ   SEQUENCE   542 AA;  58537 MW;  9D898AC180C680FC CRC64;
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  Query Match             74.0%;  Score 37;  DB 1;  Length 542;
  Best Local Similarity   75.0%;  Pred. No. 57;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            :|||:|||
Db       2 ASPGTPGT 9
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RESULT  20
YQ36_CAEEL
ID   YQ36_CAEEL     STANDARD;      PRT;   963 AA.
AC   Q09457;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Putative cuticle collagen C09G5.6.
GN   C09G5.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Palmer S.;
RL   Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE
CC       PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A
CC       BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT (BY SIMILARITY).
CC   -!- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
CC       CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
CC       LINKS (BY SIMILARITY).
CC   -!- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE
CC       COLLAGENS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z46791; CAA86755.1; -.
DR   WormPep; C09G5.6; CE01486.
DR   InterPro; IPR002486; Col_cuticle_N.
DR   InterPro; IPR000087; Collagen.
DR   Pfam; PF01391; Collagen; 2.
DR   Pfam; PF01484; Col_cuticle_N; 1.
KW   Hypothetical protein; Cuticle; Connective tissue; Repeat;
KW   Multigene family; Collagen.
FT   DOMAIN      392    423       TRIPLE-HELICAL REGION.
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FT   DOMAIN       441    503       TRIPLE-HELICAL REGION.
FT   DOMAIN       506    567       TRIPLE-HELICAL REGION.
FT   DOMAIN       663    666       POLY-PRO.
FT   DOMAIN       685    688       POLY-PRO.
SQ   SEQUENCE   963 AA;  107031 MW;  AFF895A75909F66E CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 963;
  Best Local Similarity   75.0%;  Pred. No. 1e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            |:||:|||
Db     559 SAPGAPGT 566


RESULT  21
RGSC_RAT
ID   RGSC_RAT       STANDARD;      PRT;  1387 AA.
AC   O08774; O88383;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Regulator of G-protein signaling 12 (RGS12).
GN   RGS12.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97312490; PubMed=9168931;
RA   Snow B.E., Antonio L., Suggs S., Gutstein H.B., Siderovski D.P.;
RT   "Molecular cloning and expression analysis of rat Rgs12 and Rgs14.";
RL   Biochem. Biophys. Res. Commun. 233:770-777(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98316347; PubMed=9651375;
RA   Snow B.E., Hall R.A., Krumins A.M., Brothers G.M., Bouchard D.,
RA   Brothers C.A., Chung S., Mangion J., Gilman A.G., Lefkowitz R.J.,
RA   Siderovski D.P.;
RT   "GTPase activating specificity of RGS12 and binding specificity of an
RT   alternatively spliced PDZ (PSD-95/Dlg/ZO-1) domain.";
RL   J. Biol. Chem. 273:17749-17755(1998).
CC   -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC       ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC       THEIR INACTIVE GDP-BOUND FORM.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO ISOFORMS THAT ARISE
CC       FROM ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN AND LUNG
CC       AND LOWER LEVELS IN TESTIS, HEART, AND SPLEEN.
CC   -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 PID DOMAIN.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; U92280; AAC53176.1; -.
DR   EMBL; AF035151; AAC40154.1; -.
DR   HSSP; P49799; 1AGR.
DR   InterPro; IPR003109; GoLoco.
DR   InterPro; IPR001478; PDZ.
DR   InterPro; IPR000050; PID_domain.
DR   InterPro; IPR003116; RBD.
DR   InterPro; IPR000342; RGS.
DR   Pfam; PF02188; GoLoco; 1.
DR   Pfam; PF00595; PDZ; 1.
DR   Pfam; PF00640; PID; 1.
DR   Pfam; PF02196; RBD; 2.
DR   Pfam; PF00615; RGS; 1.
DR   PRINTS; PR01301; RGSPROTEIN.
DR   ProDom; PD001580; RGS; 1.
DR   SMART; SM00390; GoLoco; 1.
DR   SMART; SM00228; PDZ; 1.
DR   SMART; SM00462; PTB; 1.
DR   SMART; SM00455; RBD; 2.
DR   SMART; SM00315; RGS; 1.
DR   PROSITE; PS50106; PDZ; 1.
DR   PROSITE; PS01179; PID; 1.
DR   PROSITE; PS50132; RGS; 1.
KW   Signal transduction inhibitor; Nuclear protein; Alternative splicing.
FT   DOMAIN       21     97       PDZ.
FT   DOMAIN      227    339       PID.
FT   DOMAIN      715    832       RGS.
FT   DOMAIN     1368   1373       POLY-PRO.
FT   VARSPLIC      1    648       MISSING (IN ISOFORM PDZ-LESS).
FT   VARSPLIC    649    666       SFGRSRRFSLTRSLDDLE -> MNLEKGLSDDSDVFIDQQ
FT                                (IN ISOFORM PDZ-LESS).
SQ   SEQUENCE   1387 AA;  150468 MW;  958047D106B08310 CRC64;


  Query Match             74.0%;  Score 37;  DB 1;  Length 1387;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            :|:|| |||
Db    1296 HSTPGPPGT 1304


RESULT  22
WA_EMENI
ID   WA_EMENI       STANDARD;      PRT;  1986 AA.
AC   Q03149;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Conidial green pigment synthase (EC 2.3.1.-).
GN   WA.
OS   Emericella nidulans (Aspergillus nidulans).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=5072;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93101122; PubMed=1465094;
RA   Mayorga M.E., Timberlake W.E.;
RT   "The developmentally regulated Aspergillus nidulans wA gene encodes a
RT   polypeptide homologous to polyketide and fatty acid synthases.";
RL   Mol. Gen. Genet. 235:205-212(1992).
CC   -!- FUNCTION: THIS PROTEIN CONDENSES CARBON UNITS TO FORM AN
CC       INTERMEDIATE YELLOW POLYKETIDE PIGMENT THAT IS POLYMERIZED
CC       BY CONIDIAL LACCASE TO FORM THE GREEN PIGMENT IN MATURE
CC       ASEXUAL SPORES (CONIDIA).
CC   -!- COFACTOR: CONTAINS 2 COVALENTLY BOUND PHOSPHOPANTETHEINES
CC       (POTENTIAL).
CC   -!- PATHWAY: BIOSYNTHESIS OF CONIDIAL GREEN PIGMENT.
CC   -!- SIMILARITY: CONTAINS 2 ACYL CARRIER DOMAINS.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
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DR   EMBL; X65866; CAA46695.1; -.
DR   PIR; S28353; S28353.
DR   InterPro; IPR001227; Acyltransf_domain.
DR   InterPro; IPR000794; Ketoacyl-synt.
DR   InterPro; IPR003880; Phosphopant_attach.
DR   Pfam; PF00698; Acyl_transf; 1.
DR   Pfam; PF00109; ketoacyl-synt; 1.
DR   Pfam; PF02801; ketoacyl-synt_C; 1.
DR   Pfam; PF00550; pp-binding; 2.
DR   PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
DR   PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR   PROSITE; PS50075; ACP_DOMAIN; 2.
KW   Transferase; Phosphopantetheine; Multifunctional enzyme; Repeat.
FT   DOMAIN      529    582       BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT   DOMAIN      991   1024       ACYL/MALONYL TRANSFERASES
FT                                (BY SIMILARITY).
FT   DOMAIN     1650   1719       ACYL CARRIER (ACP) 1.
FT   DOMAIN     1772   1841       ACYL CARRIER (ACP) 2.
FT   ACT_SITE    548    548       BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT   ACT_SITE   1001   1001       ACYL/MALONYL TRANSFERASES (BY
FT                                SIMILARITY).
FT   BINDING    1682   1682       PHOSPHOPANTETHEINE (BY SIMILARITY).
FT   BINDING    1804   1804       PHOSPHOPANTETHEINE (BY SIMILARITY).
SQ   SEQUENCE   1986 AA;  216634 MW;  74EF0940FF40EE9A CRC64;

  Query Match             74.0%;  Score 37;  DB 1;  Length 1986;
  Best Local Similarity   87.5%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            ||| ||||
Db    1749 SSPASPGT 1756


RESULT  23
SAX1_MOUSE
ID   SAX1_MOUSE     STANDARD;      PRT;   305 AA.
AC   P42580;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Homeobox protein SAX-1 (NKX-1.1).
GN   SAX1 OR NKX1-1 OR NKX-1.1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=95399317; PubMed=7669696;
RA   Schubert F.R., Fainsod A., Gruenbaum Y., Gruss P.;
RT   "Expression of the novel murine homeobox gene Sax-1 in the developing
RT   nervous system.";
RL   Mech. Dev. 51:99-114(1995).
RN   [2]
RP   SEQUENCE OF 289-305 FROM N.A.
RC   STRAIN=BALB/C;
RA   Hong S.B., Kim S.J., Noh M.J., Lee Y.M., Kim Y.S., Yoo O.J.;
RL   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY FUNCTION IN CELL SPECIFICATION, PARTICULARLY IN THE
CC       CNS.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING POSTERIOR CENTRAL
CC       NERVOUS SYSTEM. FIRST SEEN IN THE ECTODERM LATERAL TO THE
CC       PRIMITIVE STREAK, LATER IT ENCOMPASSES THE NEURAL PLATE. STARTING
CC       AT DAY 9.5 PC, IT IS EXPRESSED IN DISTINCT AREAS OF SPINAL CORD,
CC       HINDBRAIN, MIDBRAIN AND FOREBRAIN.
CC   -!- SIMILARITY: BELONGS TO THE NK-1 FAMILY OF HOMEOBOX PROTEINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X75384; CAA53153.1; -.
DR   EMBL; U58137; AAB06948.1; -.
DR   HSSP; P02836; 3HDD.
DR   MGD; MGI:104806; Sax1.
DR   InterPro; IPR001356; Homeobox.
DR   Pfam; PF00046; homeobox; 1.
DR   PRINTS; PR00024; HOMEOBOX.
DR   SMART; SM00389; HOX; 1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
KW   Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT   DOMAIN       88     96       POLY-GLU.
FT   DOMAIN      143    148       POLY-ARG.
FT   DNA_BIND    156    215       HOMEOBOX.
FT   DOMAIN      239    242       POLY-GLY.
SQ   SEQUENCE   305 AA;  32012 MW;  E02E09A40453FF1B CRC64;

  Query Match             72.0%;  Score 36;  DB 1;  Length 305;
  Best Local Similarity   75.0%;  Pred. No. 45;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            :||||||:
Db    134 ASPGSPGS 141


RESULT  24
PYCA_METJA
ID   PYCA_METJA     STANDARD;      PRT;   501 AA.
AC   Q58626;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
GN   PYCA OR MJ1229.
OS   Methanococcus jannaschii.
OC   Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC   Methanococcus.
OX   NCBI_TaxID=2190;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX   MEDLINE=96337999; PubMed=8688087;
RA   Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA   Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA   Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA   Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA   Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA   Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA   Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA   Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT   "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT   jannaschii.";
RL   Science 273:1058-1073(1996).
RN   [2]
RP   SEQUENCE OF 1-12, AND FUNCTION.
RX   MEDLINE=21034791; PubMed=11195096;
RA   Mukhopadhyay B., Patel V.J., Wolfe R.S.;
RT   "A stable archaeal pyruvate carboxylase from the hyperthermophile
RT   Methanococcus jannaschii.";
RL   Arch. Microbiol. 174:406-414(2000).
CC   -!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
CC       INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
CC       ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL
CC       GROUP TO PYRUVATE IN THE SECOND.
CC   -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
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CC       oxaloacetate.
CC   -!- COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND
CC       BICARBONATE.
CC   -!- ENZYME REGULATION: INHIBITED BY MAGNESIUM, WHEN ITS CONCENTRATION
CC       EXCEEDED THE ATP ONE, AND BY HIGH CONCENTRATION OF ATP AND ALPHA-
CC       KETOGLUTARATE.
CC   -!- PATHWAY: GLUCONEOGENESIS.
CC   -!- SUBUNIT: HETEROOCTAMER OF FOUR A AND FOUR B SUBUNITS.
CC   -!- MASS SPECTROMETRY: MW=55500; METHOD=MALDI.
CC   -!- MISCELLANEOUS: ITS OPTIMUM PH IS 8.5 AND THE OPTIMUM TEMPERATURE
CC       IS 80-90 DEGREES CELSIUS.
CC   -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC       AND CARBAMYL PHOSPHATE SYNTHETASES.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U67563; AAB99232.1; -.
DR   HSSP; P24182; 1BNC.
DR   TIGR; MJ1229; -.
DR   InterPro; IPR000901; CPSase.
DR   Pfam; PF02785; Biotin_carb_C; 1.
DR   Pfam; PF00289; CPSase_L_chain; 1.
DR   Pfam; PF02786; CPSase_L_D2; 1.
DR   PROSITE; PS00866; CPSASE_1; 1.
DR   PROSITE; PS00867; CPSASE_2; 1.
KW   Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
KW   ATP-binding; Complete proteome.
FT   NP_BIND     162    167       ATP (POTENTIAL).
FT   ACT_SITE    291    291       POTENTIAL.
SQ   SEQUENCE   501 AA;  55402 MW;  04D2E401892F872F CRC64;

  Query Match             72.0%;  Score 36;  DB 1;  Length 501;
  Best Local Similarity   75.0%;  Pred. No. 77;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPG 8
          | ||| ||
Db    357 YRSPGGPG 364


RESULT  25
GUNB_PSEFL
ID   GUNB_PSEFL     STANDARD;      PRT;   511 AA.
AC   P18126;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Endoglucanase B precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
DE   (Cellulase) (EGB).
GN   CELB.
OS   Pseudomonas fluorescens.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=294;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 30-48.
RC   STRAIN=SP. CELLULOSA;
RX   MEDLINE=90355836; PubMed=2117693;
RA   Gilbert H.J., Hall J., Hazlewood G.P., Ferreira L.M.A.;
RT   "The N-terminal region of an endoglucanase from Pseudomonas
RT   fluorescens subspecies cellulosa constitutes a cellulose-binding
RT   domain that is distinct from the catalytic centre.";
RL   Mol. Microbiol. 4:759-767(1990).
CC   -!- FUNCTION: THIS ENZYME CATALYZES THE ENDOHYDROLYSIS OF 1,4-BETA-
CC       GLUCOSIDIC LINKAGES IN CELLULOSE, LICHENIN AND CEREAL BETA-D-
CC       GLUCANS. EGB IS MOST ACTIVE AGAINST BARLEY BETA-GLUCAN, BUT SHOWED
CC       SIGNIFICANT ACTIVITY AGAINST AMORPHOUS AND CRISTALLINE CELLULOSE.
CC   -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC       linkages in cellulose.
CC   -!- SUBCELLULAR LOCATION: Periplasmic.
CC   -!- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
CC       (CBD).
CC   -!- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
CC       HYDROLASES).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X52615; CAA36844.1; -.
DR   PIR; S10527; S10527.
DR   HSSP; P43316; 2ENG.
DR   InterPro; IPR001919; CBD_2.
DR   InterPro; IPR002883; CBD_5.
DR   InterPro; IPR000334; Glyco_hydro_45.
DR   Pfam; PF00553; CBD_2; 1.
DR   Pfam; PF02013; CBD_5; 1.
DR   Pfam; PF02015; Glyco_hydro_45; 1.
DR   PROSITE; PS00561; CBD_BACTERIAL; 1.
DR   PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.
KW   Cellulose degradation; Hydrolase; Glycosidase; Signal; Periplasmic.
FT   SIGNAL        1     29
FT   CHAIN        30    511       ENDOGLUCANASE B.
FT   DOMAIN       30    131       CELLULOSE-BINDING (BY SIMILARITY).
FT   DOMAIN      132    173       SER-RICH (LINKER).
FT   DOMAIN      223    259       SER-RICH.
FT   DISULFID     32    127       BY SIMILARITY.
FT   ACT_SITE    276    276       NUCLEOPHILE (BY SIMILARITY).
FT   ACT_SITE    393    393       PROTON DONOR (BY SIMILARITY).
SQ   SEQUENCE   511 AA;  52078 MW;  3C3119D998291D8E CRC64;

  Query Match             72.0%;  Score 36;  DB 1;  Length 511;
  Best Local Similarity   55.6%;  Pred. No. 78;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          |::|| ||:
Db    360 YNAPGDPGS 368


RESULT  26
BUD8_YEAST
ID   BUD8_YEAST     STANDARD;      PRT;   603 AA.
AC   P41698; Q06482;
DT   01-NOV-1995 (Rel. 32, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Bud site selection protein BUD8.
GN   BUD8 OR YLR353W OR L9638.3.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Harkins H.A., Pringle J.R.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RA   Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA   Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA   Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA   Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
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RA   Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA   Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
RA   Wilson R., Waterston R.;
RL   Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO YEAST BUD9.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L37016; AAA64518.1; -.
DR   EMBL; U19102; AAB67749.1; -.
DR   SGD; S0004345; BUD8.
FT   DOMAIN       84     95       POLY-SER.
FT   CONFLICT    140    140       R -> W (IN REF. 1).
FT   CONFLICT    145    145       V -> M (IN REF. 1).
FT   CONFLICT    221    221       Y -> C (IN REF. 1).
FT   CONFLICT    350    350       S -> N (IN REF. 1).
FT   CONFLICT    354    354       T -> M (IN REF. 1).
FT   CONFLICT    422    422       MISSING (IN REF. 1).
FT   CONFLICT    602    602       R -> L (IN REF. 1).
SQ   SEQUENCE   603 AA;  66288 MW;  83F8843CA476E6C4 CRC64;

  Query Match             72.0%;  Score 36;  DB 1;  Length 603;
  Best Local Similarity   85.7%;  Pred. No. 93;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||:|||
Db     299 SPGAPGT 305


RESULT  27
CA1A_MOUSE
ID   CA1A_MOUSE     STANDARD;      PRT;   680 AA.
AC   Q05306;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Collagen alpha 1(X) chain precursor.
GN   COL10A1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=93143676; PubMed=8424763;
RA   Elima K., Eerola I., Rosati R., Metsaranta M., Garofalo S., Perala M.,
RA   de Crombrugghe B., Vuorio E.;
RT   "The mouse collagen X gene: complete nucleotide sequence, exon
RT   structure and expression pattern.";
RL   Biochem. J. 289:247-253(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=Liver;
RX   MEDLINE=93238750; PubMed=8477738;
RA   Kong R.Y.C., Kwan K.M., Lau E.T., Thomas J.T., Boot-Handford R.P.,
RA   Grant M.E., Cheah K.S.E.;
RT   "Intron-exon structure, alternative use of promoter and expression of
RT   the mouse collagen X gene, Col10a-1.";
RL   Eur. J. Biochem. 213:99-111(1993).
RN   [3]
RP   SEQUENCE OF 51-680 FROM N.A.
RC   STRAIN=DBA/2J;
RX   MEDLINE=92267014; PubMed=1587271;
RA   Apte S.S., Seldin M.F., Hayashi M., Olsen B.R.;
RT   "Cloning of the human and mouse type X collagen genes and mapping of
RT   the mouse type X collagen gene to chromosome 10.";
RL   Eur. J. Biochem. 206:217-224(1992).
RN   [4]
RP   SEQUENCE OF 385-627 FROM N.A.
RC   STRAIN=C57BL;
RX   MEDLINE=92182017; PubMed=1543751;
RA   Elima K., Metsaranta M., Kallio J., Peraelae M., Eerola I.,
RA   Garofalo S., de Crombrugghe B., Vuorio E.;
RT   "Specific hybridization probes for mouse alpha 2(IX) and alpha 1(X)
RT   collagen mRNAs.";
RL   Biochim. Biophys. Acta 1130:78-80(1992).
CC   -!- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC
CC       CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
CC       MINERALIZATION ZONES OF HYALINE CARTILAGE.
CC   -!- SUBUNIT: HOMOTRIMER.
CC   -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC       UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC   -!- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
CC   -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X67348; CAA47763.1; -.
DR   EMBL; X65121; CAA46237.1; -.
DR   EMBL; X63013; CAA44741.1; -.
DR   EMBL; Z21610; CAA79736.1; -.
DR   PIR; S28807; S28807.
DR   PIR; S31216; S31216.
DR   PIR; S22215; S22215.
DR   MGD; MGI:88445; Col10a1.
DR   InterPro; IPR001073; C1q.
DR   InterPro; IPR000087; Collagen.
DR   Pfam; PF00386; C1q; 1.
DR   Pfam; PF01391; Collagen; 6.
DR   PRINTS; PR00007; COMPLEMNTC1Q.
DR   SMART; SM00110; C1Q; 1.
DR   PROSITE; PS01113; C1Q; 1.
KW   Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW   Cartilage; Collagen; Signal.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    680       COLLAGEN ALPHA 1(X) CHAIN.
FT   DOMAIN       19     56       NONHELICAL REGION (NC2).
FT   DOMAIN       57    519       TRIPLE-HELICAL REGION.
FT   DOMAIN      520    680       NONHELICAL REGION (NC1).
FT   DOMAIN      545    680       C1Q.
FT   CONFLICT    248    248       P -> L (IN REF. 3).
FT   CONFLICT    286    286       A -> S (IN REF. 2).
FT   CONFLICT    306    306       L -> F (IN REF. 3).
FT   CONFLICT    417    417       T -> S (IN REF. 3).
FT   CONFLICT    451    451       R -> K (IN REF. 4).
FT   CONFLICT    500    500       H -> L (IN REF. 3).
FT   CONFLICT    567    567       A -> C (IN REF. 3).
FT   CONFLICT    569    569       I -> H (IN REF. 3).
FT   CONFLICT    571    572       FD -> IY (IN REF. 3).
FT   CONFLICT    635    635       Q -> T (IN REF. 3).
SQ   SEQUENCE   680 AA;  66775 MW;  FE984CA99AF708E2 CRC64;

  Query Match             72.0%;  Score 36;  DB 1;  Length 680;
  Best Local Similarity   75.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           | ||| ||
Db     193 YGSPGRPG 200
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RESULT  28
TRI2_STRCO
ID   TRI2_STRCO      STANDARD;      PRT;  1171 AA.
AC   Q9RKB9;
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Putative Tricorn protease homolog 2 (EC 3.4.21.-).
GN   TRI2 OR SCE87.19.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Seeger K.J., Harris D., Thomson N.R., Parkhill J., Barrell B.G.,
RA   Rajandream M.A.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Degrades oligopeptides in a sequential manner
CC       (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S41 (SERINE PROTEASE).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AL132674; CAB59664.1; -.
DR   MEROPS; S41A; -.
DR   InterPro; IPR003581; TSPc.
DR   SMART; SM00245; TSPc; 1.
KW   Hydrolase; Serine protease.
FT   DOMAIN      842    941       PDZ-LIKE.
FT   SITE       1022   1022       SUBSTRATE SPECIFICITY SWITCH (BY
FT                                SIMILARITY).
FT   ACT_SITE    827    827       BY SIMILARITY.
FT   ACT_SITE   1051   1051       SUBSTRATE-BINDING (BY SIMILARITY).
FT   ACT_SITE   1052   1052       NUCLEOPHILE (BY SIMILARITY).
SQ   SEQUENCE   1171 AA;  125660 MW;  9C53019CEC0B0A25 CRC64;


  Query Match             72.0%;  Score 36;  DB 1;  Length 1171;
  Best Local Similarity   85.7%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 SPGSPGT 9
          :||||||
Db    487 TPGSPGT 493


RESULT  29
MAP2_HUMAN
ID   MAP2_HUMAN      STANDARD;      PRT;  1827 AA.
AC   P11137; Q99976; Q99975;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein 2 (MAP 2) (MAP2B) [Contains: MAP2C].
GN   MAP2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Price R.;
RL   Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain;
RX   MEDLINE=94124038; PubMed=8294038;
RA   Albala J.S., Kalcheva N., Shafit-Zagardo B.;
RT   "Characterization of the transcripts encoding two isoforms of human
RT   microtubule-associated protein-2 (MAP-2).";
RL   Gene 136:377-378(1993).
RN   [3]
RP   SEQUENCE OF 493-1562 FROM N.A.
RX   MEDLINE=88274407; PubMed=2455776;
RA   Kosik K.S., Orecchio L.D., Bakalis S., Duffy L., Neve R.L.;
RT   "Partial sequence of MAP2 in the region of a shared epitope with
RT   Alzheimer neurofibrillary tangles.";
RL   J. Neurochem. 51:587-598(1988).
CC   -!- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
CC       STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
CC       SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
CC   -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
CC       FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
CC   -!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U01828; AAA03354.1; -.
DR   EMBL; U89330; AAB48098.1; -.
DR   EMBL; U89329; AAB48097.1; -.
DR   EMBL; M25668; AAA59552.1; -.
DR   PIR; PL0024; QRHUMT.
DR   MIM; 157130; -.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 3.
DR   PROSITE; PS00229; TAU_MAP; 2.
KW   Microtubules; Repeat; Alternative splicing; Calmodulin-binding.
FT   DOMAIN     1447   1467       CALMODULIN-BINDING (POTENTIAL).
FT   REPEAT     1661   1691       TAU/MAP MOTIF.
FT   REPEAT     1692   1722       TAU/MAP MOTIF.
FT   REPEAT     1723   1754       TAU/MAP MOTIF.
FT   VARSPLIC    152   1507       MISSING (IN ISOFORM MAP2C).
FT   CONFLICT      9      9       A -> G (IN REF. 2).
FT   CONFLICT     37     37       R -> A (IN REF. 2).
FT   CONFLICT    108    108       A -> G (IN REF. 2).
FT   CONFLICT    152    155       MISSING (IN REF. 2).
FT   CONFLICT    187    187       S -> K (IN REF. 2).
FT   CONFLICT   1655   1655       A -> GL (IN REF. 2).
FT   CONFLICT   1736   1736       V -> A (IN REF. 2).
SQ   SEQUENCE   1827 AA;  199610 MW;  BAC36D0030F5F455 CRC64;


  Query Match             72.0%;  Score 36;  DB 1;  Length 1827;
  Best Local Similarity   72.7%;  Pred. No. 3e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy      1 YSS--PGSPGT 9
          |||  ||:|||
Db   1609 YSSRTPGTPGT 1619


RESULT  30
MAP2_MOUSE
ID   MAP2_MOUSE      STANDARD;      PRT;  1828 AA.
AC   P20357;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein 2 (MAP 2).
```

```
GN   MAP2 OR MTAP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89083571; PubMed=3205744;
RA   Wang D., Lewis S.A., Cowan N.J.;
RT   "Complete sequence of a cDNA encoding mouse MAP2.";
RL   Nucleic Acids Res. 16:11369-11370(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89043973; PubMed=3142041;
RA   Lewis S.A., Wang D., Cowan N.J.;
RT   "Microtubule-associated protein MAP2 shares a microtubule binding
RT   motif with tau protein.";
RL   Science 242:936-939(1988).
CC   -!- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
CC       STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
CC       SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
CC   -!- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M21041; AAA39490.1; -.
DR   PIR; S06467; S06467.
DR   PIR; A40115; A40115.
DR   MGD; MGI:97175; Mtap2.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 3.
DR   PROSITE; PS00229; TAU_MAP; 2.
KW   Microtubules; Repeat; Calmodulin-binding.
FT   DOMAIN      1452   1472       CALMODULIN-BINDING (POTENTIAL).
FT   REPEAT      1662   1692       TAU/MAP MOTIF.
FT   REPEAT      1693   1723       TAU/MAP MOTIF.
FT   REPEAT      1724   1755       TAU/MAP MOTIF.
SQ   SEQUENCE   1828 AA;  198980 MW;  200BC59E360538CA CRC64;

  Query Match             72.0%;  Score 36;  DB 1;  Length 1828;
  Best Local Similarity   72.7%;  Pred. No. 3e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 YSS--PGSPGT 9
             |||  ||:|||
Db    1613 YSSRTPGTPGT 1623


RESULT  31
MAP2_RAT
ID   MAP2_RAT       STANDARD;      PRT;  1861 AA.
AC   P15146;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein 2 (MAP 2) (MAP2B) [Contains: MAP2C].
GN   MAP2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Brain;
RX   MEDLINE=90251471; PubMed=2339070;
RA   Kindler S., Schwanke B., Schulz B., Garner C.C.;
RT   "Complete cDNA sequence encoding rat high and low molecular weight
RT   MAP2.";
RL   Nucleic Acids Res. 18:2822-2822(1990).
RN   [2]
RP   SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Brain;
RX   MEDLINE=91060576; PubMed=2174050;
RA   Kindler S., Schulz B., Goedert M., Garner C.C.;
RT   "Molecular structure of microtubule-associated protein 2b and 2c from
RT   rat brain.";
RL   J. Biol. Chem. 265:19679-19684(1990).
RN   [3]
RP   SEQUENCE OF 1-151; 1515-1694 AND 1726-1861 FROM N.A.
RX   MEDLINE=90221819; PubMed=2326166;
RA   Doll T., Papandrikopoulou A., Matus A.;
RT   "Nucleotide and amino acid sequences of embryonic rat MAP2c.";
RL   Nucleic Acids Res. 18:361-361(1990).
RN   [4]
RP   DISCUSSION OF SEQUENCE.
RX   MEDLINE=89365159; PubMed=2770869;
RA   Papandrikopoulou A., Doll T., Tucker R.P., Garner C.C., Matus A.;
RT   "Embryonic MAP2 lacks the cross-linking sidearm sequences and
RT   dendritic targeting signal of adult MAP2.";
RL   Nature 340:650-652(1989).
RN   [5]
RP   SEQUENCE OF 1695-1725 FROM N.A.
RX   MEDLINE=94110302; PubMed=8282767;
RA   Doll T., Meichsner M., Riederer B.M., Honegger P., Matus A.;
RT   "An isoform of microtubule-associated protein 2 (MAP2) containing
RT   four repeats of the tubulin-binding motif.";
RL   J. Cell Sci. 106:633-640(1993).
CC   -!- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
CC       STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
CC       SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
CC   -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
CC       FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
CC   -!- DEVELOPMENTAL STAGE: MAP2C IS EXPRESSED DURING EMBRYONIC BRAIN
CC       DEVELOPMENT AND UNTIL POSTANATAL DAY 10. MAP2B IS EXPRESSED
CC       THROUGHOUT BRAIN DEVELOPMENT.
CC   -!- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
CC   ---------------------------------------------------------------------
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X51842; CAA36135.1; -.
DR   EMBL; X17682; CAA35667.1; -.
DR   EMBL; X71487; CAA50588.1; -.
DR   PIR; S07887; S07887.
DR   PIR; S10003; S10003.
DR   PIR; A37981; A37981.
DR   InterPro; IPR001084; Tubulin-bind.
DR   Pfam; PF00418; tubulin-binding; 4.
DR   PROSITE; PS00229; TAU_MAP; 3.
KW   Microtubules; Repeat; Alternative splicing; Calmodulin-binding.
FT   DOMAIN      1454   1474       CALMODULIN-BINDING (POTENTIAL).
FT   REPEAT      1664   1694       TAU/MAP MOTIF.
FT   REPEAT      1695   1725       TAU/MAP MOTIF.
FT   REPEAT      1726   1756       TAU/MAP MOTIF.
FT   REPEAT      1757   1788       TAU/MAP MOTIF.
FT   VARSPLIC     152   1514       MISSING (IN ISOFORM MAP2C).
FT   VARSPLIC    1695   1725       MISSING (IN ISOFORM WITH 3 TAU/MAP
FT                                 REPEATS).
SQ   SEQUENCE   1861 AA;  202409 MW;  42DCF116D21EF54E CRC64;

  Query Match             72.0%;  Score 36;  DB 1;  Length 1861;
  Best Local Similarity   72.7%;  Pred. No. 3.1e+02;
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  Matches    8;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 YSS--PGSPGT 9
           |||  ||:|||
Db    1615 YSSRTPGTPGT 1625


RESULT  32
CDN1_MOUSE
ID   CDN1_MOUSE      STANDARD;      PRT;   159 AA.
AC   P39689;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Cyclin-dependent kinase inhibitor 1 (Melanoma differentiation
DE   associated protein) (P21) (CDK-interacting protein 1).
GN   CDKN1A OR CIP1 OR WAF1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BXSB; TISSUE=Spleen;
RX   MEDLINE=94366751; PubMed=8084607;
RA   Huppi K., Siwarski D., Dosik J., Michieli P., Chedid M., Reed S.,
RA   Mock B., Givol D., Mushinski J.F.;
RT   "Molecular cloning, sequencing, chromosomal localization and
RT   expression of mouse p21 (Waf1).";
RL   Oncogene 9:3017-3020(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95316868; PubMed=7796420;
RA   El-Deiry W.S., Tokino T., Waldman T., Velculescu V., Oliner J.D.,
RA   Burell M., Hill D.E., Rees J.L., Hamilton S.R., Kinzler K.W.,
RA   Vogelstein B.;
RT   "Topological control of p21WAF1/CIP1 expression in normal and
RT   neoplastic tissues.";
RL   Cancer Res. 55:2910-2919(1995).
RN   [3]
RP   SEQUENCE OF 1-143 FROM N.A.
RX   MEDLINE=94061997; PubMed=8242752;
RA   El-Deiry W.S., Tokino T., Velculescu V.E., Levy D.B., Parsons R.,
RA   Trent J.M., Lin D., Mercer W.E., Kinzler K.W., Vogelstein B.;
RT   "WAF1, a potential mediator of p53 tumor suppression.";
RL   Cell 75:817-825(1993).
CC   -!- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES
CC       ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO
CC       DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
CC       ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
CC       KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- INDUCTION: BY P53, MEZEREIN (ANTILEUKEMIC COMPOUND) AND INTERFERON
CC       BETA.
CC   -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U09507; AAB60456.1; -.
DR   EMBL; U24173; AAC52220.1; -.
DR   PIR; A49438; A49438.
DR   HSSP; P46527; 1JSU.
DR   MGD; MGI:104556; Cdkn1a.
DR   InterPro; IPR003175; CDI.
DR   Pfam; PF02234; CDI; 1.
KW   Cell cycle; Nuclear protein; Zinc-finger.
FT   ZN_FING      12     40       C4-TYPE (POTENTIAL).
FT   CONFLICT     30     30       R -> S (IN REF. 3).
FT   CONFLICT     56     57       TP -> RQ (IN REF. 3).
SQ   SEQUENCE   159 AA;  17785 MW;  37B7C22B9A2FD089 CRC64;


  Query Match             70.0%;  Score 35;  DB 1;  Length 159;
  Best Local Similarity   85.7%;  Pred. No. 33;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
             ||| |||
Db     125 SPGGPGT 131


RESULT  33
UR2R_RAT
ID   UR2R_RAT        STANDARD;      PRT;   386 AA.
AC   P49684; P48041;
DT   01-FEB-1996 (Rel. 33, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Urotensin II receptor (UR-II-R) (G protein-coupled sensory epithelial
DE   neuropeptide-like receptor) (SENR).
GN   GPR14.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96115583; PubMed=8666380;
RA   Marchese A., Heiber M., Nguyen T., Heng H.H.Q., Saldivia V.R.,
RA   Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R.,
RA   O'Dowd B.F., Docherty J.M.;
RT   "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
RT   and GPR14, encoding receptors related to interleukin 8, neuropeptide
RT   Y, and somatostatin receptors.";
RL   Genomics 29:335-344(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Circumvallate papillae;
RX   MEDLINE=95251679; PubMed=7733947;
RA   Tal M., Ammar D.A., Karpuj M., Krizhanovsky V., Naim M.,
RA   Thompson D.A.;
RT   "A novel putative neuropeptide receptor expressed in neural tissue,
RT   including sensory epithelia.";
RL   Biochem. Biophys. Res. Commun. 209:752-759(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Urinary bladder;
RA   Suga H., Takao K.;
RT   "Expression of the rat SENR in the urinary bladder tissues.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: HIGH AFINITY RECEPTOR FOR UROTENSIN II. THE ACTIVITY OF
CC       THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATE A
CC       PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN NEURAL AND SENSORY
CC       TISSUES.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U32673; AAC52593.1; -.
DR   EMBL; U23483; AAA80111.1; -.
DR   EMBL; AB012210; BAA25251.1; -.
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DR   HSSP; P34996; 1DDD.
DR   GCRDb; GCR_1427; -.
DR   GCRDb; GCR_1443; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     54       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     55     77       1 (POTENTIAL).
FT   DOMAIN       78     87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    113       2 (POTENTIAL).
FT   DOMAIN      114    124       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    125    146       3 (POTENTIAL).
FT   DOMAIN      147    167       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    168    186       4 (POTENTIAL).
FT   DOMAIN      187    209       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    210    232       5 (POTENTIAL).
FT   DOMAIN      233    258       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    259    284       6 (POTENTIAL).
FT   DOMAIN      285    299       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    300    321       7 (POTENTIAL).
FT   DOMAIN      322    386       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     29     29       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    123    199       BY SIMILARITY.
FT   CONFLICT    315    315       F -> L (IN REF. 1).
SQ   SEQUENCE   386 AA;  42707 MW;  FA4E95CC6A4CA27C CRC64;

  Query Match             70.0%;  Score 35;  DB 1;  Length 386;
  Best Local Similarity   85.7%;  Pred. No. 85;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           ||||||:
Db     341 SPGSPGS 347


RESULT  34
IL5R_MOUSE
ID   IL5R_MOUSE     STANDARD;      PRT;   415 AA.
AC   P21183;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Interleukin-5 receptor alpha chain precursor (IL-5R-alpha).
GN   IL5RA OR IL5R.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91092260; PubMed=2265612;
RA   Takaki S., Tominaga A., Mita S., Sonoda E., Yamaguchi N.,
RA   Takatsu K.;
RT   "Molecular cloning and expression of the murine interleukin-5
RT   receptor.";
RL   EMBO J. 9:4367-4374(1990).
CC   -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC       BINDS TO IL-5.
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC       CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO
CC       ON B-CELLS.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D90205; BAA14231.1; -.
DR   PIR; S12357; S12357.
DR   MGD; MGI:96558; Il5ra.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003532; Hematopo_receptor_S_F2.
DR   PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW   Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     17
FT   CHAIN        18    415       INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT   DOMAIN       18    339       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    340    361       POTENTIAL.
FT   DOMAIN      362    415       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    131    152       BY SIMILARITY.
FT   DISULFID    179    193       BY SIMILARITY.
FT   CARBOHYD     32     32       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    128    128       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    213    213       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    241    241       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   415 AA;  46989 MW;  A4326D2922571C08 CRC64;

  Query Match             70.0%;  Score 35;  DB 1;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 PGSPGT 9
           ||||||
Db     119 PGSPGT 124


RESULT  35
HXKG_ASPNG
ID   HXKG_ASPNG     STANDARD;      PRT;   495 AA.
AC   Q92407;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Glucokinase (EC 2.7.1.2) (Glucose kinase) (GLK).
GN   GLKA.
OS   Aspergillus niger.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5061;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CBS 120.49 / N400;
RX   MEDLINE=97008939; PubMed=8856049;
RA   Panneman H., Ruijter G.J.G., van den Broeck H.C., Driever E.T.M.,
RA   Visser J.;
RT   "Cloning and biochemical characterisation of an Aspergillus niger
RT   glucokinase. Evidence for the presence of separate glucokinase and
RT   hexokinase enzymes.";
RL   Eur. J. Biochem. 240:518-525(1996).
CC   -!- FUNCTION: THE ENZYME HAS GREAT AFFINITY FOR GLUCOSE. MANNOSE, 2-
CC       DEOXYGLUCOSE AND GLUCOSAMINE CAN SERVE AS SUBSTRATES. ACTIVITY IS
CC       RELATIVELY CONSTANT BETWEEN PH 7.5 AND PH 9.0. BELOW PH 7.5, THE
CC       ACTIVITY DECREASES WITH PH.
CC   -!- CATALYTIC ACTIVITY: ATP + D-glucose = ADP + D-glucose 6-phosphate.
CC   -!- SUBUNIT: MONOMER (PROBABLE).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X99626; CAA67949.1; -.
DR   HSSP; Q26609; 1BDG.
DR   InterPro; IPR001312; Hexokinase.
DR   Pfam; PF00349; hexokinase; 1.
DR   PRINTS; PR00475; HEXOKINASE.
DR   ProDom; PD001109; Hexokinase; 1.
DR   PROSITE; PS00378; HEXOKINASES; 1.
KW   Transferase; Kinase; Glycolysis; ATP-binding.
FT   BINDING      93     93       ATP (POTENTIAL).
FT   DOMAIN      149    175       GLUCOSE-BINDING (POTENTIAL).
FT   NP_BIND     472    477       ATP (POTENTIAL).
SQ   SEQUENCE   495 AA;  54536 MW;  02C94EF07D1809F8 CRC64;


  Query Match             70.0%;  Score 35;  DB 1;  Length 495;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          |:|||  ||
Db    218 YTSPGETGT 226


RESULT  36
AMH2_HUMAN
ID   AMH2_HUMAN     STANDARD;      PRT;   573 AA.
AC   Q16671; Q13762;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Anti-mullerian hormone type II receptor precursor (EC 2.7.1.37) (AMH
DE   type II receptor) (MIS type II receptor) (MISRII) (MRII).
GN   AMHR2 OR AMHR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96083584; PubMed=7493017;
RA   Imbeaud S., Faure E., Lamarre I., Mattei M.-G., di Clemente N.,
RA   Tizard R., Carre-Eusebe D., Belville C., Tragethon L., Tonkin C.,
RA   Nelson J., McAuliffe M., Bidart J.-M., Lababidi A., Josso N.,
RA   Cate R.L., Picard J.-Y.;
RT   "Insensitivity to anti-mullerian hormone due to a mutation in the
RT   human anti-mullerian hormone receptor.";
RL   Nat. Genet. 11:382-388(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96028015; PubMed=7488027;
RA   Visser J.A., McLuskey A., van Beers T., Weghuis D.O., van Kessel A.G.,
RA   Grootegoed J.A., Themmen A.P.N.;
RT   "Structure and chromosomal localization of the human anti-mullerian
RT   hormone type II receptor gene.";
RL   Biochem. Biophys. Res. Commun. 215:1029-1036(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=20055680; PubMed=10589763;
RA   Masiakos P.T., MacLaughlin D.T., Maheswaran S., Teixeira J.,
RA   Fuller A.F. Jr., Shah P.C., Kehas D.J., Kenneally M.K.,
RA   Dombkowski D.M., Ha T.U., Preffer F.I., Donahoe P.K.;
RT   "Human ovarian cancer, cell lines, and primary ascites cells express
RT   the human Mullerian inhibiting substance (MIS) type II receptor,
RT   bind, and are responsive to MIS.";
RL   Clin. Cancer Res. 5:3488-3499(1999).
CC   -!- FUNCTION: RECEPTOR FOR ANTI-MULLERIAN HORMONE.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DISEASE: DEFECTS IN AMHR2 ARE THE CAUSE OF PERSISTENT MULLERIAN
CC       DUCT SYNDROME TYPE II (PMDS-2); A FORM OF MALE
CC       PSEUDOHERMAPHRODITISM CHARACTERIZED BY A FAILURE OF MUELLERIAN
CC       DUCT REGRESSION IN OTHERWISE NORMAL MALES.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       TGFB RECEPTOR SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X89013; CAA61418.1; -.
DR   EMBL; U29700; AAC50328.1; -.
DR   EMBL; X91156; CAA62593.1; -.
DR   EMBL; X91157; CAA62593.1; JOINED.
DR   EMBL; X91158; CAA62593.1; JOINED.
DR   EMBL; X91159; CAA62593.1; JOINED.
DR   EMBL; X91160; CAA62593.1; JOINED.
DR   EMBL; X91161; CAA62593.1; JOINED.
DR   EMBL; X91162; CAA62593.1; JOINED.
DR   EMBL; X91163; CAA62593.1; JOINED.
DR   EMBL; X91164; CAA62593.1; JOINED.
DR   EMBL; X91165; CAA62593.1; JOINED.
DR   EMBL; X91166; CAA62593.1; JOINED.
DR   EMBL; AF172932; AAD48497.1; -.
DR   MIM; 600956; -.
DR   InterPro; IPR000472; Activin_rec.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Transmembrane; Glycoprotein; Signal; Pseudohermaphroditism.
FT   SIGNAL       1     17       POTENTIAL.
FT   CHAIN       18    573       ANTI-MULLERIAN HORMONE TYPE II RECEPTOR.
FT   DOMAIN      18    149       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   150    170       POTENTIAL.
FT   DOMAIN     171    573       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     203    518       PROTEIN KINASE.
FT   NP_BIND    209    217       ATP (BY SIMILARITY).
FT   BINDING    230    230       ATP (BY SIMILARITY).
FT   ACT_SITE   333    333       BY SIMILARITY.
FT   CARBOHYD    66     66       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   119    119       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   161    161       L -> V (IN REF. 2; CAA62593).
SQ   SEQUENCE   573 AA;  62749 MW;  1347C10C2942FDBA CRC64;


  Query Match             70.0%;  Score 35;  DB 1;  Length 573;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 PGSPGT 9
          ||||||
Db    126 PGSPGT 131


RESULT  37
MRKC_KLEPN
ID   MRKC_KLEPN     STANDARD;      PRT;   828 AA.
AC   P21647;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Outer membrane usher protein mrkC precursor.
GN   MRKC.
OS   Klebsiella pneumoniae.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Klebsiella.
OX   NCBI_TaxID=573;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IA565;
RX   MEDLINE=91100388; PubMed=1670938;
RA   Allen B.L., Gerlach G.-F., Clegg S.;
RT   "Nucleotide sequence and functions of mrk determinants necessary for
RT   expression of type 3 fimbriae in Klebsiella pneumoniae.";
RL   J. Bacteriol. 173:916-920(1991).
CC   -!- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF THE TYPE 3
CC       FIMBRIAL SUBUNIT (MRKA).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC       (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55912; AAA25095.1; -.
DR   PIR; D39142; D39142.
DR   InterPro; IPR000015; Fimb_usher.
DR   Pfam; PF00577; Usher; 1.
DR   PROSITE; PS01151; FIMBRIAL_USHER; 1.
KW   Outer membrane; Transmembrane; Fimbria; Transport; Signal.
FT   SIGNAL       1     18       POTENTIAL.
FT   CHAIN       19    828       OUTER MEMBRANE USHER PROTEIN MRKC.
FT   DISULFID   813    827       POTENTIAL.
SQ   SEQUENCE   828 AA;  91049 MW;  B30EDF5798249FC9 CRC64;
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Query Match 70.0%; Score 35; DB 1; Length 828;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       4 PGSPGT 9
           ||||||
Db     693 PGSPGT 698
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RESULT  38
VGLB_HSV1F
ID   VGLB_HSV1F     STANDARD;      PRT;   903 AA.
AC   P06436;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Glycoprotein B precursor.
GN   GB OR UL27.
OS   Herpes simplex virus (type 1 / strain F).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=10304;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85083254; PubMed=2981343;
RA   Pellett P.E., Kousoulas K.G., Pereira L., Roizman B.;
RT   "Anatomy of the herpes simplex virus 1 strain F glycoprotein B gene:
RT   primary sequence and predicted protein structure of the wild type and
RT   of monoclonal antibody-resistant mutants.";
RL   J. Virol. 53:243-253(1985).
RN   [2]
RP   SEQUENCE OF 1-176 FROM N.A.
RX   MEDLINE=88306232; PubMed=2457278;
RA   Hammerschmidt W., Conraths F., Mankertz J., Buhk H.-J., Pauli G.,
RA   Ludwig H.;
RT   "Common epitopes of glycoprotein B map within the major DNA-binding
RT   proteins of bovine herpesvirus type 2 (BHV-2) and herpes simplex
RT   virus type 1 (HSV-1).";
RL   Virology 165:406-418(1988).
```

```
CC   -!- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,
CC       GB, GC, GG, GD, GI, AND GE.
CC   -!- MISCELLANEOUS: GB IS THE ONLY GLYCOPROTEIN THAT IS KNOWN TO BE
CC       REQUIRED FOR VIRAL GROWTH.
CC   -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14164; AAA45776.1; -.
DR   EMBL; M21633; AAA45788.1; -.
DR   PIR; A03750; VGBEB1.
DR   InterPro; IPR000234; Glycoprot_B.
DR   Pfam; PF00606; Glycoprotein_B; 1.
DR   ProDom; PD000693; Glycoprot_B; 1.
KW   Glycoprotein; Transmembrane; Signal.
FT   SIGNAL       1     29
FT   CHAIN       30    903       GLYCOPROTEIN B.
FT   DOMAIN      31    729       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   730    745       POTENTIAL.
FT   TRANSMEM   751    770       POTENTIAL.
FT   TRANSMEM   774    794       POTENTIAL.
FT   DOMAIN     795    903       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   140    140       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   397    397       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   429    429       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   488    488       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   673    673       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   903 AA;  100104 MW;  73BDCA7813DB35E8 CRC64;
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Query Match 70.0%; Score 35; DB 1; Length 903;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy       2 SSPGSPG 8
           ||||:||
Db      32 SSPGTPG 38
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```
RESULT  39
VGLB_HSV11
ID   VGLB_HSV11     STANDARD;      PRT;   904 AA.
AC   P10211;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Glycoprotein B precursor.
GN   GB OR UL27.
OS   Herpes simplex virus (type 1 / strain 17).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=10299;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88274327; PubMed=2839594;
RA   McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
RA   McNab D., Perry L.J., Scott J.E., Taylor P.;
RT   "The complete DNA sequence of the long unique region in the genome of
RT   herpes simplex virus type 1.";
RL   J. Gen. Virol. 69:1531-1574(1988).
CC   -!- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,
CC       GB, GC, GG, GD, GI, AND GE.
CC   -!- MISCELLANEOUS: GB IS THE ONLY GLYCOPROTEIN THAT IS KNOWN TO BE
CC       REQUIRED FOR VIRAL GROWTH.
```

```
CC   -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10879; BAA01673.1; -.
DR   EMBL; X14112; CAA32320.1; -.
DR   PIR; I30084; VGBEW7.
DR   InterPro; IPR000234; Glycoprot_B.
DR   Pfam; PF00606; Glycoprotein_B; 1.
DR   ProDom; PD000693; Glycoprot_B; 1.
KW   Glycoprotein; Transmembrane; Signal.
FT   SIGNAL        1     30
FT   CHAIN        31    904       GLYCOPROTEIN B.
FT   DOMAIN       31    730       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    731    746       POTENTIAL.
FT   TRANSMEM    752    771       POTENTIAL.
FT   TRANSMEM    775    795       POTENTIAL.
FT   DOMAIN      796    904       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     87     87       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    398    398       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    430    430       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    489    489       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    674    674       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   904 AA;  100292 MW;  2C14E8B1284C1F3A CRC64;

  Query Match             70.0%;  Score 35;  DB 1;  Length 904;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
           ||||:||
Db      33 SSPGTPG 39


RESULT  40
VGLB_HSV1P
ID   VGLB_HSV1P     STANDARD;      PRT;   904 AA.
AC   P08665;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Glycoprotein B precursor.
GN   GB OR UL27.
OS   Herpes simplex virus (type 1 / strain Patton).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=10308;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87112925; PubMed=3027364;
RA   Stuve L.L., Brown-Shimer S., Pachl C., Najarian R., Dina D.,
RA   Burke R.L.;
RT   "Structure and expression of the herpes simplex virus type 2
RT   glycoprotein gB gene.";
RL   J. Virol. 61:326-335(1987).
CC   -!- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
CC   -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GH,
CC       GB, GC, GG, GD, GI, AND GE.
CC   -!- MISCELLANEOUS: GB IS THE ONLY GLYCOPROTEIN THAT IS KNOWN TO BE
CC       REQUIRED FOR VIRAL GROWTH.
CC   -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K03541; AAA45778.1; -.
DR   InterPro; IPR000234; Glycoprot_B.
DR   Pfam; PF00606; Glycoprotein_B; 1.
DR   ProDom; PD000693; Glycoprot_B; 1.
KW   Glycoprotein; Transmembrane; Signal.
FT   SIGNAL        1     30
FT   CHAIN        31    904       GLYCOPROTEIN B.
FT   DOMAIN       31    730       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    731    746       POTENTIAL.
FT   TRANSMEM    752    772       POTENTIAL.
FT   TRANSMEM    775    795       POTENTIAL.
FT   DOMAIN      796    904       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     87     87       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    398    398       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    430    430       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    489    489       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    674    674       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   904 AA;  100115 MW;  7825E1DC830A626F CRC64;

  Query Match             70.0%;  Score 35;  DB 1;  Length 904;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
           ||||:||
Db      33 SSPGTPG 39


Search completed: May 21, 2002, 11:24:11
Job time: 331 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 21, 2002, 11:23:51 ; Search time 41.2 Seconds
(without alignments)
37.790 Million cell updates/sec

Title: US-09-734-281-2
Perfect score: 50
Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	372	11	Q91WK4	Q91wk4 mus musculu
2	42	84.0	641	3	Q9Y879	Q9y879 cryptococcu
3	41	82.0	15	6	Q9TRE5	Q9tre5 bos taurus
4	41	82.0	626	10	Q9ZRY1	Q9zry1 glycine max
5	40	80.0	376	4	Q96CK9	Q96ck9 homo sapien
6	40	80.0	435	2	O68641	O68641 oerskovia x
7	39	78.0	150	2	Q9XAE0	Q9xae0 streptomyce
8	39	78.0	272	2	Q9S283	Q9s283 streptomyce
9	39	78.0	389	6	Q9BEG5	Q9beg5 bos taurus
10	39	78.0	391	6	Q9BEG6	Q9beg6 bos taurus
11	39	78.0	405	4	Q9NWV9	Q9nwv9 homo sapien
12	39	78.0	424	4	Q9UKS6	Q9uks6 homo sapien
13	39	78.0	424	4	Q9H331	Q9h331 homo sapien
14	39	78.0	513	4	Q9BRM0	Q9brm0 homo sapien
15	39	78.0	651	4	Q9P2L4	Q9p214 homo sapien
16	39	78.0	2232	5	P91365	P91365 caenorhabdi
17	38	76.0	280	5	Q95TC5	Q95tc5 drosophila
18	38	76.0	453	11	Q63422	Q63422 rattus norv
19	38	76.0	517	17	Q974W1	Q974w1 sulfolobus
20	38	76.0	711	5	Q9U5M3	Q9u5m3 podocoryne
21	38	76.0	1019	5	Q961G7	Q961g7 drosophila
22	38	76.0	1345	1	Q54437	Q54437 staphylothe
23	37	74.0	168	5	O17289	O17289 caenorhabdi
24	37	74.0	238	4	Q9H4T5	Q9h4t5 homo sapien
25	37	74.0	302	3	O43060	O43060 schizosacch
26	37	74.0	333	4	Q15469	Q15469 homo sapien
27	37	74.0	387	11	Q9D2V9	Q9d2v9 mus musculu
28	37	74.0	387	11	Q99PD5	Q99pd5 mus musculu
29	37	74.0	393	6	Q99147	Q99147 oryctolagus
30	37	74.0	396	4	Q14631	Q14631 homo sapien
31	37	74.0	406	3	O74658	O74658 candida alb
32	37	74.0	406	3	Q9URP9	Q9urp9 candida alb
33	37	74.0	407	3	O74661	O74661 candida alb
34	37	74.0	420	4	Q14633	Q14633 homo sapien
35	37	74.0	539	4	O95196	O95196 homo sapien
36	37	74.0	539	11	Q9QY32	Q9qy32 mus musculu
37	37	74.0	541	6	Q01106	Q01106 oryctolagus
38	37	74.0	723	11	Q9D677	Q9d677 mus musculu
39	37	74.0	734	4	O75112	O75112 homo sapien
40	37	74.0	742	11	Q9CW54	Q9cw54 mus musculu
41	37	74.0	847	4	Q16584	Q16584 homo sapien
42	37	74.0	850	11	Q9JJ15	Q9jj15 mus musculu
43	37	74.0	1523	3	Q9HFX4	Q9hfx4 candida alb
44	37	74.0	3494	4	Q96RU9	Q96ru9 homo sapien
45	37	74.0	3620	6	Q9TU53	Q9tu53 canis famil
46	37	74.0	3623	4	O60494	O60494 homo sapien
47	37	74.0	6875	6	Q28733	Q28733 oryctolagus
48	37	74.0	26926	4	Q10466	Q10466 homo sapien
49	36	72.0	114	10	Q9ATC9	Q9atc9 malus domes
50	36	72.0	119	10	Q43548	Q43548 malus domes
51	36	72.0	149	11	Q9JKX0	Q9jkx0 mus musculu
52	36	72.0	179	11	Q9JKW9	Q9jkw9 mus musculu
53	36	72.0	209	16	Q98K79	Q98k79 rhizobium l
54	36	72.0	216	11	Q9JKX1	Q9jkx1 mus musculu
55	36	72.0	221	2	Q9RJC5	Q9rjc5 streptomyce

ALIGNMENTS

RESULT 1
Q91WK4
ID Q91WK4 PRELIMINARY; PRT; 372 AA.
AC Q91WK4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN TAU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE, AND RETINA;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC014748; AAH14748.1; -.
SQ SEQUENCE 372 AA; 38861 MW; B027745D23BC62A2 CRC64;

Query Match 100.0%; Score 50; DB 11; Length 372;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 128 YSSPGSPGT 136

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RESULT   2
Q9Y879
ID   Q9Y879      PRELIMINARY;      PRT;   641 AA.
AC   Q9Y879;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CALCINEURIN A CATALYTIC SUBUNIT.
GN   CNA1.
OS   Cryptococcus neoformans var. neoformans.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=40410;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JEC21;
RX   MEDLINE=20107115; PubMed=10639477;
RA   Cruz M.C., Sia R.A.L., Olson M., Cox G.M., Heitman J.;
RT   "Comparison of the Roles of Calcineurin in Physiology and Virulence in
RT   Serotype D and Serotype A Strains of Cryptococcus neoformans.";
RL   Infect. Immun. 68:982-985(2000).
CC   -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC       ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC   -!- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
DR   EMBL; AF159511; AAD44336.1; -.
DR   HSSP; P48452; 1TCO.
DR   InterPro; IPR000934; Ser_thr_phosphtse.
DR   Pfam; PF00149; STphosphatase; 1.
DR   PRINTS; PR00114; STPHPHTASE.
DR   SMART; SM00156; PP2Ac; 1.
DR   PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW   Hydrolase; Iron; Manganese.
SQ   SEQUENCE   641 AA;  71813 MW;  DD68607843D8E6DB CRC64;

  Query Match             84.0%;  Score 42;  DB 3;  Length 641;
  Best Local Similarity   77.8%;  Pred. No. 18;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           : |||||||
Db     554 FGSPGSPGT 562


RESULT   3
Q9TRE5
ID   Q9TRE5      PRELIMINARY;      PRT;    15 AA.
AC   Q9TRE5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   TAU PROTEIN (FRAGMENT).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94043150; PubMed=8226879;
RA   Paudel H.K., Lew J., Ali Z., Wang J.H.;
RT   "Brain proline-directed protein kinase phosphorylates tau on sites
RT   that are abnormally phosphorylated in tau associated with Alzheimer's
RT   paired helical filaments.";
RL   J. Biol. Chem. 268:23512-23518(1993).
SQ   SEQUENCE   15 AA;  1449 MW;  FBCBEEFEEBC2B342 CRC64;

  Query Match             82.0%;  Score 41;  DB 6;  Length 15;
  Best Local Similarity   87.5%;  Pred. No. 0.5;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           ||||| ||
Db       3 YSSPGXPG 10


RESULT   4
Q9ZRY1
ID   Q9ZRY1      PRELIMINARY;      PRT;   626 AA.
AC   Q9ZRY1;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   NDX1 HOMEOBOX PROTEIN (FRAGMENT).
GN   NDX1.
OS   Glycine max (Soybean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jorgensen J.E., Gronlund M., Pallisgaard N., Larsen K., Marcker K.A.,
RA   Jensen E.;
RT   "A new class of plant homeobox genes is expressed in specific regions
RT   of determinate symbiotic root nodules.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ011831; CAA09794.1; -.
DR   InterPro; IPR001356; Homeobox.
DR   SMART; SM00389; HOX; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
KW   Homeobox; DNA-binding; Nuclear protein.
FT   NON_TER       1       1
SQ   SEQUENCE   626 AA;  69101 MW;  0DCF8C371CD61B11 CRC64;

  Query Match             82.0%;  Score 41;  DB 10;  Length 626;
  Best Local Similarity   87.5%;  Pred. No. 26;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           | ||||||
Db     498 YDSPGSPG 505


RESULT   5
Q96CK9
ID   Q96CK9      PRELIMINARY;      PRT;   376 AA.
AC   Q96CK9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SIMILAR TO ZINC FINGER PROTEIN 16 (KOX 9).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG CARCINOMA;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC014165; AAH14165.1; -.
SQ   SEQUENCE   376 AA;  41145 MW;  68B1A638CC0758BC CRC64;

  Query Match             80.0%;  Score 40;  DB 4;  Length 376;
  Best Local Similarity   87.5%;  Pred. No. 23;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||:|||
Db      20 SSPGTPGT 27
```

```
RESULT   6
O68641
ID   O68641      PRELIMINARY;      PRT;   435 AA.
AC   O68641;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BETA-1,3-GLUCANASE II.
GN   BGLII.
OS   Oerskovia xanthineolytica.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Micrococcineae; Cellulomonadaceae; Oerskovia.
OX   NCBI_TaxID=1826;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LL G109;
RA   Ventom A.M., Asenjo J.A.;
RT   "Characterization of yeast lytic enzymes from Oerskovia
RT   xanthineolytica LL-G109.";
RL   Enzyme Microb. Technol. 13:71-75(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LL G109;
RX   MEDLINE=96409238; PubMed=8814220;
RA   Parrado J., Escuredo P.R., Conejero-Lara F., Kotik M., Ponting C.P.,
RA   Asenjo J.A., Dobson C.M.;
RT   "Molecular characterisation of a thermoactive beta-1,3-glucanase from
RT   Oerskovia xanthineolytica.";
RL   Biochim. Biophys. Acta 1296:145-151(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LL G109;
RX   MEDLINE=96250169; PubMed=8659924;
RA   Ferrer P., Hedegaard L., Halkier T., Diers I., Savva D., Asenjo J.A.;
RT   "Molecular cloning of a lytic beta-1,3-glucanase gene from Oerskovia
RT   xanthineolytica LL G109.";
RL   Ann. N. Y. Acad. Sci. 782:555-566(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LL G109;
RA   Ferrer P., Andrews B.A., Asenjo J.A., Hedegaard L., Diers I.;
RT   "BglII codes for a yeast-lytic beta-1,3-glucanase from Oerskovia
RT   xanthineolytica LL G109 (Cellulomonas cellulans) having a mannose-
RT   binding domain.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF052745; AAC38290.1; -.
DR   HSSP; P23904; 1AJK.
DR   InterPro; IPR000757; Glyco_hydro_16.
DR   InterPro; IPR000772; Ricin_B_lectin.
DR   Pfam; PF00722; Glyco_hydro_16; 1.
DR   Pfam; PF00652; Ricin_B_lectin; 1.
DR   SMART; SM00458; RICIN; 1.
DR   PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
DR   PROSITE; PS50231; RICIN_B_LECTIN; 1.
SQ   SEQUENCE   435 AA;  46097 MW;  00F087BE644C0F58 CRC64;

  Query Match           80.0%;  Score 40;  DB 2;  Length 435;
  Best Local Similarity  87.5%;  Pred. No. 27;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||:|||
Db     297 SSPGNPGT 304


RESULT   7
Q9XAE0
ID   Q9XAE0      PRELIMINARY;      PRT;   150 AA.
AC   Q9XAE0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 16.1 KDA PROTEIN.
GN   SC6G9.42C.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Seeger K.J., Harris D.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=97000351; PubMed=8843436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA   Kinashi H., Hopwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
DR   EMBL; AL079356; CAB45633.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   150 AA;  16072 MW;  7A8D93D1C6A48A0D CRC64;

  Query Match           78.0%;  Score 39;  DB 2;  Length 150;
  Best Local Similarity  87.5%;  Pred. No. 13;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           |||| |||
Db       3 SSPGKPGT 10


RESULT   8
Q9S283
ID   Q9S283      PRELIMINARY;      PRT;   272 AA.
AC   Q9S283;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PUTATIVE EXPRESSION REGULATOR (FRAGMENT).
GN   SCI11.37C.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Saunders D., Harris D.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=97000351; PubMed=8843436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA   Kinashi H., Hopwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
DR   EMBL; AL096849; CAB50963.1; -.
```

```
DR   InterPro; IPR001450; 4Fe4S_ferredoxin.
DR   InterPro; IPR000561; EGF-like.
DR   PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
FT   NON_TER       1      1
SQ   SEQUENCE   272 AA;  27508 MW;  6E8523635D929BB5 CRC64;
```

Query Match 78.0%; Score 39; DB 2; Length 272;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 YSSPGSPGT 9
          |: ||:|||
Db    170 YAPPGAPGT 178
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RESULT   9
Q9BEG5
ID   Q9BEG5      PRELIMINARY;      PRT;   389 AA.
AC   Q9BEG5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   ECTODYSPLASIN 1, ISOFORM A2.
GN   ED1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HOLSTEIN;
RA   Droegemueller C., Distl O., Leeb T.;
RT   "Identification of a highly polymorphic microsatellite within the
RT   bovine ectodysplasin A (ED1) gene on BTA Xq22-24.";
RL   Anim. Genet. 31:416-416(2000).
DR   EMBL; AJ300468; CAC29152.1; -.
DR   EMBL; AJ300469; CAC29152.1; JOINED.
DR   EMBL; AJ278907; CAC29152.1; JOINED.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR000478; TNF_family.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   389 AA;  41339 MW;  60BE0077C7C83986 CRC64;
```

Query Match 78.0%; Score 39; DB 6; Length 389;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 YSSPGSPGT 9
          :| ||:|||
Db     78 FSGPGTPGT 86
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RESULT  10
Q9BEG6
ID   Q9BEG6      PRELIMINARY;      PRT;   391 AA.
AC   Q9BEG6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   ECTODYSPLASIN 1, ISOFORM A1.
GN   ED1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HOLSTEIN;
RA   Droegemueller C., Distl O., Leeb T.;
RT   "Identification of a highly polymorphic microsatellite within the
RT   bovine ectodysplasin A (ED1) gene on BTA Xq22-24.";
RL   Anim. Genet. 31:416-416(2000).
DR   EMBL; AJ300468; CAC29151.1; -.
DR   EMBL; AJ300469; CAC29151.1; JOINED.
DR   EMBL; AJ278907; CAC29151.1; JOINED.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR000478; TNF_family.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   391 AA;  41567 MW;  1F87AD67A04EB7AA CRC64;
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Query Match 78.0%; Score 39; DB 6; Length 391;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 YSSPGSPGT 9
          :| ||:|||
Db     78 FSGPGTPGT 86
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RESULT  11
Q9NWV9
ID   Q9NWV9      PRELIMINARY;      PRT;   405 AA.
AC   Q9NWV9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   CDNA FLJ20570 FIS, CLONE REC00956 (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,
RA   Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T.,
RA   Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK000577; BAA91267.1; -.
DR   InterPro; IPR001060; FCH.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00611; FCH; 1.
DR   SMART; SM00055; FCH; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50002; SH3; 1.
FT   NON_TER     405    405
SQ   SEQUENCE   405 AA;  46494 MW;  6EA81D7782B53D92 CRC64;
```

Query Match 78.0%; Score 39; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      3 SPGSPGT 9
          |||||||
Db    341 SPGSPGT 347
```

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RESULT  12
Q9UKS6
ID   Q9UKS6      PRELIMINARY;      PRT;   424 AA.
AC   Q9UKS6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   SH3 DOMAIN-CONTAINING PROTEIN 6511.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20002705; PubMed=10531379;
RA   Howard L., Nelson K.K., Maciewicz R.A., Blobel C.P.;
RT   "Interaction of the metalloprotease disintegrins MDC9 and MDC15 with
RT   two SH3 domain-containing proteins, endophilin I and SH3PX1.";
RL   J. Biol. Chem. 274:31693-31699(1999).
DR   EMBL; AF130979; AAF04472.1; -.
DR   HSSP; P29355; 1SEM.
DR   InterPro; IPR001060; FCH.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00611; FCH; 1.
DR   Pfam; PF00018; SH3; 1.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   SMART; SM00055; FCH; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50002; SH3; 1.
SQ   SEQUENCE   424 AA;  48515 MW;  924A7BF79C8DC395 CRC64;


  Query Match             78.0%;  Score 39;  DB 4;  Length 424;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 SPGSPGT 9
          |||||||
Db    341 SPGSPGT 347


RESULT  13
Q9H331
ID   Q9H331      PRELIMINARY;      PRT;   424 AA.
AC   Q9H331;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PACSIN3 (PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE 3) (UNKNOWN)
DE   (PROTEIN FOR MGC:19935) (PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE
DE   IN NEURONS 3).
GN   PACSIN3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=11082044;
RA   Modregger J., Ritter B., Witter B., Paulsson M., Plomann M.;
RT   "All three PACSIN isoforms bind to endocytic proteins and inhibit
RT   endocytosis.";
RL   J. Cell Sci. 113:4511-4521(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21100457; PubMed=11179684;
RA   Sumoy L., Pluvinet R., Andreu N., Estivill X., Escarceller M.;
RT   "PACSIN 3 is a novel SH3 domain cytoplasmic adapter protein of the
RT   pacsin-syndapin-FAP52 gene family.";
RL   Gene 262:199-205(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MELANOMA;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=UTERUS, LEIOMYOSARCOMA;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF149825; AAG31023.1; -.
DR   EMBL; AF242530; AAK29207.1; -.
DR   EMBL; BC011889; AAH11889.1; -.
DR   EMBL; BC007914; AAH07914.1; -.
DR   HSSP; P29355; 1SEM.
DR   InterPro; IPR001060; FCH.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00018; SH3; 1.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   SMART; SM00055; FCH; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Kinase.
SQ   SEQUENCE   424 AA;  48486 MW;  6DBD940AE6D1F352 CRC64;


  Query Match             78.0%;  Score 39;  DB 4;  Length 424;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 SPGSPGT 9
          |||||||
Db    341 SPGSPGT 347


RESULT  14
Q9BRM0
ID   Q9BRM0      PRELIMINARY;      PRT;   513 AA.
AC   Q9BRM0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   HYPOTHETICAL PROTEIN (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=UTERUS, AND LEIOMYOSARCOMA;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006174; AAH06174.1; -.
DR   InterPro; IPR001798; Kelch.
DR   Pfam; PF01344; Kelch; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   513 AA;  54599 MW;  21FD050215015520 CRC64;


  Query Match             78.0%;  Score 39;  DB 4;  Length 513;
  Best Local Similarity   87.5%;  Pred. No. 48;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 SSPGSPGT 9
          |||||||:
Db    379 SSPGSPGS 386


RESULT  15
Q9P2L4
ID   Q9P2L4      PRELIMINARY;      PRT;   651 AA.
AC   Q9P2L4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   KIAA1332 PROTEIN (FRAGMENT).
GN   KIAA1332.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=20181126; PubMed=10718198;
RA   Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
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RT   "Prediction of the coding sequences of unidentified human genes.XVI.
RT   The complete sequences of 150 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 7:65-73(2000).
DR   EMBL; AB037753; BAA92570.1; -.
DR   InterPro; IPR001798; Kelch.
DR   Pfam; PF01344; Kelch; 2.
FT   NON_TER       1      1
SQ   SEQUENCE   651 AA;  70304 MW;  1CF1DEB5F03DCB3C CRC64;

  Query Match             78.0%;  Score 39;  DB 4;  Length 651;
  Best Local Similarity   87.5%;  Pred. No. 62;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           |||||||:
Db     517 SSPGSPGS 524


RESULT  16
P91365
ID   P91365      PRELIMINARY;      PRT;  2232 AA.
AC   P91365;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   K06A9.1 PROTEIN.
GN   K06A9.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Geisel C., Gattung S.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) MAY BE PRODUCED BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN IS THAT
CC       OF THE A FORM.
DR   EMBL; U80846; AAC70889.1; -.
DR   EMBL; U80846; AAC70890.1; -.
KW   Alternative splicing.
FT   VARSPLIC     842    866       VASSSPAPSTSQNPNPSTSSGSSMI -> LATTSAPKPSVT
FT                                 CLFMYD (IN ISOFORM B).
FT   VARSPLIC     870   1051       PYPSQSTSPVESSTTPSPGSPGTTLTSTSPSPSQSTTIGST
FT                                 QGSTSPGISTTSEEMTSQGSTQTPGSTGSTVTQPSTVSDST
FT                                 SSGSTVTVGSTEGSSSPIPSTSQNTNPSTSSGSSMSTQTPQ
FT                                 SSQSTSPVESSTSGATSSSGSPGTTLTSISPSPSPSSTIGS
FT                                 SQGSTSPVVSTISQGSTE -> KEIDQTAINTYKTYFNFAL
FT                                 LVASKLNNESILTGYIDNFGYSAGLNDHQYYPTDDYNGIKS
FT                                 VPFPIDGTDDDIDLDLKDVDKSLATADWTPPVADQTCMIFI
FT                                 SAAPEDEYGGTTIKSTYTYFETVVGVLVGGAKSIPGLSIDK
FT                                 NIVITNNTMNDRDASAVVSKLLELLPTA (IN ISOFORM
FT                                 B).
SQ   SEQUENCE   2232 AA;  213840 MW;  08D69FA638E14CC8 CRC64;

  Query Match             78.0%;  Score 39;  DB 5;  Length 2232;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db     886 SPGSPGT 892


RESULT  17
Q95TC5
ID   Q95TC5      PRELIMINARY;      PRT;  280 AA.
AC   Q95TC5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   GH02414P.
GN   CG3960.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Y, CN BW SP;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA   Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA   Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA   Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY060231; AAL25270.1; -.
SQ   SEQUENCE   280 AA;  29901 MW;  571CBAAE823B3BE2 CRC64;

  Query Match             76.0%;  Score 38;  DB 5;  Length 280;
  Best Local Similarity   75.0%;  Pred. No. 38;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           |: |||||
Db     125 YNQPGSPG 132


RESULT  18
Q63422
ID   Q63422      PRELIMINARY;      PRT;  453 AA.
AC   Q63422;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PROTON-DEPENDENT PEPTIDE TRANSPORTER (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=SMALL INTESTINE;
RX   MEDLINE=96067558; PubMed=7488096;
RA   Erickson R.H., Gum J.R. Jr., Lindstrom M.M., McKean D., Kim Y.S.;
RT   "Regional expression and dietary regulation of rat small intestinal
RT   peptide and amino acid transporter mRNAs.";
RL   Biochem. Biophys. Res. Commun. 216:249-257(1995).
DR   EMBL; L46873; AAC42076.1; -.
DR   InterPro; IPR002637; Ham1p_like.
DR   InterPro; IPR000109; PTR2.
DR   Pfam; PF00854; PTR2; 1.
DR   PROSITE; PS01022; PTR2_1; 1.
DR   PROSITE; PS01023; PTR2_2; 1.
FT   NON_TER       1      1
FT   NON_TER     453    453
SQ   SEQUENCE   453 AA;  49905 MW;  0706EE059904B082 CRC64;

  Query Match             76.0%;  Score 38;  DB 11;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
           |||||||
Db     420 SSPGSPG 426


RESULT  19
Q974W1
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ID   Q974W1      PRELIMINARY;      PRT;   517 AA.
AC   Q974W1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL PROTEIN ST0549.
GN   ST0549.
OS   Sulfolobus tokodaii.
OC   Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX   NCBI_TaxID=111955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JCM 10545 / 7;
RX   PubMed=11572479;
RA   Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA   Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA   Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA   Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA   Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA   Oshima T., Kikuchi H.;
RT   "Complete genome sequence of an aerobic thermoacidophilic
RT   Crenarchaeon, Sulfolobus tokodaii strain7.";
RL   DNA Res. 8:123-140(2001).
DR   EMBL; AP000982; BAB65546.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   517 AA;  57965 MW;  E129448C73A27A24 CRC64;
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  Query Match             76.0%;  Score 38;  DB 17;  Length 517;
  Best Local Similarity   66.7%;  Pred. No. 73;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |:|| :|||
Db     204 YASPSTPGT 212
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RESULT  20
Q9U5M3
ID   Q9U5M3      PRELIMINARY;      PRT;   711 AA.
AC   Q9U5M3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PAIRED BOX PROTEIN.
GN   PAX-B.
OS   Podocoryne carnea.
OC   Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC   Hydractiniidae; Podocoryne.
OX   NCBI_TaxID=6096;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20302558; PubMed=10842067;
RA   Groeger H., Callaerts P., Gehring W.J., Schmid V.;
RT   "Characterization and expression analysis of an ancestor-type Pax gene
RT   in the hydrozoan jellyfish Podocoryne carnea.";
RL   Mech. Dev. 94:157-169(2000).
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
CC   -!- SIMILARITY: WITH OTHER HOMEOBOX PROTEINS.
DR   EMBL; AJ249563; CAB61522.1; -.
DR   HSSP; P26367; 6PAX.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR001523; Paired_box.
DR   Pfam; PF00046; homeobox; 1.
DR   Pfam; PF00292; PAX; 1.
DR   PRINTS; PR00027; PAIREDBOX.
DR   SMART; SM00389; HOX; 1.
DR   SMART; SM00351; PAX; 1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
DR   PROSITE; PS00034; PAIRED_BOX; 1.
KW   DNA-binding; Developmental protein; Homeobox; Nuclear protein;
KW   Paired box; Transcription regulation.
SQ   SEQUENCE   711 AA;  79326 MW;  AC1D9099E25249B1 CRC64;
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  Query Match             76.0%;  Score 38;  DB 5;  Length 711;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPG 8
           |||||||
Db     211 SSPGSPG 217
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RESULT  21
Q961G7
ID   Q961G7      PRELIMINARY;      PRT;  1019 AA.
AC   Q961G7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   GH23906P.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Y, CN BW SP;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA   Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA   Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA   Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY051598; AAK93022.1; -.
SQ   SEQUENCE   1019 AA;  112156 MW;  207885C035945EAF CRC64;
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  Query Match             76.0%;  Score 38;  DB 5;  Length 1019;
  Best Local Similarity   75.0%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           |: |||||
Db     864 YNQPGSPG 871
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RESULT  22
Q54437
ID   Q54437      PRELIMINARY;      PRT;  1345 AA.
AC   Q54437;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   STABLE PROTEASE PRECURSOR.
OS   Staphylothermus marinus.
OC   Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC   Staphylothermus.
OX   NCBI_TaxID=2280;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=F1;
RX   MEDLINE=95139068; PubMed=7837271;
RA   Peters J., Nitsch M., Kuhlmorgen B., Golbik R., Lupas A.,
RA   Kellermann J., Engelhardt H., Pfander J.-P., Muller S., Goldie K.,
RA   Engel A., Stetter K.-O., Baumeister W.;
RT   "Tetrabrachion: a filamentous archaebacterial surface protein assembly
RT   of unusual structure and extreme stability.";
RL   J. Mol. Biol. 245:385-401(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=F1;
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RA   Mayr J., Lupas A., Kellermann J., Eckerskorn C., Baumeister W.,
RA   Peters J.;
RT   "A hyperthermostable protease of the subtilisin family bound to the
RT   surface layer of the archaeon Staphylothermus marinus.";
RL   Curr. Biol. 0:0-0(1996).
DR   EMBL; U57968; AAB02323.1; -.
DR   MEROPS; S08.096; -.
DR   InterPro; IPR000209; Peptidase_S8.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00082; Peptidase_S8; 3.
DR   PRINTS; PR00723; SUBTILISIN.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
DR   PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
DR   PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.
KW   Signal; Protease.
FT   SIGNAL        1     24       POTENTIAL.
SQ   SEQUENCE   1345 AA;  148446 MW;  D40878E437A52EC3 CRC64;

  Query Match             76.0%;  Score 38;  DB 1;  Length 1345;
  Best Local Similarity   77.8%;  Pred. No. 2e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           ||| |:|||
Db     596 YSSNGAPGT 604


RESULT  23
O17289
ID   O17289      PRELIMINARY;      PRT;   168 AA.
AC   O17289;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 18.6 KDA PROTEIN.
GN   R52.4.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Du Z., Goela D., Ozersky P.;
RT   "The sequence of C. elegans cosmid R52.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RT   "Direct Submission.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF025471; AAB71062.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   168 AA;  18604 MW;  4D72C56A94F38F88 CRC64;

  Query Match             74.0%;  Score 37;  DB 5;  Length 168;
  Best Local Similarity   75.0%;  Pred. No. 34;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ::||||||
Db      40 TTPGSPGT 47


RESULT  24
Q9H4T5
ID   Q9H4T5      PRELIMINARY;      PRT;   238 AA.
AC   Q9H4T5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BA93B14.3 (NEUROTENSIN RECEPTOR 1 (HIGH AFFINITY)(NTR))
DE   (FRAGMENT).
GN   NTSR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Heath P.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL357033; CAC14923.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
FT   NON_TER     238    238
SQ   SEQUENCE   238 AA;  25503 MW;  258BE57EACCF6EF0 CRC64;

  Query Match             74.0%;  Score 37;  DB 4;  Length 238;
  Best Local Similarity   75.0%;  Pred. No. 49;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           |:||:|||
Db       6 SAPGTPGT 13


RESULT  25
O43060
ID   O43060      PRELIMINARY;      PRT;   302 AA.
AC   O43060;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   HYPOTHETICAL 33.3 KDA PROTEIN C4C3.07 IN CHROMOSOME II.
GN   SPBC4C3.07.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Wood V., Rajandream M.A., Barrell B.G., Lauber J., Hilbert H.,
RA   Duesterhoeft A.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO PROTEASOME REGULATORY SUBUNIT S12/MOV-34.
DR   EMBL; AL021730; CAA16829.1; -.
DR   InterPro; IPR000555; Mov34.
DR   InterPro; IPR003640; Mov34_2.
DR   Pfam; PF01398; Mov34; 1.
DR   ProDom; PD005425; Mov34_2; 1.
DR   SMART; SM00232; JAB_MPN; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   302 AA;  33251 MW;  A046E087CF083D84 CRC64;

  Query Match             74.0%;  Score 37;  DB 3;  Length 302;
  Best Local Similarity   66.7%;  Pred. No. 63;
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  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |:||  |||
Db     123 YASPAEPGT 131


RESULT  26
Q15469
ID   Q15469       PRELIMINARY;      PRT;   333 AA.
AC   Q15469;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SOLUBLE INTERLEUKIN-5  RECEPTOR PRECURSOR.
GN   HSIL5R4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL BLOOD;
RX   MEDLINE=92121815; PubMed=1732409;
RA   Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT   "Molecular cloning and expression of the human interleukin 5
RT   receptor.";
RL   J. Exp. Med. 175:341-351(1992).
DR   EMBL; X62156; CAA44081.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003532; Hematopo_receptor_S_F2.
DR   PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW   Signal; Receptor.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    333       SOLUBLE INTERLEUKIN-5  RECEPTOR.
SQ   SEQUENCE   333 AA;  37722 MW;  8D9239845E16985B CRC64;


  Query Match             74.0%;  Score 37;  DB 4;  Length 333;
  Best Local Similarity   66.7%;  Pred. No. 69;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 HAPPGSPGT 127


RESULT  27
Q9D2V9
ID   Q9D2V9       PRELIMINARY;      PRT;   387 AA.
AC   Q9D2V9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   0610009M14RIK PROTEIN.
GN   0610009M14RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK018735; BAB31377.1; -.
DR   HSSP; P80220; 1DIP.
DR   MGD; MGI:1926079; 0610009M14Rik.
DR   InterPro; IPR000580; TSC-22_Dip_Bun.
DR   Pfam; PF01166; TSC22; 1.
DR   ProDom; PD007152; TSC-22_Dip_Bun; 1.
DR   PROSITE; PS01289; TSC22; 1.
SQ   SEQUENCE   387 AA;  39978 MW;  D4160FA3AB2DFB90 CRC64;


  Query Match             74.0%;  Score 37;  DB 11;  Length 387;
  Best Local Similarity   75.0%;  Pred. No. 81;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           |  |||||
Db      19 YEGPGSPG 26


RESULT  28
Q99PD5
ID   Q99PD5       PRELIMINARY;      PRT;   387 AA.
AC   Q99PD5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   LEUCINE ZIPPER PROTEIN THG-1PIT.
GN   0610009M14RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Fiorenza M.T., Mukhopdhyay M., Westphal H.;
RT   "Thg-1pit, a putative Lhx3 target gene.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF315352; AAK02018.1; -.
DR   HSSP; P80220; 1DIP.
DR   MGD; MGI:1926079; 0610009M14Rik.
DR   InterPro; IPR000580; TSC-22_Dip_Bun.
DR   Pfam; PF01166; TSC22; 1.
DR   ProDom; PD007152; TSC-22_Dip_Bun; 1.
DR   PROSITE; PS01289; TSC22; 1.
SQ   SEQUENCE   387 AA;  39908 MW;  D047B988643CE237 CRC64;


  Query Match             74.0%;  Score 37;  DB 11;  Length 387;
  Best Local Similarity   75.0%;  Pred. No. 81;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPG 8
           |  |||||
Db      19 YEGPGSPG 26


RESULT  29
Q99147
ID   Q99147       PRELIMINARY;      PRT;   393 AA.
AC   Q99147;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
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DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TITIN (FRAGMENT).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NEW ZEALAND WHITE; TISSUE=HEART;
RX   MEDLINE=91305130; PubMed=1712941;
RA   Fritz J.D., Greaser M.L., Wolff J.;
RT   "A novel 3' Extension Technique using Random Primers in RNA-PCR.";
RL   Nucleic Acids Res. 19:3747-3747(1991).
DR   EMBL; X59596; CAA42165.1; -.
DR   InterPro; IPR003962; FnIII_repeat.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00041; fn3; 2.
DR   PRINTS; PR00014; FNTYPEIII.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00410; IG_like; 1.
KW   Repeat.
FT   NON_TER       1      1
FT   NON_TER     393    393
SQ   SEQUENCE   393 AA;  43475 MW;  0672492F4091CBE7 CRC64;
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  Query Match             74.0%;  Score 37;  DB 6;  Length 393;
  Best Local Similarity   66.7%;  Pred. No. 83;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            |  || |||
Db      55 YKEPGPPGT 63
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RESULT  30
Q14631
ID   Q14631      PRELIMINARY;      PRT;   396 AA.
AC   Q14631;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-5 RECEPTOR  TYPE 2 PRECURSOR.
GN   HSIL5R2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL BLOOD;
RX   MEDLINE=92121815; PubMed=1732409;
RA   Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT   "Molecular cloning and expression of the human interleukin 5
RT   receptor.";
RL   J. Exp. Med. 175:341-351(1992).
DR   EMBL; X61177; CAA43484.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003532; Hematopo_receptor_S_F2.
DR   PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW   Signal; Receptor.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    396       INTERLEUKIN-5 RECEPTOR  TYPE 2.
SQ   SEQUENCE   396 AA;  44998 MW;  1AB60619842ACDA5 CRC64;
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  Query Match             74.0%;  Score 37;  DB 4;  Length 396;
  Best Local Similarity   66.7%;  Pred. No. 83;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
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            :: ||||||
Db     119 HAPPGSPGT 127
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RESULT  31
O74658
ID   O74658      PRELIMINARY;      PRT;   406 AA.
AC   O74658;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AGGLUTININ-LIKE PROTEIN (FRAGMENT).
GN   ALS2.
OS   Candida albicans (Yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=5476;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1161;
RX   MEDLINE=98440424; PubMed=9765564;
RA   Hoyer L.L., Payne T.L., Hecht J.E.;
RT   "Identification of Candida albicans ALS2 and ALS4 and localization of
RT   als proteins to the fungal cell surface.";
RL   J. Bacteriol. 180:5334-5343(1998).
DR   EMBL; AF024581; AAC64236.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   406 AA;  40585 MW;  9A6C92C1B2A93A81 CRC64;
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  Query Match             74.0%;  Score 37;  DB 3;  Length 406;
  Best Local Similarity   75.0%;  Pred. No. 86;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            |:||:|||
Db     189 SNPGAPGT 196
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RESULT  32
Q9URP9
ID   Q9URP9      PRELIMINARY;      PRT;   406 AA.
AC   Q9URP9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   AGGLUTININ-LIKE PROTEIN (FRAGMENT).
GN   ALS4.
OS   Candida albicans (Yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=5476;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1161;
RX   MEDLINE=98440424; PubMed=9765564;
RA   Hoyer L.L., Payne T.L., Hecht J.E.;
RT   "Identification of Candida albicans ALS2 and ALS4 and localization of
RT   als proteins to the fungal cell surface.";
RL   J. Bacteriol. 180:5334-5343(1998).
DR   EMBL; AF024585; AAC64240.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   406 AA;  40592 MW;  E0117B4CE4ECB4C3 CRC64;
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```
  Query Match             74.0%;  Score 37;  DB 3;  Length 406;
  Best Local Similarity   75.0%;  Pred. No. 86;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            |:||:|||
Db     189 SNPGAPGT 196
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RESULT  33
O74661
ID   O74661      PRELIMINARY;      PRT;   407 AA.
AC   O74661;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AGGLUTININ-LIKE PROTEIN (FRAGMENT).
GN   ALS4.
OS   Candida albicans (Yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=5476;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1161;
RX   MEDLINE=98440424; PubMed=9765564;
RA   Hoyer L.L., Payne T.L., Hecht J.E.;
RT   "Identification of Candida albicans ALS2 and ALS4 and localization of
RT   als proteins to the fungal cell surface.";
RL   J. Bacteriol. 180:5334-5343(1998).
DR   EMBL; AF024587; AAC64242.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   407 AA;  40649 MW;  FC846B7A1640CF44 CRC64;

  Query Match           74.0%;  Score 37;  DB 3;  Length 407;
  Best Local Similarity  75.0%;  Pred. No. 86;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
          |:||:|||
Db     189 SNPGAPGT 196


RESULT  34
Q14633
ID   Q14633      PRELIMINARY;      PRT;   420 AA.
AC   Q14633;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-5 RECEPTOR  PRECURSOR.
GN   HSIL5R.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL BLOOD;
RX   MEDLINE=92121815; PubMed=1732409;
RA   Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT   "Molecular cloning and expression of the human interleukin 5
RT   receptor.";
RL   J. Exp. Med. 175:341-351(1992).
DR   EMBL; X61176; CAA43483.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003532; Hematopo_receptor_S_F2.
DR   PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW   Signal; Receptor.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    420       INTERLEUKIN-5 RECEPTOR.
SQ   SEQUENCE   420 AA;  47670 MW;  8DC56DFC8BEFF524 CRC64;

  Query Match           74.0%;  Score 37;  DB 4;  Length 420;
  Best Local Similarity  66.7%;  Pred. No. 89;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 HAPPGSPGT 127


RESULT  35
O95196
ID   O95196      PRELIMINARY;      PRT;   539 AA.
AC   O95196;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   NEUROGLYCAN C.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=99133557; PubMed=9950058;
RA   Yasuda Y., Tokita Y., Aono S., Matsui F., Ono T., Sonta S.,
RA   Watanabe E., Nakanishi Y., Oohira A.;
RT   "Cloning and chromosomal mapping of the human gene of neuroglycan C
RT   (NGC), a neural transmembrane chondroitin sulfate proteoglycan with an
RT   EGF module.";
RL   Neurosci. Res. 32:313-322(1998).
DR   EMBL; AF059274; AAC69612.1; -.
DR   InterPro; IPR000561; EGF-like.
DR   SMART; SM00181; EGF; 1.
SQ   SEQUENCE   539 AA;  57024 MW;  5B22E9E8DE34290E CRC64;

  Query Match           74.0%;  Score 37;  DB 4;  Length 539;
  Best Local Similarity  87.5%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           | ||||||
Db     227 SFPGSPGT 234


RESULT  36
Q9QY32
ID   Q9QY32      PRELIMINARY;      PRT;   539 AA.
AC   Q9QY32;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   NEUROGLYCAN C.
GN   CSPG5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BLACK/6; TISSUE=BRAIN;
RX   MEDLINE=20085050; PubMed=10617623;
RA   Aono S., Keino H., Ono T., Yasuda Y., Tokita Y., Matsui F.,
RA   Taniguchi M., Sonta S.-I., Oohira A.;
RT   "Genomic Organization and Expression Pattern of Mouse Neuroglycan C in
RT   the Cerebellar Development.";
RL   J. Biol. Chem. 275:337-342(2000).
DR   EMBL; AF133700; AAF23362.1; -.
DR   MGD; MGI:1352747; Cspg5.
DR   InterPro; IPR000561; EGF-like.
DR   SMART; SM00181; EGF; 1.
SQ   SEQUENCE   539 AA;  57352 MW;  7D566881555460ED CRC64;

  Query Match           74.0%;  Score 37;  DB 11;  Length 539;
  Best Local Similarity  87.5%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       2 SSPGSPGT 9
            | ||||||
Db     228 SFPGSPGT 235


RESULT  37
Q01106
ID   Q01106      PRELIMINARY;      PRT;   541 AA.
AC   Q01106;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TITIN (FRAGMENT).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART MUSCLE;
RX   MEDLINE=92258380; PubMed=1582406;
RA   Labeit S., Gautel M., Lakey A., Trinick J.;
RT   "Towards a molecular understanding of titin.";
RL   EMBO J. 11:1711-1716(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART MUSCLE;
RA   Fritz J.D., Greaser M.L., Wolff J.;
RT   "A novel 3' extension method using random primers.";
RL   Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; M98338; AAA31480.1; -.
DR   InterPro; IPR003962; FnIII_repeat.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00041; fn3; 4.
DR   PRINTS; PR00014; FNTYPEIII.
DR   SMART; SM00060; FN3; 4.
DR   SMART; SM00409; IG; 1.
KW   Repeat.
FT   NON_TER       1      1
SQ   SEQUENCE   541 AA;  60088 MW;  0DAA2541E1318B99 CRC64;


  Query Match             74.0%;  Score 37;  DB 6;  Length 541;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            |  || |||
Db      55 YKEPGPPGT 63


RESULT  38
Q9D677
ID   Q9D677      PRELIMINARY;      PRT;   723 AA.
AC   Q9D677;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   4632412M04RIK PROTEIN.
GN   4632412M04RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=SKIN;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
DR   EMBL; AK014569; BAB29434.1; -.
DR   HSSP; P49799; 1AGR.
DR   MGD; MGI:1924302; 4632412M04Rik.
DR   InterPro; IPR003109; GoLoco.
DR   InterPro; IPR003116; RBD.
DR   InterPro; IPR000342; RGS.
DR   Pfam; PF02188; GoLoco; 1.
DR   Pfam; PF02196; RBD; 2.
DR   Pfam; PF00615; RGS; 1.
DR   PRINTS; PR01301; RGSPROTEIN.
DR   ProDom; PD001580; RGS; 1.
DR   SMART; SM00390; GoLoco; 1.
DR   SMART; SM00455; RBD; 2.
DR   SMART; SM00315; RGS; 1.
DR   PROSITE; PS50132; RGS; 1.
SQ   SEQUENCE   723 AA;  78539 MW;  EBCBFD7D5A56BF51 CRC64;


  Query Match             74.0%;  Score 37;  DB 11;  Length 723;
  Best Local Similarity   66.7%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            :|:|| |||
Db     632 HSTPGPPGT 640


RESULT  39
O75112
ID   O75112      PRELIMINARY;      PRT;   734 AA.
AC   O75112;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   KIAA0613 PROTEIN (FRAGMENT).
GN   KIAA0613.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=98403880; PubMed=9734811;
RA   Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA   Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. X.
RT   The complete sequences of 100 new cDNA clones from brain which can
RT   code for large proteins in vitro.";
RL   DNA Res. 5:169-176(1998).
CC   -!- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC       IONS.
DR   EMBL; AB014513; BAA31588.1; -.
DR   HSSP; Q05158; 1QLI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001781; LIM.
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DR   InterPro; IPR001478; PDZ.
DR   InterPro; IPR002965; P_rich_extensn.
DR   Pfam; PF00412; LIM; 3.
DR   Pfam; PF00595; PDZ; 1.
DR   PRINTS; PR01217; PRICHEXTENSN.
DR   ProDom; PD000094; LIM; 3.
DR   SMART; SM00132; LIM; 3.
DR   SMART; SM00228; PDZ; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR   PROSITE; PS50023; LIM_DOMAIN_2; 3.
DR   PROSITE; PS50106; PDZ; 1.
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AC   Q9CW54;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
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DR   MGD; MGI:1918979; 1200016K18Rik.
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Job time: 341 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 21, 2002, 11:18:35 ; Search time 21.42 Seconds
(without alignments)
10.263 Million cell updates/sec

Title: US-09-734-281-2
Perfect score: 50
Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	50	100.0	9	4	US-08-617-987A-2	Sequence 2, Appli
3	50	100.0	27	2	US-08-244-951A-5	Sequence 5, Appli
4	50	100.0	31	2	US-08-244-951A-4	Sequence 4, Appli
5	50	100.0	34	2	US-08-602-264A-10	Sequence 10, Appl
6	50	100.0	34	3	US-08-461-018A-10	Sequence 10, Appl
7	50	100.0	34	4	US-09-216-958-10	Sequence 10, Appl
8	50	100.0	67	2	US-08-244-951A-1	Sequence 1, Appli
9	50	100.0	67	2	US-08-389-011-1	Sequence 1, Appli
10	50	100.0	67	3	US-08-403-917A-1	Sequence 1, Appli
11	50	100.0	67	4	US-09-348-952A-1	Sequence 1, Appli
12	50	100.0	106	3	US-08-776-404B-1	Sequence 1, Appli
13	50	100.0	112	3	US-08-666-360-1	Sequence 1, Appli
14	50	100.0	351	1	US-08-159-969-2	Sequence 2, Appli
15	50	100.0	352	2	US-08-726-306A-17	Sequence 17, Appl
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17	50	100.0	391	2	US-08-389-011-23	Sequence 23, Appl
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23	39	78.0	23	2	US-08-244-951A-3	Sequence 3, Appli
24	39	78.0	33	2	US-08-244-951A-2	Sequence 2, Appli
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47	36	72.0	62	1	US-08-397-633A-43	Sequence 43, Appl
48	36	72.0	63	1	US-08-642-255-121	Sequence 121, App
49	36	72.0	63	1	US-08-397-633A-32	Sequence 32, Appl
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52	36	72.0	71	1	US-08-642-255-108	Sequence 108, App
53	36	72.0	71	1	US-08-642-255-115	Sequence 115, App
54	36	72.0	71	1	US-08-397-633A-21	Sequence 21, Appl
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ALIGNMENTS

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RESULT 1
US-08-617-987A-1
; Sequence 1, Application US/08617987A
; Patent No. 6238892
; GENERAL INFORMATION:
;  APPLICANT:  MERCKEN, MARC
;  APPLICANT:  MANDELKOW, EVA-MARIA
;  APPLICANT:  VANDERMEEREN, MARC
;  APPLICANT:  VANMECHELEN, EUGEEN
;  APPLICANT:  VAN DE VOORDE, ANDRE
;  TITLE OF INVENTION:  MONOCLONAL ANTIBODIES DIRECTED AGAINST THE
;  TITLE OF INVENTION:  MICROTUBULE-ASSOCIATED PROTEIN TAU
;  FILE REFERENCE:  12546.4USF1
;  CURRENT APPLICATION NUMBER: US/08/617,987A
;  CURRENT FILING DATE:  1996-03-15
;  PRIOR APPLICATION NUMBER:  08/108,758
;  PRIOR FILING DATE:  1993-09-02
;  PRIOR APPLICATION NUMBER:  91402871.7
;  PRIOR FILING DATE:  1991-10-25
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US-08-617-987A-1


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Db      1 YSSPGSPGT 9


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; GENERAL INFORMATION:
;  APPLICANT:  MERCKEN, MARC
;  APPLICANT:  MANDELKOW, EVA-MARIA
;  APPLICANT:  VANDERMEEREN, MARC
;  APPLICANT:  VANMECHELEN, EUGEEN
;  APPLICANT:  VAN DE VOORDE, ANDRE
;  TITLE OF INVENTION:  MONOCLONAL ANTIBODIES DIRECTED AGAINST THE
;  TITLE OF INVENTION:  MICROTUBULE-ASSOCIATED PROTEIN TAU
;  FILE REFERENCE:  12546.4USF1
;  CURRENT APPLICATION NUMBER: US/08/617,987A
;  CURRENT FILING DATE:  1996-03-15
;  PRIOR APPLICATION NUMBER:  08/108,758
;  PRIOR FILING DATE:  1993-09-02
;  PRIOR APPLICATION NUMBER:  91402871.7
;  PRIOR FILING DATE:  1991-10-25
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US-08-617-987A-2


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;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
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;      FILING DATE:  19-JAN-1995
;      CLASSIFICATION:  435
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;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27
;      TYPE:  Amino Acid
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;      TOPOLOGY:  Unknown
US-08-244-951A-5


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Db      5 YSSPGSPGT 13


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;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
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;      FILING DATE:  19-JAN-1995
;      CLASSIFICATION:  435
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;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
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;       TELEFAX:  (212) 661-8002
;     INFORMATION FOR SEQ ID NO:  4:
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; Patent No. 5837853
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;    APPLICANT:  Akihiko TAKASHIMA et al.
;    TITLE OF INVENTION:  PREVENTIVE OR THERAPEUTIC AGENTS FOR
;    TITLE OF INVENTION:  ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
;    TITLE OF INVENTION:  tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WENDEROTH, LIND & PONACK
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      COUNTRY:  D.C.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch,
;      MEDIUM TYPE:  144 mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
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;      APPLICATION NUMBER:  US/08/602,264A
;      FILING DATE:  February 20, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/204,091
;      FILING DATE:  March 2, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-602-264A-10


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Db       7 YSSPGSPGT 15


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; Patent No. 6071694
;  GENERAL INFORMATION:
;    APPLICANT:  Akihiko TAKASHIMA et al.
;    TITLE OF INVENTION:  SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
;    TITLE OF INVENTION:  ALZHEIMER'S DISEASE (AS AMENDED)
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WENDEROTH, LIND & PONACK
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      COUNTRY:  D.C.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  1.44 mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
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;      FILING DATE:  June 5, 1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/204,091
;      FILING DATE:  March 2, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-461-018A-10


  Query Match             100.0%;  Score 50;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db       7 YSSPGSPGT 15


RESULT   7
US-09-216-958-10
; Sequence 10, Application US/09216958
; Patent No. 6248559
;  GENERAL INFORMATION:
;    APPLICANT:  Akihiko TAKASHIMA et al.
;    TITLE OF INVENTION:  SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
;    TITLE OF INVENTION:  ALZHEIMER'S DISEASE (AS AMENDED)
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WENDEROTH, LIND & PONACK
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      COUNTRY:  D.C.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,958
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,018
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-216-958-10

Query Match 100.0%; Score 50; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 7 YSSPGSPGT 15

RESULT 8
US-08-244-951A-1
; Sequence 1, Application US/08244951A
; Patent No. 5843779
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,951A
; FILING DATE: 19-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; FEATURE:
; NAME/KEY: human tau protein 155-211
US-08-244-951A-1

Query Match 100.0%; Score 50; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
|||||||||
Db 43 YSSPGSPGT 51

RESULT 9
US-08-389-011-1
; Sequence 1, Application US/08389011
; Patent No. 5861257
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,011
; FILING DATE: 15-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,917
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,916
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: linear
US-08-389-011-1

Query Match 100.0%; Score 50; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||||||||| |
Db 43 YSSPGSPGT 51

RESULT 10
US-08-403-917A-1
; Sequence 1, Application US/08403917A
; Patent No. 6010913
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEEN;
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,917A
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
US-08-403-917A-1

Query Match 100.0%; Score 50; DB 3; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||||||||| |
Db 43 YSSPGSPGT 51

RESULT 11
US-09-348-952A-1
; Sequence 1, Application US/09348952A
; Patent No. 6232437
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEEN;
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/348,952A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,917
; FILING DATE: 19-JAN-1995
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown

US-09-348-952A-1

Query Match 100.0%; Score 50; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||||||||||
Db 43 YSSPGSPGT 51

RESULT 12
US-08-776-404B-1
; Sequence 1, Application US/08776404B
; Patent No. 6121003
; GENERAL INFORMATION:
; APPLICANT: VANMECHELEN, EUGEEN
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR AN EPITOPE OF
; TITLE OF INVENTION: A PARTICULAR SUBCLASS OR FORM OF PHOSPHORYLATED TAU,
; TITLE OF INVENTION: HYBRIDOMAS SECRETING THEM, ANTIGEN RECOGNITION OF THESE
; TITLE OF INVENTION: ANTIBODIES AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,404B
; FILING DATE: 27 Jan 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03032
; FILING DATE: 31 Jul 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870131.3
; FILING DATE: 29 Jul 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:003
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-776-404B-1

Query Match 100.0%; Score 50; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||||||||||
Db 52 YSSPGSPGT 60

RESULT 13
US-08-666-360-1
; Sequence 1, Application US/08666360
; Patent No. 6008024
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Monoclonal antibodies specific for PHF-tau,
; TITLE OF INVENTION: hybridomas secreting them, antigen recognition of these
; TITLE OF INVENTION: antibodies and their applications
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,360
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-666-360-1

Query Match 100.0%; Score 50; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||||||||||
Db 55 YSSPGSPGT 63

RESULT 14
US-08-159-969-2
; Sequence 2, Application US/08159969
; Patent No. 5492812
; GENERAL INFORMATION:
; APPLICANT: Voorheis, Paul H.
; TITLE OF INVENTION: Diagnostic Method for Alzheimer's
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,969
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/738,778
; FILING DATE: 01-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S.Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 4697-040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```
;    MOLECULE TYPE:  protein
US-08-159-969-2


  Query Match             100.0%;  Score 50;  DB 1;  Length 351;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     139 YSSPGSPGT 147


RESULT  15
US-08-726-306A-17
; Sequence 17, Application US/08726306A
; Patent No. 5958684
;  GENERAL INFORMATION:
;    APPLICANT:  van Leeuwen, Frederik Willem
;    APPLICANT:  Burbach, Johannes Peter Henri
;    APPLICANT:  Grosveld, Franklin G.
;    TITLE OF INVENTION:  DIAGNOSIS METHOD AND REAGENTS
;    NUMBER OF SEQUENCES:  189
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  1 Financial Center
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/726,306A
;      FILING DATE:  02-Oct-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 95/20080.4
;      FILING DATE:  02-Oct-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/009,832
;      FILING DATE:  01-Jan-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  96,048-A (3255/00784)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-726-306A-17


  Query Match             100.0%;  Score 50;  DB 2;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     139 YSSPGSPGT 147


RESULT  16
US-08-244-951A-10
; Sequence 10, Application US/08244951A
; Patent No. 5843779
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,951A
;      FILING DATE:  19-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  391
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
;    FEATURE:
;      NAME/KEY:  mTHFMPH-taul fusion protein
US-08-244-951A-10


  Query Match             100.0%;  Score 50;  DB 2;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     178 YSSPGSPGT 186


RESULT  17
US-08-389-011-23
; Sequence 23, Application US/08389011
; Patent No. 5861257
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
```

; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,011
; FILING DATE: 15-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,917
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,916
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
US-08-389-011-23

Query Match 100.0%; Score 50; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||||||||| |
Db 178 YSSPGSPGT 186

RESULT 18
US-08-403-917A-23
; Sequence 23, Application US/08403917A
; Patent No. 6010913
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEEN;
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,917A
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
US-08-403-917A-23

Query Match 100.0%; Score 50; DB 3; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||||||||| |
Db 178 YSSPGSPGT 186

RESULT 19
US-09-348-952A-23
; Sequence 23, Application US/09348952A
; Patent No. 6232437
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEEN;
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/348,952A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/403,917
;      FILING DATE:  19-JAN-1995
;      APPLICATION NUMBER:  08/256,167
;      FILING DATE:  27-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/244,951
;      FILING DATE:  13-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  391
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
US-09-348-952A-23


  Query Match             100.0%;  Score 50;  DB 4;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     178 YSSPGSPGT 186


RESULT  20
US-08-244-603A-1
; Sequence 1, Application US/08244603A
; Patent No. 6200768
;  GENERAL INFORMATION:
;    APPLICANT:  Mandelkow, Eva-Maria
;    APPLICANT:  Mandelkow, Eckhard
;    APPLICANT:  Lichtenberg-Kraag, Birgit
;    APPLICANT:  Biernat, Jacek
;    APPLICANT:  Drewes, Gerard
;    APPLICANT:  Steiner, Barbara
;    TITLE OF INVENTION:  No. 6200768el Tools For The Diagnosis And
;    TITLE OF INVENTION:  Treatment Of Alzheimer's Disease
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  233 South Waker Drive, 6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Tape
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,603A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph A. Williams, Jr.
;      REGISTRATION NUMBER:  38,659
;      REFERENCE/DOCKET NUMBER:  28384/32778
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;      TELEFAX:  312-484-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  441 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-244-603A-1


  Query Match             100.0%;  Score 50;  DB 4;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     197 YSSPGSPGT 205


RESULT  21
US-09-159-106-2
; Sequence 2, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
;  APPLICANT: Ferrer, Pau
;  APPLICANT: Diers, Ivan
;  APPLICANT: Halkier, Torben
;  APPLICANT: Hedegaard, Lisbeth
;  TITLE OF INVENTION: An Enzyme With  -1,3-Glucanase
;  TITLE OF INVENTION: Activity
;  FILE REFERENCE: 4693.204-US
;  CURRENT APPLICATION NUMBER: US/09/159,106
;  CURRENT FILING DATE: 1998-09-23
;  EARLIER APPLICATION NUMBER: 0427/96
;  EARLIER FILING DATE: 1996-12-04
;  EARLIER APPLICATION NUMBER: 0885/96
;  EARLIER FILING DATE: 1996-08-23
;  EARLIER APPLICATION NUMBER: PCT/DK97/00160
;  EARLIER FILING DATE: 1997-04-14
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 263
;   TYPE: PRT
;   ORGANISM: Oerskovia xanthineolytica
US-09-159-106-2


  Query Match             80.0%;  Score 40;  DB 4;  Length 263;
  Best Local Similarity   87.5%;  Pred. No. 33;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||:|||
Db     244 SSPGNPGT 251


RESULT  22
US-09-159-106-11
; Sequence 11, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
;  APPLICANT: Ferrer, Pau
;  APPLICANT: Diers, Ivan
```

```
;  APPLICANT: Halkier, Torben
;  APPLICANT: Hedegaard, Lisbeth
;  TITLE OF INVENTION: An Enzyme With  -1,3-Glucanase
;  TITLE OF INVENTION: Activity
;  FILE REFERENCE: 4693.204-US
;  CURRENT APPLICATION NUMBER: US/09/159,106
;  CURRENT FILING DATE: 1998-09-23
;  EARLIER APPLICATION NUMBER: 0427/96
;  EARLIER FILING DATE: 1996-12-04
;  EARLIER APPLICATION NUMBER: 0885/96
;  EARLIER FILING DATE: 1996-08-23
;  EARLIER APPLICATION NUMBER: PCT/DK97/00160
;  EARLIER FILING DATE: 1997-04-14
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;    LENGTH: 435
;    TYPE: PRT
;    ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11


  Query Match             80.0%;  Score 40;  DB 4;  Length 435;
  Best Local Similarity   87.5%;  Pred. No. 56;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            ||||:|||
Db     297 SSPGNPGT 304


RESULT  23
US-08-244-951A-3
; Sequence 3, Application US/08244951A
; Patent No. 5843779
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,951A
;      FILING DATE:  19-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
;    FEATURE:
;      NAME/KEY:  human tau protein 199-221
US-08-244-951A-3


  Query Match             78.0%;  Score 39;  DB 2;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
            |||||||
Db       1 SPGSPGT 7


RESULT  24
US-08-244-951A-2
; Sequence 2, Application US/08244951A
; Patent No. 5843779
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,951A
;      FILING DATE:  19-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
;    FEATURE:
;      NAME/KEY:  human tau protein 199-231
US-08-244-951A-2
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  Query Match           78.0%;  Score 39;  DB 2;  Length 33;
  Best Local Similarity 100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db       1 SPGSPGT 7


RESULT  25
US-08-389-011-2
; Sequence 2, Application US/08389011
; Patent No. 5861257
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/389,011
;      FILING DATE:  15-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/403,917
;      FILING DATE:  19-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/403,916
;      FILING DATE:  19-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/244,951
;      FILING DATE:  13-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003-1-CON
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
US-08-389-011-2


  Query Match           78.0%;  Score 39;  DB 2;  Length 33;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db       1 SPGSPGT 7


RESULT  26
US-08-403-917A-2
; Sequence 2, Application US/08403917A
; Patent No. 6010913
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN;
;    APPLICANT:  VAN'DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATION
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,917A
;      FILING DATE:  19-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/256,167
;      FILING DATE:  27-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/244,951
;      FILING DATE:  13-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
US-08-403-917A-2


  Query Match           78.0%;  Score 39;  DB 3;  Length 33;
  Best Local Similarity 100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db       1 SPGSPGT 7


RESULT  27
US-09-348-952A-2
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; Sequence 2, Application US/09348952A
; Patent No. 6232437
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN;
;    APPLICANT:  VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATION
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/348,952A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/403,917
;      FILING DATE:  19-JAN-1995
;      APPLICATION NUMBER:  08/256,167
;      FILING DATE:  27-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/244,951
;      FILING DATE:  13-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
US-09-348-952A-2


  Query Match             78.0%;  Score 39;  DB 4;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db       1 SPGSPGT 7


RESULT  28
US-08-244-951A-6
; Sequence 6, Application US/08244951A
; Patent No. 5843779
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,951A
;      FILING DATE:  19-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
US-08-244-951A-6


  Query Match             78.0%;  Score 39;  DB 2;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 6.1;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db       3 SPGSPGT 9


RESULT  29
US-08-836-561-106
; Sequence 106, Application US/08836561
; Patent No. 6018032
;  GENERAL INFORMATION:
;    APPLICANT:  KOIKE, Masamichi
;    APPLICANT:  FURUYA, Akiko
;    APPLICANT:  NAKAMURA, Kazuyasu
;    APPLICANT:  IIDA, Akihiro
;    APPLICANT:  ANAZAWA, Hideharu
;    APPLICANT:  HANAI, No. 6018032uo
;    APPLICANT:  TAKATSU, Kiyoshi
;    TITLE OF INVENTION:  Antibody Against Human Interleukin-5
;    TITLE OF INVENTION:  Receptor Alpha Chain
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
```

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;       COUNTRY:  USA
;       ZIP:  10036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/836,561
;       FILING DATE:  09-MAY-1997
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 232384/95
;       FILING DATE:  11-SEP-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lawrence, III, Stanton T
;       REGISTRATION NUMBER:  25,736
;       REFERENCE/DOCKET NUMBER:  7005-115-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-790-9090
;       TELEFAX:  212-869-9741
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  106:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  313 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-836-561-106


  Query Match             74.0%;  Score 37;  DB 3;  Length 313;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db      99 HAPPGSPGT 107


RESULT  30
US-07-947-130-2
; Sequence 2, Application US/07947130
; Patent No. 5455337
;  GENERAL INFORMATION:
;    APPLICANT:  Devos, Rene
;    APPLICANT:  Fiers, Walter
;    APPLICANT:  Tavernier, Jan
;    TITLE OF INVENTION:  Chimeric Interleukin-5
;    TITLE OF INVENTION:  Receptor/Immunoglobulin Polypeptides
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mr. George M. Gould, Esq.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/947,130
;      FILING DATE:  19920916
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 91810738.4
;      FILING DATE:  18-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Malaska, Stephen L.
;      REGISTRATION NUMBER:  32,655
;      REFERENCE/DOCKET NUMBER:  4105/144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-235-6326
;      TELEFAX:  201-235-3500
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  leukemia
;      CELL TYPE:  Promyelocytes
;      CELL LINE:  HL-60
;    IMMEDIATE SOURCE:
;      LIBRARY:  human HL-60
;      CLONE:  lambda gt11-hIL5Ralpha12
US-07-947-130-2


  Query Match             74.0%;  Score 37;  DB 1;  Length 335;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 HAPPGSPGT 127


RESULT  31
US-08-421-822-2
; Sequence 2, Application US/08421822
; Patent No. 5668256
;  GENERAL INFORMATION:
;    APPLICANT:  Devos, Rene
;    APPLICANT:  Fiers, Walter
;    APPLICANT:  Tavernier, Jan
;    TITLE OF INVENTION:  Chimeric Interleukin-5
;    TITLE OF INVENTION:  Receptor/Immunoglobulin Polypeptides
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mr. George M. Gould, Esq.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/421,822
;      FILING DATE:  13-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/947,130
;      FILING DATE:  16-SEP-1992
;      APPLICATION NUMBER:  EP 91810738.4
;      FILING DATE:  18-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Malaska, Stephen L.
;      REGISTRATION NUMBER:  32,655
;      REFERENCE/DOCKET NUMBER:  4105/144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-235-6326
;      TELEFAX:  201-235-3500
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;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  leukemia
;      CELL TYPE:  Promyelocytes
;      CELL LINE:  HL-60
;     IMMEDIATE SOURCE:
;      LIBRARY:  human HL-60
;      CLONE:  lambda gt11-hIL5Ralpha12
;
US-08-421-822-2

  Query Match             74.0%;  Score 37;  DB 1;  Length 335;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            :: ||||||
Db     119 HAPPGSPGT 127


RESULT  32
US-08-421-823-2
; Sequence 2, Application US/08421823
; Patent No. 5712121
;  GENERAL INFORMATION:
;    APPLICANT:  Devos, Rene
;    APPLICANT:  Fiers, Walter
;    APPLICANT:  Tavernier, Jan
;    TITLE OF INVENTION:  Chimeric Interleukin-5
;    TITLE OF INVENTION:  Receptor/Immunoglobulin Polypeptides
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mr. George M. Gould, Esq.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/421,823
;      FILING DATE:  13-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/947,130
;      FILING DATE:  16-SEP-1992
;      APPLICATION NUMBER:  EP 91810738.4
;      FILING DATE:  18-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Malaska, Stephen L.
;      REGISTRATION NUMBER:  32,655
;      REFERENCE/DOCKET NUMBER:  4105/144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-235-6326
;      TELEFAX:  201-235-3500
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  leukemia
;      CELL TYPE:  Promyelocytes
;      CELL LINE:  HL-60
;     IMMEDIATE SOURCE:
;      LIBRARY:  human HL-60
;      CLONE:  lambda gt11-hIL5Ralpha12
US-08-421-823-2

  Query Match             74.0%;  Score 37;  DB 1;  Length 335;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            :: ||||||
Db     119 HAPPGSPGT 127


RESULT  33
US-07-757-390-14
; Sequence 14, Application US/07757390
; Patent No. 5453491
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/757,390
;      FILING DATE:  19910910
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  396 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-757-390-14

  Query Match             74.0%;  Score 37;  DB 1;  Length 396;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy      1 YSSPGSPGT 9
          :: ||||||
Db    119 HAPPGSPGT 127


RESULT  34
US-08-442-282-14
; Sequence 14, Application US/08442282
; Patent No. 5760204
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,282
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/757,390
;      FILING DATE:  10-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  396 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-442-282-14


  Query Match           74.0%;  Score 37;  DB 1;  Length 396;
  Best Local Similarity  66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          :: ||||||
Db    119 HAPPGSPGT 127


RESULT  35
US-08-442-281-14
; Sequence 14, Application US/08442281
; Patent No. 5807991
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,281
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/757,390
;      FILING DATE:  10-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  396 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-442-281-14


  Query Match           74.0%;  Score 37;  DB 1;  Length 396;
  Best Local Similarity  66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          :: ||||||
Db    119 HAPPGSPGT 127


RESULT  36
US-08-939-727-14
; Sequence 14, Application US/08939727
; Patent No. 5916767
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/939,727
;      FILING DATE:
;      CLASSIFICATION:
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/757,390
;      FILING DATE:  10-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  396 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-939-727-14


  Query Match             74.0%;  Score 37;  DB 2;  Length 396;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 HAPPGSPGT 127


RESULT  37
US-07-757-390-13
; Sequence 13, Application US/07757390
; Patent No. 5453491
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/757,390
;      FILING DATE:  19910910
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  420 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-757-390-13


  Query Match             74.0%;  Score 37;  DB 1;  Length 420;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 HAPPGSPGT 127


RESULT  38
US-08-442-282-13
; Sequence 13, Application US/08442282
; Patent No. 5760204
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,282
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/757,390
;      FILING DATE:  10-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  420 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-442-282-13


  Query Match             74.0%;  Score 37;  DB 1;  Length 420;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
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Db     119 HAPPGSPGT 127


RESULT  39
US-08-442-281-13
; Sequence 13, Application US/08442281
; Patent No. 5807991
;  GENERAL INFORMATION:
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;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,281
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/757,390
;      FILING DATE:  10-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  420 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-442-281-13


  Query Match             74.0%;  Score 37;  DB 1;  Length 420;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
            :: ||||||
Db     119 HAPPGSPGT 127


RESULT  40
US-08-939-727-13
; Sequence 13, Application US/08939727
; Patent No. 5916767
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/939,727
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/757,390
;      FILING DATE:  10-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  420 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-939-727-13


  Query Match             74.0%;  Score 37;  DB 2;  Length 420;
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  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
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Db     119 HAPPGSPGT 127


Search completed: May 21, 2002, 11:18:36
Job time: 196 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 21, 2002, 11:15:20 ; Search time 21.42 Seconds
(without alignments)
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Title: US-09-734-281-1
Perfect score: 50
Sequence: 1 YSSPGSPGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	50	100.0	9	4	US-08-617-987A-2	Sequence 2, Appli
3	50	100.0	27	2	US-08-244-951A-5	Sequence 5, Appli
4	50	100.0	31	2	US-08-244-951A-4	Sequence 4, Appli
5	50	100.0	34	2	US-08-602-264A-10	Sequence 10, Appl
6	50	100.0	34	3	US-08-461-018A-10	Sequence 10, Appl
7	50	100.0	34	4	US-09-216-958-10	Sequence 10, Appl
8	50	100.0	67	2	US-08-244-951A-1	Sequence 1, Appli
9	50	100.0	67	2	US-08-389-011-1	Sequence 1, Appli
10	50	100.0	67	3	US-08-403-917A-1	Sequence 1, Appli
11	50	100.0	67	4	US-09-348-952A-1	Sequence 1, Appli
12	50	100.0	106	3	US-08-776-404B-1	Sequence 1, Appli
13	50	100.0	112	3	US-08-666-360-1	Sequence 1, Appli
14	50	100.0	351	1	US-08-159-969-2	Sequence 2, Appli
15	50	100.0	352	2	US-08-726-306A-17	Sequence 17, Appl
16	50	100.0	391	2	US-08-244-951A-10	Sequence 10, Appl
17	50	100.0	391	2	US-08-389-011-23	Sequence 23, Appl
18	50	100.0	391	3	US-08-403-917A-23	Sequence 23, Appl
19	50	100.0	391	4	US-09-348-952A-23	Sequence 23, Appl
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21	40	80.0	263	4	US-09-159-106-2	Sequence 2, Appli
22	40	80.0	435	4	US-09-159-106-11	Sequence 11, Appl
23	39	78.0	23	2	US-08-244-951A-3	Sequence 3, Appli
24	39	78.0	33	2	US-08-244-951A-2	Sequence 2, Appli
25	39	78.0	33	2	US-08-389-011-2	Sequence 2, Appli
26	39	78.0	33	3	US-08-403-917A-2	Sequence 2, Appli
27	39	78.0	33	4	US-09-348-952A-2	Sequence 2, Appli
28	39	78.0	35	2	US-08-244-951A-6	Sequence 6, Appli
29	37	74.0	313	3	US-08-836-561-106	Sequence 106, App
30	37	74.0	335	1	US-07-947-130-2	Sequence 2, Appli
31	37	74.0	335	1	US-08-421-822-2	Sequence 2, Appli
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33	37	74.0	396	1	US-07-757-390-14	Sequence 14, Appl
34	37	74.0	396	1	US-08-442-282-14	Sequence 14, Appl
35	37	74.0	396	1	US-08-442-281-14	Sequence 14, Appl
36	37	74.0	396	2	US-08-939-727-14	Sequence 14, Appl
37	37	74.0	420	1	US-07-757-390-13	Sequence 13, Appl
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39	37	74.0	420	1	US-08-442-281-13	Sequence 13, Appl
40	37	74.0	420	2	US-08-939-727-13	Sequence 13, Appl
41	36	72.0	61	1	US-08-175-155-67	Sequence 67, Appl
42	36	72.0	61	1	US-08-477-509B-102	Sequence 102, App
43	36	72.0	61	2	US-08-707-237A-74	Sequence 74, Appl
44	36	72.0	61	3	US-08-482-085B-102	Sequence 102, App
45	36	72.0	61	4	US-09-444-791A-102	Sequence 102, App
46	36	72.0	62	1	US-08-642-255-100	Sequence 100, App
47	36	72.0	62	1	US-08-397-633A-43	Sequence 43, Appl
48	36	72.0	63	1	US-08-642-255-121	Sequence 121, App
49	36	72.0	63	1	US-08-397-633A-32	Sequence 32, Appl
50	36	72.0	65	1	US-08-642-255-125	Sequence 125, App
51	36	72.0	65	1	US-08-397-633A-46	Sequence 46, Appl
52	36	72.0	71	1	US-08-642-255-108	Sequence 108, App
53	36	72.0	71	1	US-08-642-255-115	Sequence 115, App
54	36	72.0	71	1	US-08-397-633A-21	Sequence 21, Appl
55	36	72.0	71	1	US-08-397-633A-27	Sequence 27, Appl

ALIGNMENTS

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RESULT 1
US-08-617-987A-1
; Sequence 1, Application US/08617987A
; Patent No. 6238892
; GENERAL INFORMATION:
;  APPLICANT:  MERCKEN, MARC
;  APPLICANT:  MANDELKOW, EVA-MARIA
;  APPLICANT:  VANDERMEEREN, MARC
;  APPLICANT:  VANMECHELEN, EUGEEN
;  APPLICANT:  VAN DE VOORDE, ANDRE
;  TITLE OF INVENTION:  MONOCLONAL ANTIBODIES DIRECTED AGAINST THE
;  TITLE OF INVENTION:  MICROTUBULE-ASSOCIATED PROTEIN TAU
;  FILE REFERENCE:  12546.4USF1
;  CURRENT APPLICATION NUMBER: US/08/617,987A
;  CURRENT FILING DATE:  1996-03-15
;  PRIOR APPLICATION NUMBER:  08/108,758
;  PRIOR FILING DATE:  1993-09-02
;  PRIOR APPLICATION NUMBER:  91402871.7
;  PRIOR FILING DATE:  1991-10-25
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (3)
;   OTHER INFORMATION: No. 6238892e = "S is phosphorylated"
;   NAME/KEY: MOD_RES
;   LOCATION: (6)
;   OTHER INFORMATION: No. 6238892e = "S is phosphorylated"
US-08-617-987A-1


  Query Match             100.0%;  Score 50;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
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Db      1 YSSPGSPGT 9


RESULT   2
US-08-617-987A-2
; Sequence 2, Application US/08617987A
; Patent No. 6238892
; GENERAL INFORMATION:
;  APPLICANT:  MERCKEN, MARC
;  APPLICANT:  MANDELKOW, EVA-MARIA
;  APPLICANT:  VANDERMEEREN, MARC
;  APPLICANT:  VANMECHELEN, EUGEEN
;  APPLICANT:  VAN DE VOORDE, ANDRE
;  TITLE OF INVENTION:  MONOCLONAL ANTIBODIES DIRECTED AGAINST THE
;  TITLE OF INVENTION:  MICROTUBULE-ASSOCIATED PROTEIN TAU
;  FILE REFERENCE:  12546.4USF1
;  CURRENT APPLICATION NUMBER: US/08/617,987A
;  CURRENT FILING DATE:  1996-03-15
;  PRIOR APPLICATION NUMBER:  08/108,758
;  PRIOR FILING DATE:  1993-09-02
;  PRIOR APPLICATION NUMBER:  91402871.7
;  PRIOR FILING DATE:  1991-10-25
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (6)
;   OTHER INFORMATION: No. 6238892e = "S is phosphorylated"
US-08-617-987A-2


  Query Match             100.0%;  Score 50;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          |||||||||
Db      1 YSSPGSPGT 9


RESULT   3
US-08-244-951A-5
; Sequence 5, Application US/08244951A
; Patent No. 5843779
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,951A
;      FILING DATE:  19-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
US-08-244-951A-5


  Query Match             100.0%;  Score 50;  DB 2;  Length 27;
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  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
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Db      5 YSSPGSPGT 13


RESULT   4
US-08-244-951A-4
; Sequence 4, Application US/08244951A
; Patent No. 5843779
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,951A
;      FILING DATE:  19-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
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;       TELEFAX:  (212) 661-8002
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  31
;       TYPE:  Amino Acid
;       STRANDEDNESS:  Unknown
;       TOPOLOGY:  Unknown
US-08-244-951A-4


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  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db       7 YSSPGSPGT 15


RESULT   5
US-08-602-264A-10
; Sequence 10, Application US/08602264A
; Patent No. 5837853
;  GENERAL INFORMATION:
;    APPLICANT:  Akihiko TAKASHIMA et al.
;    TITLE OF INVENTION:  PREVENTIVE OR THERAPEUTIC AGENTS FOR
;    TITLE OF INVENTION:  ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
;    TITLE OF INVENTION:  tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WENDEROTH, LIND & PONACK
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      COUNTRY:  D.C.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch,
;      MEDIUM TYPE:  144 mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,264A
;      FILING DATE:  February 20, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/204,091
;      FILING DATE:  March 2, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-602-264A-10


  Query Match             100.0%;  Score 50;  DB 2;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db       7 YSSPGSPGT 15


RESULT   6
US-08-461-018A-10
; Sequence 10, Application US/08461018A
; Patent No. 6071694
;  GENERAL INFORMATION:
;    APPLICANT:  Akihiko TAKASHIMA et al.
;    TITLE OF INVENTION:  SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
;    TITLE OF INVENTION:  ALZHEIMER'S DISEASE (AS AMENDED)
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WENDEROTH, LIND & PONACK
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      COUNTRY:  D.C.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch,
;      MEDIUM TYPE:  1.44 mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,018A
;      FILING DATE:  June 5, 1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/204,091
;      FILING DATE:  March 2, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-461-018A-10


  Query Match             100.0%;  Score 50;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       7 YSSPGSPGT 15


RESULT   7
US-09-216-958-10
; Sequence 10, Application US/09216958
; Patent No. 6248559
;  GENERAL INFORMATION:
;    APPLICANT:  Akihiko TAKASHIMA et al.
;    TITLE OF INVENTION:  SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
;    TITLE OF INVENTION:  ALZHEIMER'S DISEASE (AS AMENDED)
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WENDEROTH, LIND & PONACK
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      COUNTRY:  D.C.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Diskette, 3.5 inch,
;       MEDIUM TYPE:  1.44 mb
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  Wordperfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/216,958
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/461,018
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warren M. Cheek, Jr.
;       REGISTRATION NUMBER:  33,367
;       REFERENCE/DOCKET NUMBER:
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:
;       TELEFAX:
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  34 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-216-958-10


  Query Match             100.0%;  Score 50;  DB 4;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db       7 YSSPGSPGT 15


RESULT   8
US-08-244-951A-1
; Sequence 1, Application US/08244951A
; Patent No. 5843779
;  GENERAL INFORMATION:
;     APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;     APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;     TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;     TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;     TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;     TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;     TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;     NUMBER OF SEQUENCES:  10
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  BIERMAN & MUSERLIAN
;       STREET:  600 THIRD AVENUE
;       CITY:  NEW YORK
;       STATE:  NEW YORK
;       COUNTRY:  USA
;       ZIP:  10016
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  FLOPPY DISK
;       COMPUTER:  IBM PC COMPATIBLE
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  ASCII
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/244,951A
;       FILING DATE:  19-JAN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/EP93/03499
;       FILING DATE:  10-DEC-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  EP/92/403403.6
;       FILING DATE:  14-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  CHARLES A. MUSERLIAN
;       REGISTRATION NUMBER:  19,683
;       REFERENCE/DOCKET NUMBER:  410.003A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 661-8000
;       TELEFAX:  (212) 661-8002
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  67
;       TYPE:  Amino Acid
;       STRANDEDNESS:  Unknown
;       TOPOLOGY:  Unknown
;     FEATURE:
;       NAME/KEY:  human tau protein 155-211
US-08-244-951A-1


  Query Match             100.0%;  Score 50;  DB 2;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db      43 YSSPGSPGT 51


RESULT   9
US-08-389-011-1
; Sequence 1, Application US/08389011
; Patent No. 5861257
;  GENERAL INFORMATION:
;     APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;     APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;     TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;     TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;     TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;     TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;     TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
;     NUMBER OF SEQUENCES:  24
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  BIERMAN & MUSERLIAN
;       STREET:  600 THIRD AVENUE
;       CITY:  NEW YORK
;       STATE:  NEW YORK
;       COUNTRY:  USA
;       ZIP:  10016
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  FLOPPY DISK
;       COMPUTER:  IBM PC COMPATIBLE
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  ASCII
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/389,011
;       FILING DATE:  15-FEB-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/403,917
;       FILING DATE:  19-JAN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/403,916
;       FILING DATE:  19-JAN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/244,951
;       FILING DATE:  13-JUN-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/EP93/03499
;       FILING DATE:  10-DEC-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  EP/92/403403.6
;       FILING DATE:  14-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
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;       NAME:  CHARLES A. MUSERLIAN
;       REGISTRATION NUMBER:  19,683
;       REFERENCE/DOCKET NUMBER:  410.003-1-CON
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 661-8000
;       TELEFAX:  (212) 661-8002
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  67
;       TYPE:  Amino Acid
;       STRANDEDNESS:  Unknown
;       TOPOLOGY:  linear
US-08-389-011-1


  Query Match             100.0%;  Score 50;  DB 2;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db      43 YSSPGSPGT 51


RESULT  10
US-08-403-917A-1
; Sequence 1, Application US/08403917A
; Patent No. 6010913
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN;
;    APPLICANT:  VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATION
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,917A
;      FILING DATE:  19-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/256,167
;      FILING DATE:  27-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/244,951
;      FILING DATE:  13-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  67
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
US-08-403-917A-1


  Query Match             100.0%;  Score 50;  DB 3;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db      43 YSSPGSPGT 51


RESULT  11
US-09-348-952A-1
; Sequence 1, Application US/09348952A
; Patent No. 6232437
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN;
;    APPLICANT:  VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATION
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/348,952A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/403,917
;      FILING DATE:  19-JAN-1995
;      APPLICATION NUMBER:  08/256,167
;      FILING DATE:  27-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/244,951
;      FILING DATE:  13-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  67
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
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US-09-348-952A-1

Query Match 100.0%; Score 50; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||||||||||
Db 43 YSSPGSPGT 51

RESULT 12
US-08-776-404B-1
; Sequence 1, Application US/08776404B
; Patent No. 6121003
; GENERAL INFORMATION:
; APPLICANT: VANMECHELEN, EUGEEN
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR AN EPITOPE OF
; TITLE OF INVENTION: A PARTICULAR SUBCLASS OR FORM OF PHOSPHORYLATED TAU,
; TITLE OF INVENTION: HYBRIDOMAS SECRETING THEM, ANTIGEN RECOGNITION OF THESE
; TITLE OF INVENTION: ANTIBODIES AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,404B
; FILING DATE: 27 Jan 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03032
; FILING DATE: 31 Jul 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870131.3
; FILING DATE: 29 Jul 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:003
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-776-404B-1

Query Match 100.0%; Score 50; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||||||||||
Db 52 YSSPGSPGT 60

RESULT 13
US-08-666-360-1
; Sequence 1, Application US/08666360
; Patent No. 6008024
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Monoclonal antibodies specific for PHF-tau,
; TITLE OF INVENTION: hybridomas secreting them, antigen recognition of these
; TITLE OF INVENTION: antibodies and their applications
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,360
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-666-360-1

Query Match 100.0%; Score 50; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSSPGSPGT 9
||||||||||
Db 55 YSSPGSPGT 63

RESULT 14
US-08-159-969-2
; Sequence 2, Application US/08159969
; Patent No. 5492812
; GENERAL INFORMATION:
; APPLICANT: Voorheis, Paul H.
; TITLE OF INVENTION: Diagnostic Method for Alzheimer's
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,969
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/738,778
; FILING DATE: 01-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S.Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 4697-040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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;    MOLECULE TYPE:  protein
US-08-159-969-2


  Query Match             100.0%;  Score 50;  DB 1;  Length 351;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     139 YSSPGSPGT 147


RESULT  15
US-08-726-306A-17
; Sequence 17, Application US/08726306A
; Patent No. 5958684
;  GENERAL INFORMATION:
;    APPLICANT:  van Leeuwen, Frederik Willem
;    APPLICANT:  Burbach, Johannes Peter Henri
;    APPLICANT:  Grosveld, Franklin G.
;    TITLE OF INVENTION:  DIAGNOSIS METHOD AND REAGENTS
;    NUMBER OF SEQUENCES:  189
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  1 Financial Center
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/726,306A
;      FILING DATE:  02-Oct-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 95/20080.4
;      FILING DATE:  02-Oct-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/009,832
;      FILING DATE:  01-Jan-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Ph.D., Kathleen M.
;      REGISTRATION NUMBER:  34,380
;      REFERENCE/DOCKET NUMBER:  96,048-A (3255/00784)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 345-9100
;      TELEFAX:  (617) 345-9111
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-726-306A-17


  Query Match             100.0%;  Score 50;  DB 2;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     139 YSSPGSPGT 147


RESULT  16
US-08-244-951A-10
; Sequence 10, Application US/08244951A
; Patent No. 5843779
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,951A
;      FILING DATE:  19-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  391
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
;    FEATURE:
;      NAME/KEY:  mTHFMPH-taul fusion protein
US-08-244-951A-10


  Query Match             100.0%;  Score 50;  DB 2;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     178 YSSPGSPGT 186


RESULT  17
US-08-389-011-23
; Sequence 23, Application US/08389011
; Patent No. 5861257
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  BIERMAN & MUSERLIAN
;       STREET:  600 THIRD AVENUE
;       CITY:  NEW YORK
;       STATE:  NEW YORK
;       COUNTRY:  USA
;       ZIP:  10016
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  FLOPPY DISK
;       COMPUTER:  IBM PC COMPATIBLE
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  ASCII
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/389,011
;       FILING DATE:  15-FEB-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/403,917
;       FILING DATE:  19-JAN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/403,916
;       FILING DATE:  19-JAN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/244,951
;       FILING DATE:  13-JUN-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/EP93/03499
;       FILING DATE:  10-DEC-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  EP/92/403403.6
;       FILING DATE:  14-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  CHARLES A. MUSERLIAN
;       REGISTRATION NUMBER:  19,683
;       REFERENCE/DOCKET NUMBER:  410.003-1-CON
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 661-8000
;       TELEFAX:  (212) 661-8002
;   INFORMATION FOR SEQ ID NO:  23:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  391
;       TYPE:  Amino Acid
;       STRANDEDNESS:  Unknown
;       TOPOLOGY:  Unknown
US-08-389-011-23


  Query Match             100.0%;  Score 50;  DB 2;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     178 YSSPGSPGT 186


RESULT  18
US-08-403-917A-23
; Sequence 23, Application US/08403917A
; Patent No. 6010913
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN;
;    APPLICANT:  VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATION
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,917A
;      FILING DATE:  19-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/256,167
;      FILING DATE:  27-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/244,951
;      FILING DATE:  13-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  391
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
US-08-403-917A-23


  Query Match             100.0%;  Score 50;  DB 3;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     178 YSSPGSPGT 186


RESULT  19
US-09-348-952A-23
; Sequence 23, Application US/09348952A
; Patent No. 6232437
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN;
;    APPLICANT:  VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATION
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/348,952A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/403,917
;      FILING DATE:  19-JAN-1995
;      APPLICATION NUMBER:  08/256,167
;      FILING DATE:  27-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/244,951
;      FILING DATE:  13-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  391
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
US-09-348-952A-23


  Query Match             100.0%;  Score 50;  DB 4;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     178 YSSPGSPGT 186


RESULT  20
US-08-244-603A-1
; Sequence 1, Application US/08244603A
; Patent No. 6200768
;  GENERAL INFORMATION:
;    APPLICANT:  Mandelkow, Eva-Maria
;    APPLICANT:  Mandelkow, Eckhard
;    APPLICANT:  Lichtenberg-Kraag, Birgit
;    APPLICANT:  Biernat, Jacek
;    APPLICANT:  Drewes, Gerard
;    APPLICANT:  Steiner, Barbara
;    TITLE OF INVENTION:  No. 6200768el Tools For The Diagnosis And
;    TITLE OF INVENTION:  Treatment Of Alzheimer's Disease
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  233 South Waker Drive, 6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Tape
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,603A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph A. Williams, Jr.
;      REGISTRATION NUMBER:  38,659
;      REFERENCE/DOCKET NUMBER:  28384/32778
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;      TELEFAX:  312-484-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  441 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-244-603A-1


  Query Match             100.0%;  Score 50;  DB 4;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           |||||||||
Db     197 YSSPGSPGT 205


RESULT  21
US-09-159-106-2
; Sequence 2, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
;  APPLICANT: Ferrer, Pau
;  APPLICANT: Diers, Ivan
;  APPLICANT: Halkier, Torben
;  APPLICANT: Hedegaard, Lisbeth
;  TITLE OF INVENTION: An Enzyme With  -1,3-Glucanase
;  TITLE OF INVENTION: Activity
;  FILE REFERENCE: 4693.204-US
;  CURRENT APPLICATION NUMBER: US/09/159,106
;  CURRENT FILING DATE: 1998-09-23
;  EARLIER APPLICATION NUMBER: 0427/96
;  EARLIER FILING DATE: 1996-12-04
;  EARLIER APPLICATION NUMBER: 0885/96
;  EARLIER FILING DATE: 1996-08-23
;  EARLIER APPLICATION NUMBER: PCT/DK97/00160
;  EARLIER FILING DATE: 1997-04-14
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 263
;   TYPE: PRT
;   ORGANISM: Oerskovia xanthineolytica
US-09-159-106-2


  Query Match             80.0%;  Score 40;  DB 4;  Length 263;
  Best Local Similarity   87.5%;  Pred. No. 33;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
           ||||:|||
Db     244 SSPGNPGT 251


RESULT  22
US-09-159-106-11
; Sequence 11, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
;  APPLICANT: Ferrer, Pau
;  APPLICANT: Diers, Ivan
```

```
;  APPLICANT: Halkier, Torben
;  APPLICANT: Hedegaard, Lisbeth
;  TITLE OF INVENTION: An Enzyme With  -1,3-Glucanase
;  TITLE OF INVENTION: Activity
;  FILE REFERENCE: 4693.204-US
;  CURRENT APPLICATION NUMBER: US/09/159,106
;  CURRENT FILING DATE: 1998-09-23
;  EARLIER APPLICATION NUMBER: 0427/96
;  EARLIER FILING DATE: 1996-12-04
;  EARLIER APPLICATION NUMBER: 0885/96
;  EARLIER FILING DATE: 1996-08-23
;  EARLIER APPLICATION NUMBER: PCT/DK97/00160
;  EARLIER FILING DATE: 1997-04-14
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;    LENGTH: 435
;    TYPE: PRT
;    ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11


  Query Match             80.0%;  Score 40;  DB 4;  Length 435;
  Best Local Similarity   87.5%;  Pred. No. 56;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 SSPGSPGT 9
            ||||:|||
Db     297 SSPGNPGT 304


RESULT  23
US-08-244-951A-3
; Sequence 3, Application US/08244951A
; Patent No. 5843779
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,951A
;      FILING DATE:  19-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
;    FEATURE:
;      NAME/KEY:  human tau protein 199-221
US-08-244-951A-3


  Query Match             78.0%;  Score 39;  DB 2;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
            |||||||
Db       1 SPGSPGT 7


RESULT  24
US-08-244-951A-2
; Sequence 2, Application US/08244951A
; Patent No. 5843779
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/244,951A
;      FILING DATE:  19-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
;    FEATURE:
;      NAME/KEY:  human tau protein 199-231
US-08-244-951A-2
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  Query Match           78.0%;  Score 39;  DB 2;  Length 33;
  Best Local Similarity  100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db       1 SPGSPGT 7


RESULT  25
US-08-389-011-2
; Sequence 2, Application US/08389011
; Patent No. 5861257
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/389,011
;      FILING DATE:  15-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/403,917
;      FILING DATE:  19-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/403,916
;      FILING DATE:  19-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/244,951
;      FILING DATE:  13-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003-1-CON
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
US-08-389-011-2


  Query Match           78.0%;  Score 39;  DB 2;  Length 33;
  Best Local Similarity  100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db       1 SPGSPGT 7


RESULT  26
US-08-403-917A-2
; Sequence 2, Application US/08403917A
; Patent No. 6010913
;  GENERAL INFORMATION:
;    APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;    APPLICANT:  VANMECHELEN, EUGEEN;
;    APPLICANT:  VAN DE VOORDE, ANDRE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;    TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATION
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIERMAN & MUSERLIAN
;      STREET:  600 THIRD AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10016
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,917A
;      FILING DATE:  19-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/256,167
;      FILING DATE:  27-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/244,951
;      FILING DATE:  13-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP93/03499
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP/92/403403.6
;      FILING DATE:  14-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CHARLES A. MUSERLIAN
;      REGISTRATION NUMBER:  19,683
;      REFERENCE/DOCKET NUMBER:  410.003-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 661-8000
;      TELEFAX:  (212) 661-8002
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Unknown
;      TOPOLOGY:  Unknown
US-08-403-917A-2


  Query Match           78.0%;  Score 39;  DB 3;  Length 33;
  Best Local Similarity  100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db       1 SPGSPGT 7


RESULT  27
US-09-348-952A-2
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; Sequence 2, Application US/09348952A
; Patent No. 6232437
; GENERAL INFORMATION:
;   APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;   APPLICANT:  VANMECHELEN, EUGEEN;
;   APPLICANT:  VAN DE VOORDE, ANDRE
;   TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;   TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;   TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;   TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;   TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATION
;   NUMBER OF SEQUENCES:  24
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  BIERMAN & MUSERLIAN
;     STREET:  600 THIRD AVENUE
;     CITY:  NEW YORK
;     STATE:  NEW YORK
;     COUNTRY:  USA
;     ZIP:  10016
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  FLOPPY DISK
;     COMPUTER:  IBM PC COMPATIBLE
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  ASCII
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/348,952A
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/403,917
;     FILING DATE:  19-JAN-1995
;     APPLICATION NUMBER:  08/256,167
;     FILING DATE:  27-JUN-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/244,951
;     FILING DATE:  13-JUN-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/EP93/03499
;     FILING DATE:  10-DEC-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  EP/92/403403.6
;     FILING DATE:  14-DEC-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  CHARLES A. MUSERLIAN
;     REGISTRATION NUMBER:  19,683
;     REFERENCE/DOCKET NUMBER:  410.003-1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212) 661-8000
;     TELEFAX:  (212) 661-8002
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  33
;     TYPE:  Amino Acid
;     STRANDEDNESS:  Unknown
;     TOPOLOGY:  Unknown
US-09-348-952A-2


  Query Match             78.0%;  Score 39;  DB 4;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db       1 SPGSPGT 7


RESULT  28
US-08-244-951A-6
; Sequence 6, Application US/08244951A
; Patent No. 5843779
; GENERAL INFORMATION:
;   APPLICANT:  VANDERMEEREN, MARC; MERCKEN, MARC;
;   APPLICANT:  VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
;   TITLE OF INVENTION:  MONOCLONAL ANTIBODIES
;   TITLE OF INVENTION:  DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
;   TITLE OF INVENTION:  PROTEIN TAU, HYBRIDOMAS SECRETING THESE
;   TITLE OF INVENTION:  ANTIBODIES, ANTIGEN RECOGNITION BY THESE
;   TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
;   NUMBER OF SEQUENCES:  10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  BIERMAN & MUSERLIAN
;     STREET:  600 THIRD AVENUE
;     CITY:  NEW YORK
;     STATE:  NEW YORK
;     COUNTRY:  USA
;     ZIP:  10016
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  FLOPPY DISK
;     COMPUTER:  IBM PC COMPATIBLE
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  ASCII
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/244,951A
;     FILING DATE:  19-JAN-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/EP93/03499
;     FILING DATE:  10-DEC-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  EP/92/403403.6
;     FILING DATE:  14-DEC-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  CHARLES A. MUSERLIAN
;     REGISTRATION NUMBER:  19,683
;     REFERENCE/DOCKET NUMBER:  410.003A
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212) 661-8000
;     TELEFAX:  (212) 661-8002
; INFORMATION FOR SEQ ID NO:  6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  35
;     TYPE:  Amino Acid
;     STRANDEDNESS:  Unknown
;     TOPOLOGY:  Unknown
US-08-244-951A-6


  Query Match             78.0%;  Score 39;  DB 2;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 6.1;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 SPGSPGT 9
           |||||||
Db       3 SPGSPGT 9


RESULT  29
US-08-836-561-106
; Sequence 106, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
;   APPLICANT:  KOIKE, Masamichi
;   APPLICANT:  FURUYA, Akiko
;   APPLICANT:  NAKAMURA, Kazuyasu
;   APPLICANT:  IIDA, Akihiro
;   APPLICANT:  ANAZAWA, Hideharu
;   APPLICANT:  HANAI, No. 6018032uo
;   APPLICANT:  TAKATSU, Kiyoshi
;   TITLE OF INVENTION:  Antibody Against Human Interleukin-5
;   TITLE OF INVENTION:  Receptor Alpha Chain
;   NUMBER OF SEQUENCES:  106
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Pennie & Edmonds LLP
;     STREET:  1155 Avenue of the Americas
;     CITY:  New York
;     STATE:  NY
```

```
;       COUNTRY:  USA
;       ZIP:  10036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/836,561
;       FILING DATE:  09-MAY-1997
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 232384/95
;       FILING DATE:  11-SEP-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lawrence, III, Stanton T
;       REGISTRATION NUMBER:  25,736
;       REFERENCE/DOCKET NUMBER:  7005-115-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-790-9090
;       TELEFAX:  212-869-9741
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  106:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  313 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-836-561-106


  Query Match             74.0%;  Score 37;  DB 3;  Length 313;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db      99 HAPPGSPGT 107


RESULT  30
US-07-947-130-2
; Sequence 2, Application US/07947130
; Patent No. 5455337
;  GENERAL INFORMATION:
;    APPLICANT:  Devos, Rene
;    APPLICANT:  Fiers, Walter
;    APPLICANT:  Tavernier, Jan
;    TITLE OF INVENTION:  Chimeric Interleukin-5
;    TITLE OF INVENTION:  Receptor/Immunoglobulin Polypeptides
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mr. George M. Gould, Esq.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/947,130
;      FILING DATE:  19920916
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 91810738.4
;      FILING DATE:  18-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Malaska, Stephen L.
;      REGISTRATION NUMBER:  32,655
;      REFERENCE/DOCKET NUMBER:  4105/144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-235-6326
;      TELEFAX:  201-235-3500
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  leukemia
;      CELL TYPE:  Promyelocytes
;      CELL LINE:  HL-60
;    IMMEDIATE SOURCE:
;      LIBRARY:  human HL-60
;      CLONE:  lambda gt11-hIL5Ralpha12
US-07-947-130-2


  Query Match             74.0%;  Score 37;  DB 1;  Length 335;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 HAPPGSPGT 127


RESULT  31
US-08-421-822-2
; Sequence 2, Application US/08421822
; Patent No. 5668256
;  GENERAL INFORMATION:
;    APPLICANT:  Devos, Rene
;    APPLICANT:  Fiers, Walter
;    APPLICANT:  Tavernier, Jan
;    TITLE OF INVENTION:  Chimeric Interleukin-5
;    TITLE OF INVENTION:  Receptor/Immunoglobulin Polypeptides
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mr. George M. Gould, Esq.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/421,822
;      FILING DATE:  13-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/947,130
;      FILING DATE:  16-SEP-1992
;      APPLICATION NUMBER:  EP 91810738.4
;      FILING DATE:  18-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Malaska, Stephen L.
;      REGISTRATION NUMBER:  32,655
;      REFERENCE/DOCKET NUMBER:  4105/144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-235-6326
;      TELEFAX:  201-235-3500
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;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  leukemia
;      CELL TYPE:  Promyelocytes
;      CELL LINE:  HL-60
;    IMMEDIATE SOURCE:
;      LIBRARY:  human HL-60
;      CLONE:  lambda gt11-hIL5Ralpha12
US-08-421-822-2


  Query Match             74.0%;  Score 37;  DB 1;  Length 335;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 HAPPGSPGT 127


RESULT  32
US-08-421-823-2
; Sequence 2, Application US/08421823
; Patent No. 5712121
;  GENERAL INFORMATION:
;    APPLICANT:  Devos, Rene
;    APPLICANT:  Fiers, Walter
;    APPLICANT:  Tavernier, Jan
;    TITLE OF INVENTION:  Chimeric Interleukin-5
;    TITLE OF INVENTION:  Receptor/Immunoglobulin Polypeptides
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mr. George M. Gould, Esq.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/421,823
;      FILING DATE:  13-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/947,130
;      FILING DATE:  16-SEP-1992
;      APPLICATION NUMBER:  EP 91810738.4
;      FILING DATE:  18-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Malaska, Stephen L.
;      REGISTRATION NUMBER:  32,655
;      REFERENCE/DOCKET NUMBER:  4105/144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-235-6326
;      TELEFAX:  201-235-3500
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  leukemia
;      CELL TYPE:  Promyelocytes
;      CELL LINE:  HL-60
;    IMMEDIATE SOURCE:
;      LIBRARY:  human HL-60
;      CLONE:  lambda gt11-hIL5Ralpha12
US-08-421-823-2


  Query Match             74.0%;  Score 37;  DB 1;  Length 335;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 HAPPGSPGT 127


RESULT  33
US-07-757-390-14
; Sequence 14, Application US/07757390
; Patent No. 5453491
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/757,390
;      FILING DATE:  19910910
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  396 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-757-390-14


  Query Match             74.0%;  Score 37;  DB 1;  Length 396;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy      1 YSSPGSPGT 9
          :: ||||||
Db    119 HAPPGSPGT 127


RESULT  34
US-08-442-282-14
; Sequence 14, Application US/08442282
; Patent No. 5760204
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,282
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/757,390
;      FILING DATE:  10-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  396 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-442-282-14


  Query Match             74.0%;  Score 37;  DB 1;  Length 396;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          :: ||||||
Db    119 HAPPGSPGT 127


RESULT  35
US-08-442-281-14
; Sequence 14, Application US/08442281
; Patent No. 5807991
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,281
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/757,390
;      FILING DATE:  10-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  396 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-442-281-14


  Query Match             74.0%;  Score 37;  DB 1;  Length 396;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 YSSPGSPGT 9
          :: ||||||
Db    119 HAPPGSPGT 127


RESULT  36
US-08-939-727-14
; Sequence 14, Application US/08939727
; Patent No. 5916767
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/939,727
;      FILING DATE:
;      CLASSIFICATION:
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/757,390
;      FILING DATE:  10-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  396 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-939-727-14


  Query Match             74.0%;  Score 37;  DB 2;  Length 396;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 HAPPGSPGT 127


RESULT  37
US-07-757-390-13
; Sequence 13, Application US/07757390
; Patent No. 5453491
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/757,390
;      FILING DATE:  19910910
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  420 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-757-390-13


  Query Match             74.0%;  Score 37;  DB 1;  Length 420;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 YSSPGSPGT 9
           :: ||||||
Db     119 HAPPGSPGT 127


RESULT  38
US-08-442-282-13
; Sequence 13, Application US/08442282
; Patent No. 5760204
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,282
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/757,390
;      FILING DATE:  10-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  420 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-442-282-13


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; Sequence 13, Application US/08442281
; Patent No. 5807991
;  GENERAL INFORMATION:
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;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,281
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/757,390
;      FILING DATE:  10-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
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US-08-442-281-13


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Db     119 HAPPGSPGT 127


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; Patent No. 5916767
;  GENERAL INFORMATION:
;    APPLICANT:  Takatsu, Kiyoshi
;    APPLICANT:  Tominaga, Akira
;    APPLICANT:  Takagi, Satoshi
;    APPLICANT:  Murata, Yoshiyuki
;    TITLE OF INVENTION:  Human And Murine Interleukin-5 Receptor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/939,727
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/757,390
;      FILING DATE:  10-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7005-030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 790-9090
;      TELEFAX:  212 8698864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  420 amino acids
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;    MOLECULE TYPE:  peptide
US-08-939-727-13


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Search completed: May 21, 2002, 11:18:35
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09/734,281

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File 103:Energy SciTec 1974-2002/Apr B2
(c) 2002 Contains copyrighted material
*File 103: For access restrictions see Help Restrict.
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File 144:Pascal 1973-2002/May W3
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*File 155: This file has been reloaded. Accession numbers have changed.
File 156:ToxFile 1966-2002/Feb W4
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*File 162: Truncating CC codes is recommended for full retrieval.
See Help News162 for details.
File 172:EMBASE Alert 2002/May W3
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File 305:Analytical Abstracts 1980-2002/Apr W4
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*File 305: Frequency of updates and Alerts changing to weekly.
See HELP NEWS 305.
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File 370:Science 1996-1999/Jul W3
(c) 1999 AAAS
*File 370: This file is closed (no updates). Use File 47 for more current information.
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*File 399: Use is subject to the terms of your user/customer agreement.
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(c) 1998 Inst for Sci Info

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959154 MONOCLONAL
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08798405 BIOSIS NO.: 199395087756
The antineoplastic agent estramustine and the derivative estramustine phosphate inhibit secretion of interleukin-3 in leukemic cells: Possible roles of MAPs.
AUTHOR: Martinez Jorge(a); Santibanez Juan Francisco; Vial Clarisa; Maccioni Ricardo B
AUTHOR ADDRESS: (a)Inst. Nutricion y Tecnol. de Alimentos, Univ. de Chile, Casilla 138-11, Santiago**Chile
JOURNAL: Molecular and Cellular Biochemistry 117 (2):p165-173
%%%1992%%%

ISSN: 0300-8177
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The antineoplasic drug estramustine is an adduct of estradiol and
nor-nitrogen mustard. It has been shown that this drug interferes with microtubule assembly, an effect mediated by estramustine interaction with microtubule-associated proteins (MAPs). In the present report we demonstrate that estramustine and the %%%phosphorylated%%% derivative of
the drug, estramustine-phosphate, inhibit the secretion of interleukin-3 by WEHI-3B cells. These studies also show that the estramustine derivative specifically interacts with a MAPs component found in these cells, which exhibited characteristics resembling those of %%%tau%%% protein isoforms. Western blots using a unique %%%monoclonal%%% antibody
MTB6.22 that recognizes microtubule-binding domains on MAPs, indicated that this WEHI protein factor contained the antigenic determinant that are functionally significant for microtubule assembly. ELISA assays using this antibody, also showed a decrease in the levels of the immunoreactive protein in WEHI cells after treatment with EMP. Interestingly, it has been recently described that the action of estramustine-phosphate is mediated by a direct interaction with MAP-binding sites on the microtubule surface, which are recognized by the site-specific %%%monoclonal%%% antibody. These findings together with immuno-precipitation experiments using anti-interleukin-3 antibodies and the inhibitory effect of the estramustine derivative on WEHI secretion process suggest that this anti-mitotic agent may block IL-3 secretion by a mechanism involving its interaction with a '%%%tau%%%-like' MAPs component present in these cells.

4/7/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08787925 BIOSIS NO.: 199395077276
%%%Phosphorylation%%% sites on %%%tau%%% by %%%tau%%% protein kinase I, a
bovine derived kinase generating an epitope of paired helical filaments.
AUTHOR: Ishiguro Koichi(a); Omori Akira; Takamatsu Masako; Sato Kazuki; Arioka Manabu; Uchida Tsuneko; Imahori Kazutomo
AUTHOR ADDRESS: (a)Mitsubishi Kasei Inst. Life Sci., 11 Minamiooya, Machida-shi, Tokyo, 194**Japan
JOURNAL: Neuroscience Letters 148 (1-2):p202-206 %%%1992%%%
ISSN: 0304-3940
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Tau%%% protein kinase I (TPKI) isolated from bovine brain has
been determined to %%%phosphorylte%%% %%%tau%%% at four distinct sites by
detecting modified Ser and Thr residues with protein sequencer. Ser199, Thr231, Ser396 and Ser413 were all found to have been %%%phosphorylated%%% by TPKI (numbering of amino acids was done in relation to the longest human %%%tau%%% (Neuron, 3 (1989) 519-526)). These phophorylations generate an epitope of PHF (paired helical filaments) and eliminate the recognition of %%%tau%%% by the %%%monoclonal%%% antibody, %%%tau%%%-1. These results suggested that TPKI
might be reponsible for at least some of the %%%phosphorylation%%% of %%%tau%%% to induce PHF formation

4/7/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08775405 BIOSIS NO.: 199395064756
Glycogen synthase kinase-3 induces Alzheimer's disease-like %%%phosphorylation%%% of %%%tau%%%: Generation of paired helical filament
epitopes and neuronal localisation of the kinase.
AUTHOR: Hanger Diane P(a); Hughes Kenneth; Woodgett James R; Brion Jean-Pierre; Anderton Brian H
AUTHOR ADDRESS: (a)Dep. Neurosci., Inst. Psychiatry, De Crespigny Park, Denmark Hill, London SE5 8AF**UK
JOURNAL: Neuroscience Letters 147 (1):p58-62 %%%1992%%%
ISSN: 0304-3940
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Glycogen synthase kinase-3 (GSK-3) reduced the mobility of human
%%%tau%%% on SDS-PAGE, prevented binding of the %%%monoclonal%%% antibody
(%%%mAb%%%), %%%Tau%%%.1, and induced binding of the %%%mAb%%% 8D8.
Recombinant %%%tau%%% %%%phosphorylated%%% by GSK-3 aligned on SDS-PAGE
with the abnormally %%%phosphorylated%%% %%%tau%%% (PHF-%%%tau%%%)
associated with the paired helical filaments in Alzheimer's disease brain. %%%Phosphorylated%%% serine-396 (numbering of the largest human
brain %%%tau%%% isoform) was identified as a binding site on %%%tau%%%
for %%%mAb%%% 8D8. The localisation of GSK-3 within granular structures
in pyramidal cells indicates that GSK-3-alpha and GSK-3-beta may have a role in the production of PHF-%%%tau%%% in Alzheimer's disease.

4/7/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08740909 BIOSIS NO.: 199395030260
Proline-directed %%%phosphorylation%%% of human %%%tau%%% protein.
AUTHOR: Vulliet Richard(a); Halloran S Mitchell; Braun Ruedi K; Smith Alan J; Lee Gloria
AUTHOR ADDRESS: (a)Dep. Vet. Pharmacol. Toxicol., Univ. Calif., Davis, Calif. 95616**ussia
JOURNAL: Journal of Biological Chemistry 267 (31):p22570-22574 %%%1992%%%
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The primary sequence of the microtubule-associated proetin %%%tau%%% contains multiple repeats of the sequence -X-Ser-/Thr-Pro-X-,
the consensus sequence for the proline-directed protein kinase (p34-cdc2/p58-cyclin A). When %%%phosphorylated%%% by proline-directed
protein kinase in vitro, %%%tau%%% was found to incorporate up to 4.4 mol
of phosphate/mol of protein. Isoelectric focusing of the tryptic phosphopeptides demonstrated the presence of five distinct peptides with pI values of approximately 6.9, 6.5, 5.6-5.9, 4.7, and 3.6. Mapping of the tryptic phosphopeptides by high performance liquid chromatography techniques demonstrated three distinct peaks. Data from gas phase sequencing, amino acid analysis, and phosphoamino acid analysis suggest that proline-directed protein kinase %%%phosphorylates%%% %%%tau%%% at
four sites. Each site demonstrates the presence of a proline residue on the carboxyl-terminal side of the %%%phosphorylated%%% residue. Two %%%phosphorylation%%% sites are located adjacent to the three-repeat microtubule-binding domain that has been found to be required for the in vivo co-localization of %%%tau%%% protein to microtubules. Two other putative %%%phosphorylation%%% sites are located within the identified epitope of the %%%monoclonal%%% antibody %%%Tau%%%-1. %%%Phosphorylation%%% of these sites altered the immunoreactivity of %%%tau%%% to %%%Tau%%%-1 antibody. Since the neuronal microtubule-associated protein %%%tau%%% is multiply %%%phosphorylated%%%

in Alzheimer's disease, and %%%Tau%%%-1 immunoreactivity is similarly reduced in neurofibrillary tangles and enhanced after dephosphorylation, phosphophorylation at one or more of three sites may correlate with abnormally %%%phosphorylated%%% sites in %%%tau%%% protein in Alzheimer's disease.

4/7/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08729888 BIOSIS NO.: 199395019239
A serine fwdarw proline change in the Alzheimer's disease-associated epitope %%%Tau%%%-2 results in altered secondary structure, but %%%phosphorylation%%% overcomes the conformational gap.
AUTHOR: Lang Emma; Otvos Laszlo Jr(a)
AUTHOR ADDRESS: (a)Wistar Institute Anatomy Biology, 3601 Spruce Street, Philadelphia, Pa. 19104
JOURNAL: Biochemical and Biophysical Research Communications 188 (1):p 162-169 %%%1992%%%
ISSN: 0006-291X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Monoclonal%%% antiboddy %%%Tau%%% 2 was raised against bovine %%%tau%%% protein, was reported to recognize a conformational epitope, and stained %%%tau%%% was found in neurofibrillary tangles of Alzheimer's disease, but not normal human %%%tau%%%. We synthesized tetradeka peptides corresponding to the original bovine sequence, its serine fwdarw proline substitued analog, the genuine human sequence of this region, and the bovine epitope %%%phosphorylated%%% on the crucial serine. The secondary structure of the peptides was determined by circular dichroism. It was found that only the original bovine epitope showed a tendency to form the beta-pleated sheets characteristic of the neurofibrillary tangles. The spectra of the human peptide, it analog, and the %%%phosphorylated%%% bovine sequence were very similar, featuring a weak, helical beta-turn character. Eventual %%%phosphorylation%%% of epitopes of this otherwise heavily %%%phosphorylated%%% protein may overcome inter-species conformational gaps.

4/7/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08717649 BIOSIS NO.: 199395007000
Immunological and conformational characterization of a %%%phosphorylated%%% immunodominant epitope on the paired helical filaments found in Alzheimer's disease.
AUTHOR: Lang Emma; Szendrei Gyorgyi I; Lee Virginia M-Y; Otvos Laszlo Jr(a)
AUTHOR ADDRESS: (a)Wistar Institute Anatomy Biology, 3601 Spruce Street, Philadelphia, Pa. 19104
JOURNAL: Biochemical and Biophysical Research Communications 187 (2):p 783-790 %%%1992%%%
ISSN: 0006-291X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The immunological recognition pattern of one of the most commonly used %%%monoclonal%%% antibodies, PHF-1, which detects the paired helical filaments of Alzheimer's disease, exhibits a high degree of similarity with the recognition of a polyclonal antibody, anti-T3P, raised against a synthetic phosphopeptide, GAEIVYKS(Phospho)PVVSGD, corresponding to amino acids 389-402 of the microtubule-associated protein %%%tau%%%. A panel of 16 synthetic non-%%%phosphorylated%%% and %%%phosphorylated%%% peptides, excised from different regions of %%%tau%%% and peptide analogs thereof, were used to show that PHF-1 is indeed directed against the T3 fragment. Circular dichroism spectroscopy shows that the %%%phosphorylated%%% peptide exhibits a limited propensity to form intramolecular beta-pleated sheets, and alteration is found in the reverse-turn structure that dominates the middle section of the molecule. The shift in the turn-forming amino acids may also allow a stacking procedure, may interfere with microtubule assembly, and, consequently, may be accountable for deposit formation.

4/7/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08427296 BIOSIS NO.: 000094134500
%%%MONOCLONAL%%% ANTIBODIES WITH SELECTIVE SPECIFICITY FOR ALZHEIMER %%%TAU%%% ARE DIRECTED AGAINST PHOSPHATASE-SENSITIVE EPITOPES
AUTHOR: MERCKEN M; VANDERMEEREN M; LUEBKE U; SIX J; BOONS J; VAN DE VOORDE A; MARTIN J-J; GHEUENS J
AUTHOR ADDRESS: LABORATORY MOLECULAR NEUROSCIENCE AGING RESEARCH, MAILMAN RESEARCH CENTER, MCLEAN HOSPITAL, BELMONT, MASS. 02178, USA.
JOURNAL: ACTA NEUROPATHOL 84 (3). 1992. 265-272. %%%1992%%%
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A modified form of the microtubule-associated protein %%%Tau%%% is the major component of the paired helical filaments (PHF) found in Alzheimer's disease. The characterization of these posttranslational %%%Tau%%% modifications is hindered by the lack of sufficient PHF-%%%Tau%%%-specific markers. Here we describe several %%%monoclonal%%% antibodies, prepared by immunization with PHF, two of which showed a selective specificity for PHF-%%%Tau%%% without cross-reactivity with normal %%%Tau%%%. Epitope recognition by these two monoclonals was sensitive to alkaline phosphatase treatment. In Western blotting these %%%monoclonal%%% antibodies reacted specifically with the abnormally %%%phosphorylated%%% epitopes on Alzheimer's disease-associated PHF-%%%Tau%%%. One of the new antibodies can be used for the construction of a sandwich enzyme-linked immunosorbent assay for the specific detection of PHF-%%%Tau%%% without cross-reactivity to normal %%%Tau%%% proteins.

4/7/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08405595 BIOSIS NO.: 000094123249
%%%TAU%%% AND UBIQUITIN IN THE HUMAN HYPOTHALAMUS IN AGING AND ALZHEIMER'S DISEASE
AUTHOR: SWAAB D F; GRUNDKE-IQBAL I; IQBAL K; KREMER H P H; RAVID R; VAN DE NES J A P
AUTHOR ADDRESS: NETHERLANDS INST. BRAIN RESEARCH, MEIBERGDREEF 33, 1105 AZ AMSTERDAM-ZUIDOOST, NETHERLANDS.
JOURNAL: BRAIN RES 590 (1-2). 1992. 239-249. %%%1992%%%
FULL JOURNAL NAME: Brain Research
CODEN: BRREA

RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Immunocytochemical staining of hypothalamic cell groups with four
antibodies to Alzheimer paired helical filaments (PHF) (i.e., anti-PHF
serum 60e and %%%monoclonal%%% antibody (%%%mAb%%%) Alz-50, both directed
against normal and abnormally %%%phosphorylated%%% .%%%tau%%%.; %%%mAb%%%
.%%%tau%%%.-1, which recognizes .%%%tau%%%.; and %%%mAb%%% 3-39 to PHF,
which recognizes the carboxy terminal domain of ubiquitin) revealed a clear distinction between 12 Alzheimer's disease (AD) patients and seven controls in the hypothalamus. Dystrophic neurites, which appeared to be the most specific components in AD, were most conspicuous after Alz-50 staining. Alz-50 also stained neuronal cytoplasm and normal, thin, beaded neurites in the paraventricular nucleus (PVN) of controls, even of young cases. This staining was clearly distinct from the staining of cytoplasm and dystrophic neurites in the PVN of Alzheimer patients. The abundant staining of dystrophic neurites and cell bodies in the nucleus tuberalis lateralis (NTL) in AD, in which no neuronal loss is observed, suggests that alterations in cytoskeletal markers do not necessarily indicate impending cell death. Moreover, the cytoskeletal changes in the NTL, sexually dimorphic and suprachiasmatic nuclei in AD indicate that this condition is not restricted to cortical areas of nuclei projecting to the cortex. Consequently, the pathophysiological implications of cytoskeletal staining in AD are at present far from clear. The human hypothalamus may not only provide a better insight into the pathogenesis of Alzheimer's disease, but could also be of help in the neuropathological diagnosis of this condition.

4/7/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08380441 BIOSIS NO.: 000094110945
IMPLICATION OF BRAIN CDC2 AND MAP2 KINASES IN THE %%%PHOSPHORYLATION%%% OF
%%%TAU%%% PROTEIN IN ALZHEIMER'S DISEASE
AUTHOR: LEDESMA M D; CORREAS I; AVILA J; DIAZ-NIDO J
AUTHOR ADDRESS: CENT. BIOL. MOL., UNIV. AUTONOMA, 28049 MADRID, SPAIN.
JOURNAL: FEBS (FED EUR BIOCHEM SOC) LETT 308 (2). 1992. 218-224. %%%1992%%%
FULL JOURNAL NAME: FEBS (Federation of European Biochemical Societies)
Letters
CODEN: FEBLA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Brain %%%tau%%% protein is %%%phosphorylated%%% in vitro by cdc2
and MAP2 kinases, obtained through immunoaffinity purification from rat brain extracts. The %%%phosphorylation%%% sites are located on the %%%tau%%% molecule both upstream and downstream of the tubulin-binding
motifs. A synthetic peptide comprising residues 194-213 of the %%%tau%%%
sequence, which contains the epitope recognized by the %%%monoclonal%%%
antibody %%%tau%%%-1, is also efficiently %%%phosphorylated%%% in vitro
by cdc2 and MAP2 kinases. %%%Phosphorylation%%% of this peptide markedly
reduces its interaction with the antibody %%%tau%%%-1, as it has been described for %%%tau%%% protein in Alzheimer's disease. Both cdc2 and MAP2 kinases are present in brain extracts obtained from Alzheimer's disease patients. Interestingly, the level of cdc2 kinase may be increased in patient brains as compared with non-demented controls. These results suggest a role for cdc2 and MAP2 kinases in %%%phosphorylating%%%
%%%tau%%% protein at the %%%tau%%%-1 epitope in Alzheimer's disease.

4/7/10 (Item 10 from file: 5)
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08336193 BIOSIS NO.: 000094087441
BRAIN LEVELS OF MICROTUBULE-ASSOCIATED PROTEIN %%%TAU%%% ARE ELEVATED IN
ALZHEIMER'S DISEASE A RADIOIMMUNO-SLOT-BLOT ASSAY FOR NANOGRAMS OF THE
PROTEIN
AUTHOR: KHATOON S; GRUNDKE-IQBAL I; IQBAL K
AUTHOR ADDRESS: NEW YORK STATE INST. BASIC RES. DEVELOPMENTAL DISABILITIES,
1050 FOREST HILL RAOD, STATEN ISLAND N.Y. 10314.
JOURNAL: J NEUROCHEM 59 (2). 1992. 750-753. %%%1992%%%
FULL JOURNAL NAME: Journal of Neurochemistry
CODEN: JONRA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The microtubule-associated protein .%%%tau%%%., which stimulates
the assembly of .alpha.-.beta. tubulin heterodimers into microtubules, is abnormally %%%phosphorylated%%% in Alzheimer's disease (AD) brain and is
the major component of paired helical filaments. In the present study, the levels of .%%%tau%%%. and abnormally %%%phosphorylated%%% .%%%tau%%%.
were determined in brain homogenates of AD and age-matched control cases.
A radioimmuno-slot-blot assay was developed, using a primary %%%monoclonal%%% antibody, %%%Tau%%%-1, and a secondary antibody, anti-mouse 125I-immunoglobulin G. To assay the abnormally %%%phosphorylated%%% .%%%tau%%%., the blots were treated with alkaline
phosphatase before immunolabeling. The levels of total .%%%tau%%%. were
about eightfold higher in AD (7.3 .+-. 2.7 ng/.mu.g of protein) than in control cases (0.9 .+-. 0.2 ng/.mu.g), and this increase was in the form of the abnormally %%%phosphorylated%%% protein. These studies indicate that the abnormal %%%phosphorylation%%% - not a decrease in the level of
.%%%tau%%%. - is a likely cause of neurofibrillary degeneration in AD.

4/7/11 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08293779 BIOSIS NO.: 000094065077
%%%PHOSPHORYLATION%%%-DEPENDENT EPITOPES OF NEUROFILAMENT ANTIBODIES ON
%%%TAU%%% PROTEIN AND RELATIONSHIP WITH ALZHEIMER %%%TAU%%%
AUTHOR: LICHTENBERG-KRAAG B; MANDELKOW E-M; BIERNAT J; STEINER B; SCHROETER
C; GUSTKE N; MEYER H E; MANDELKOW E
AUTHOR ADDRESS: MAX-PLANK-UNIT FOR STRUCTURAL MOLECULAR BIOL., C/O DESY,
NOTKESTRASSE 85, D-2000 HAMBURG 52, WEST GERMANY.
JOURNAL: PROC NATL ACAD SCI U S A 89 (12). 1992. 5384-5388. %%%1992%%%
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have studied the %%%phosphorylation%%% of %%%tau%%% protein
from Alzheimer paired helical filaments, of %%%tau%%% from normal human
brain, and of recombinant %%%tau%%% isoforms. As a tool we used %%%monoclonal%%% antibodies against neurofilament protein that

crossreact
with %%%tau%%% in a %%%phosphorylation%%%-dependent manner. This allowed
us to deduce the state of %%%phosphorylation%%% in normal and pathological %%%tau%%%, as well as antibody epitopes. The epitope of antibody SMI33 is at the first Lys-Ser-Pro sequence motif (residues 234-236) and requires an unphosphorylated Ser-235. Antibody SMI31 binds
between Ser-396 (in the second Lys-Ser-Pro motif) and Ser-404, both of which must be %%%phosphorylated%%%. SMI34 has a conformational epitope
that depends on the interaction between regions on either side of the microtubule-binding region; it also requires %%%phosphorylation%%%. The %%%phosphorylatable%%% serines detected by the SMI antibodies are part of
Ser-Pro motifs and can be %%%phosphorylated%%% by a protein kinase activity that can be used to induce a paired helical filament-like state in human brain %%%tau%%% in vitro. The phosphates are incorporated in several stages that can be identified by antibody reactivity and gel shift. This sguggests a role for the %%%phosphorylation%%% sites in Alzheimer disease, as well as the involvement of a Ser-Pro-directed protein kinase.

4/7/12 (Item 12 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08183925 BIOSIS NO.: 000094007698
THE SWITCH OF %%%TAU%%% PROTEIN TO AN ALZHEIMER-LIKE STATE INCLUDES THE
%%%PHOSPHORYLATION%%% OF TWO SERINE PROLINE MOTIFS UPSTREAM OF THE
MICROTUBULE BINDING REGION
AUTHOR: BIERNAT J; MANDELKOW E-M; SCHROETER C; LICHTENBERG-KRAAG B; STEINER
B; BERLING B; MEYER H; MERCKEN M; VANDERMEEREN A; GOEDERT M; MANDELKOW E
AUTHOR ADDRESS: MAX-PLANCK-UNIT STRUCTURAL MOL. BIOL., C/O DESY,
NOTKESTRASSE 85, D-2000 HAMBURG 52, GER.
JOURNAL: EMBO (EUR MOL BIOL ORGAN) J 11 (4). 1992. 1593-1597. %%%1992%%%
FULL JOURNAL NAME: EMBO (European Molecular Biology Organization) Journal
CODEN: EMJOD
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The paired helical filaments (PHFs) of Alzheimer's disease consist mainly of the microtubule-associated protein %%%tau%%%. PHF %%%tau%%% differs from normal human brain %%%tau%%% in that it has a
higher Mr and a special state of %%%phosphorylation%%%. However, the protein kinase(s) involved, the %%%phosphorylation%%% sites on %%%tau%%%
and the resulting conformational changes are only poorly understood. Here we show that a new %%%monoclonal%%% antibody, AT8, records the PHF-like
state of %%%tau%%% in vitro, and we describe a kinase activity that turns normal %%%tau%%% into a PHF-like state. The epitope of AT8 is around residue 200, outside the region of internal repeats and requires the %%%phosphorylation%%% of serines 199 and/or 202. Both of these are followed by a proline, suggesting that the kinase activity belongs to the family of proline-directed kinases. The epitope of AT8 is nearly coincident with that of another %%%phosphorylation%%%-dependent antibody,
TAU1 [Binder, L.I., Frankfurter, A. and Rebhun, L. (1985) J. Cell Biol., 101, 1371-1378], but the two are complementary since TAU1 requires a dephosphorylated epitope.

4/7/13 (Item 13 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07889611 BIOSIS NO.: 000092138901
EFFECTS OF INJECTED ALZHEIMER BETA AMYLOID CORES IN RAT BRAIN
AUTHOR: FRAUTSCHY S A; BAIRD A; COLE G M
AUTHOR ADDRESS: DEP. MOL. CELLULAR GROWTH BIOL., WHITTIER INST. DIABETICS
ENDOCRINOL., 9894 GENESEE, LA JOLLA, CALIF. 92037.
JOURNAL: PROC NATL ACAD SCI U S A 88 (19). 1991. 8362-8366. %%%1991%%%
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Although amyloid deposits have long been known to accumulate in
Alzheimer disease (AD) brain, their origin and significance remain speculative. Because of the lack of an in vivo model where amyloid deposits can be induced, the relationship of the extracellular .beta.-amyloid deposits to another AD pathology has never been directly investigated. Therefore, we injected SDS-isolated amyloid cores into rat cortex and hippocampus. Similarly isolated lipofuscin fractions from control human brains were injected on the contralateral side. Rats were perfused and brains were examined immunohistochemically at 2 days, 7 days, and 1 month after injection. Alz-50, a %%%monoclonal%%% antibody against abnormally %%%phosphorylated%%% %%%tau%%% proteins, stained
neurons along the cortical needle track at 2 but not 7 days after injection of either amyloid or lipofuscin. At 1 month, however, ubiquitin, Alz-50 antigen, and silver-positive structures were observed only in response to amyloid. In 7 of 10 animals, there was considerable neuronal loss in the hippocampal layers. In each instance, these effects were in the immediate vicinity of .beta.-protein immunoreactive material. Marked neuronal loss was never observed at any time after lipofuscin injection. These results indicate a neuronal response to amyloid. When preparations of mature plaque amyloid isolated from the AD brain are injected into the rat brain, they exert neurotoxic effects and induce antigen found in the AD brain.

4/7/14 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07867990 BIOSIS NO.: 000092127356
MOLECULAR MILESTONES THAT SIGNAL AXONAL MATURATION AND THE COMMITMENT OF
HUMAN SPINAL CORD PRECURSOR CELLS TO THE NEURONAL OR GLIAL PHENOTYPE IN
DEVELOPMENT
AUTHOR: TOHYAMA T; LEE V M-Y; RORKE L B; TROJANOWSKI J Q
AUTHOR ADDRESS: DEP. PATHOLOGY, CHILDREN'S HOSP. PHILADELPHIA,
PHILADELPHIA, PA. 19104.
JOURNAL: J COMP NEUROL 310 (3). 1991. 285-299. %%%1991%%%
FULL JOURNAL NAME: Journal of Comparative Neurology
CODEN: JCNEA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Insights into the programmatic induction of neuronal and glial genes during human embryogenesis have depended largely on extrapolations of data derived from experimental mammals. However, the assumptions upon
which these extrapolations are based have not been rigorously tested. Indeed, practically no information is available even on the human counterparts if the relatively small subset of well-characterized, developmentally regulated neuron and glial specific genes of the mammalian CNS. Thus, the developmental programs upon which human neural
embryogenesis are based remain largely undeciphered. We have addressed this problem in immunohistochemical studied conducted on 22 human fetal spinal cords with gestational ages (GAs) that ranged from 6 to 40 weeks by using %%%monoclonal%%% antibodies to several classes of neuron or

glial specific polypeptides. These polypeptides included: representatives of four different types (Types I-IV) of intermediate filament proteins, i.e., vimentin filament protein (VFP), glial fibrillary acidic protein (GFAP), different phospho-isoforms of the high (NF-H), middle (NF-M), and low (NF-L) molecular weight (Mr) neurofilament (NF) subunits, both acidic and basic cytokeratin (CK) proteins; three different microtubule associated proteins (MAPs), i.e., MAP2, MAP5, and %%%tau%%%; two different synaptic or coated vesicle proteins, i.e., synaptophysin (SYP) and clathrin light chain B (LCb); an oligodendroglial specific protein, i.e., myelin basic protein (MBP); and a receptor for a CNS trophic factor, i.e., the nerve growth factor receptor (NGFR). The major findings derived from these studies may be summarized as follows: 1) the most primitive neuroepithelial cells only expressed VFP ans MAP5; 2) postmitotic, postmigratory neurons transiently expressed NGFR in the earliest development stages, while NF-H, NF-M, NF-L, MAP2, MAP5, clathrin LCb, and SYP were expressed throughout development although the time of initial onset of each of these proteins differed; for example, NF-M isoforms generally appeared before NF-L and NF-H isoforms, and the most highly %%%phosphorylated%%% NF-H variants emerged much later than NF-M; moreover, the induction of SYP in anterior horn cells followed the induction of proteins that are thought to determine neuronal polarity (e.g., NF-L, NF-M, NF-H, MAP2, %%%tau%%%); 3) GFAP positive astrocytes became evident after the appearance of many neuron specific proteins although radial glia transiently expressed VFP earlier in development; 4) MBP appeared in the cell bodies of glial cells contemporaneously with GFAP, and in the myelin sheaths of white matter well before axons acquired a fully mature complement of cytoskeletal proteins; and 5) although programmed neuron death undoubtedly occurred durring the GAs examined here, this process was not associated with presence of debris containing any of the developmentally regulaed polypeptides examined in this study. We concluded that human neurogenesis and gliogenesis in the developing spinal cord is a highly orchestrated process in which neuron specific and glial specific genes are induced in a manner quite similar to that described in previous studies of other experimental animals. However, unlike some reports on neurogenesis in rodents and birds, the acquisition of the molecular, neuronal phenotypes in the human spinal cord was exclusively a postmitotic, postmigratory series of events. Nevertheless, as in these other species, the induction of neuron specific gene products in human spinal cord neurons occurred in a step-wise, asynchronous manner. Finally, the absence of cellular debris containing any of the developmentally regulated antigens we studied here, at a time during which massive neuron death is likely to be in progress, suggests that the induction of these neuron specific genes may identify subsets of neurons destined to survive into maturity.

4/7/15 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07710219 BIOSIS NO.: 000092046000
ALTERED %%%PHOSPHORYLATION%%% OF %%%TAU%%% PROTEIN IN HEAT-SHOCKED RATS AND PATIENTS WITH ALZHEIMER DISEASE
AUTHOR: PAPASOZOMENOS S C; SU Y
AUTHOR ADDRESS: DEP. PATHOL. LAB. MED., UNIV. TEXAS MED. SCH., HOUSTON, TEX. 77030.
JOURNAL: PROC NATL ACAD SCI U S A 88 (10). 1991. 4543-4547. %%%1991%%%
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Six hours after heat shocking 2- to 3-month-old male and female Sprague-Dawley rats at 42.degree. C for 15 min, we analyzed .%%%tau%%%. protein immunoreactivity in SDS extracts of cerebrums and peripheral nerves by using immunoblot analysis and immunohistochemistry with the anti-.%%%tau%%%. %%%monoclonal%%% antibody %%%Tau%%%-1, which recognizes a phosphate-dependent non-%%%phosphorylated%%% epitope, and with 125I-labeled protein A. In the cerebral extracts, we found altered %%%phosphorylation%%% of .%%%tau%%%. in heat-shocked females, characterized by a marked reduction in the amount of nonphosphorylated . %%%tau%%%., a doubling of the ratio of total (%%%phosphorylated%%% plus nonphosphorylated) .%%%tau%%%. to nonphosphorylated .%%%tau%%%., and the appearance of the slowest moving %%%phosphorylated%%% .%%%tau%%%. polypeptide (68 kDa). Similar, but milder, changes were observed in male rats. These changes progressively increased in females from 3 to 6 h after heat shocking. In contrast, both %%%phosphorylated%%% .%%%tau%%%. and nonphosphorylated .%%%tau%%%. were reduced in peripheral nerves after heat shocking. In immunoblots of SDS extracts from Alzheimer disease-affected brain, the two slowest moving %%%phosphorylated%%% . %%%tau%%%. polypeptides (62 kDa and 66 kDa, respectively) were detected by %%%Tau%%%-1 after dephosphorylation and by %%%Tau%%%-2 (an anti-. %%%tau%%%. %%%monoclonal%%% antibody that recognizes a phosphate-independent epitope) without prior dephosphorylation only in regions that contained .%%%tau%%%. immunoreactivity in histologic preparations. In addition, quantitative immunoblot analysis of cortex and the underlying white matter with %%%Tau%%%-1 and 125I-labeled protein A showed that the amount of %%%phosphorylated%%% .%%%tau%%%. progressively increased in the Alzheimer disease-affected cerebral cortex, while concurrently a proportionally lesser amount of .%%%tau%%%. entered the white matter axons. The similar findings for the rat heat-shock model and Alzheimer disease suggest that life stressors may play a role in the etiopathogenesis of Alzheimer disease.

4/7/16 (Item 16 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07615129 BIOSIS NO.: 000091133013
%%%TAU%%% IN ALZHEIMER'S DISEASE AND DOWN'S SYNDROME IS INSOLUBLE AND ABNORMALLY %%%PHOSPHORYLATED%%%
AUTHOR: HANGER D P; BRION J-P; GALLO J-M; CAIRNS N J; LUTHERT P J; ANDERTON B H
AUTHOR ADDRESS: DEP. NEUROSCIENCE, INSTITUTE PSYCHIATRY, DE CRESPIGNY PARK, DENMARK HILL, LONDON SE5 8AF, U.K.
JOURNAL: BIOCHEM J 275 (1). 1991. 99-104. %%%1991%%%
FULL JOURNAL NAME: Biochemical Journal
CODEN: BIJOA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Some investigators have described the presence in Alzheimer's disease brain extracts of several abnormal forms of the microtubule-associated protein %%%tau%%%, based on their unusual mobility in SDS-PAGE. It has been proposed that these abnormal forms of %%%tau%%% may be the result of aberrant %%%tau%%% %%%phosphorylation%%%. In this study we show that %%%tau%%% in extracts of Alzheimer's disease brain can be separated into two fractions based upon its solubility (100,000 g .times. 1 h supernatant) in non-denaturing conditions (100 mM-Mes, pH 6.5, 0.5 mM-MgCl2, 1 mM-EGTA and 1 M-NaCl). The %%%tau%%% isoforms with decreased mobility in SDS/PAGE are predominantly in an insoluble fraction, whereas the soluble %%%tau%%% is indistinguishable by its mobility in SDS/PAGE from %%%tau%%% in soluble extracts of control

brain.
Insoluble %%%tau%%% displaying abnormal mobility on SDS/PAGE was only found in Alzheimer and adult Down's syndrome brains and was absent from the brains of age-matched controls and from fetal and infant Down's syndrome brains. There was a good correlation between the presence of insoluble %%%tau%%% in brain extracts and the abundance of neurofibrillary tangles and senile neuritic plaques. The %%%monoclonal%%% antibody %%%Tau%%%.1 stained insoluble %%%tau%%% on Western blots only after treatment of the nitrocellulose transfers with alkaline phosphatase, implying that this insoluble %%%tau%%% is in a particular state of %%%phosphorylation%%%. We conclude that, in Alzheimer's disease, a fraction of %%%tau%%% has a modified %%%phosphorylation%%% state and a decreased solubility; these modifications may precede formation of the neurofibrillary tangles characteristic of Alzheimer's disease and Down's syndrome in adults.

4/7/17 (Item 17 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07526493 BIOSIS NO.: 000091089622
ABNORMAL %%%PHOSPHORYLATION%%% OF %%%TAU%%% UBIQUITINATION IN NEUROFIBRILLARY PATHOLOGY OF ALZHEIMER DISEASE
AUTHOR: BANCHER C; GRUNDKE-IQBAL I; IQBAL K; FRIED V A; SMITH H T; WISNIEWSKI H M
AUTHOR ADDRESS: INSTITUTE BASIC RESEARCH, 1050 FOREST HILL ROAD, STATEN ISLAND, NY 10314, USA.
JOURNAL: BRAIN RES 539 (1). 1991. 11-18. %%%1991%%%
FULL JOURNAL NAME: Brain Research
CODEN: BRREA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: On tissue sections of Alzheimer brain, 4 antibodies to %%%tau%%% immunolabel not only neurofibrillary tangles, neuritic plaques and neuropil threads but also the tangle-free cytoplasm of a subset of hippocampal and cortical neurons we believe to be at a stage of alteration preceding the formation of paired helical filaments (PHF). Pretreatment of tissue sections with alkaline phosphatase leads to an increase in staining intensity and in number of immunoreactive lesions with antibodies directed to an amino terminal and to a mid-region of the %%%tau%%% molecule. The diffuse neuronal staining could not be observed with any of 7 %%%monoclonal%%% antibodies recognizing ubiquitin. We conclude (1) that abnormal %%%phosphorylation%%% of %%%tau%%% occurs prior to its incorporation into PHF and leads to its accumulation in the nerve cell body and (2) that ubiquitin is seen associated only when a neurofibrillary tangle is already formed.

4/7/18 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07430728 BIOSIS NO.: 000091036717
CYCLIC AMP AGONISTS INDUCE THE %%%PHOSPHORYLATION%%% OF PHOSPHOLIPASE C-%%%TAU%%% AND OF A 76-KDA PROTEIN CO-PRECIPITATED BY ANTI-PHOSPHOLIPASE C-%%%TAU%%% %%%MONOCLONAL%%% ANTIBODIES IN BALB-C-3T3 CELLS RELATIONSHIP TO INOSITOL PHOSPHATE FORMATION
AUTHOR: OLASHAW N E; RHEE S G; PLEDGER W J
AUTHOR ADDRESS: DEP. CELL BIOL., VANDERBILT UNIV. SCH. MED., NASHVILLE, TENN. 37232, USA.
JOURNAL: BIOCHEM J 272 (2). 1990. 297-304. %%%1990%%%
FULL JOURNAL NAME: Biochemical Journal
CODEN: BIJOA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Previous studies have demonstrated enhanced %%%phosphorylation%%% of phospholipase C-.%%%tau%%%. (PLC-.%%%tau%%%.), a key regulatory enzyme in phosphoinositide metabolism, in cells treated with platelet-derived growth factor (PDGF) and epidermal growth factor, both of which act via specific receptor tyrosine kinases. Our studies on BALB/c-3T3 cells show that agents that promote cellular cyclic AMP accumulation also increase the %%%phosphorylation%%%, specifically the serine %%%phosphorylation%%%, of this enzyme. Increased %%%phosphorylation%%% of PLC-.%%%tau%%%. (2-3-fold) was evident within 5-10 min of addition of isobutylmethylxanthine (IBMX) and either cholera toxin or forskolin to cells, and persisted for at least 3 h. Treatment of cells with cyclic AMP agonists also enhanced, with similar kinetics, the %%%phosphorylation%%% of a 76 kDa protein co-precipitated by anti-PLC-.%%%tau%%%. %%%monoclonal%%% antibodies. Brief exposure of cells to cholera toxin/IBMX or forskolin/IBMX decreased inositol phosphate formation induced by the GTP-binding protein (G-protein) activator aluminium fluoride by approx. 50%, but was without effect on PDGF-stimulated inositol phosphate formation. These findings suggest that PLC-.%%%tau%%%., and perhaps the 76 kDa co-precipitated protein, are substrates of cyclic AMP-dependent protein kinase in BALB/c-3T3 cells; however, the lack of effect of cyclic AMP elevation on PDGF-stimulated inositol phosphate formation indicates that the intrinsic activity of PLC-.%%%tau%%%. is unaltered by cyclic AMP-mediated %%%phosphorylation%%%.

4/7/19 (Item 19 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07358870 BIOSIS NO.: 000090137781
ALZ-50 RECOGNIZES A %%%PHOSPHORYLATED%%% EPITOPE OF %%%TAU%%% PROTEIN
AUTHOR: UEDA K; MASLIAH E; SAITOH T; BAKALIS S L; SCOBLE H; KOSIK K S
AUTHOR ADDRESS: DEP. NEUROSCIENCES, SCHOOL MEDICINE, UNIVERSITY CALIFORNIA AT SAN DIEGO, LA JOLLA, CALIF. 92093.
JOURNAL: J NEUROSCI 10 (10). 1990. 3295-3304. %%%1990%%%
FULL JOURNAL NAME: Journal of Neuroscience
CODEN: JNRSD
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Alz-50 is a %%%monoclonal%%% antibody that detects antigens enriched in the brain tissue of Alzheimer's disease (AD) patients. Although Alz-50 recognizes .%%%tau%%%., an identified integral constituent of the AD paired helical filament (PHF), the exact nature of the antigenic site is unknown. An immunoblot analysis demonstrated that the antigenic sites to Alz-50 are diminished by acid phosphatase treatment. Consistent with this finding, Alz-50 antigens were more concentrated in brain homogenates prepared with phosphatase inhibitors. The epitope in .%%%tau%%%. with which Alz-50 reacts is located in the carboxy terminus within a 14-amino acid region from just beyond the microtubule-binding repeats to the carboxy terminus. An isolated carboxy-terminal chymotryptic peptide from bovine brain .%%%tau%%%.-reactive with Alz-50 was analyzed by fast-atom-bombardment mass spectroscopy (FAB-MS) and was found to be present as both a monophosphopeptide and a nonphosphorylated peptide. The immunohistological analysis has demonstrated that Alz-50 staining of neurofibrillary tangles (NFTs) is sensitive to acid phosphatase but not to alkaline phosphatase. Furthermore, Alz-50 staining of NFTs was effectively adsorbed by a high concentration of phosphoserine but not by serine or phosphothreonine. These results strongly suggest that Alz-50 recognizes a %%%phosphorylated%%% epitope in the carboxy terminus of .%%%tau%%%. which has not been previously detected by using alkaline

phosphatase. The strong Alz-50 staining in AD samples may represent another association between a %%%phosphorylation%%% state and neurofibrillary lesions. As a marker of the inchoate tangle-bearing neuron, the characterization of the Alz-50 epitope in .%%%tau%%%. offers
a partial molecular basis for the modifications that contribute to the assembly of PHFs.

4/7/20 (Item 20 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07298210 BIOSIS NO.: 000090078097
PATHOLOGICAL PROTEINS %%%TAU%%% 64 AND 69 ARE SPECIFICALLY EXPRESSED IN THE
SOMATODENDRITIC DOMAIN OF THE DEGENERATING CORTICAL NEURONS DURING
ALZHEIMER'S DISEASE DEMONSTRATION WITH A PANEL OF ANTIBODIES AGAINST
%%%TAU%%% PROTEINS
AUTHOR: DELACOURTE A; FLAMENT S; DIBE E M; HUBLAU P; SABLONNIERE B; HEMON B
; SHERRER V; DEFOSSEZ A
AUTHOR ADDRESS: A.D.E.R.M.A., UNITE INSERM 156, FAC. MED. LILLE, F-59045
LILLE CEDEX, FR.
JOURNAL: ACTA NEUROPATHOL 80 (2). 1990. 111-117. %%%1990%%%
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Bundles of paired helical filaments (PHF) accumulate in the pyramidal neurons that degenerate during Alzheimer's disease. This neurofibrillary degeneration is highly correlated with clinical signs of dementia. During this degeneration process, %%%Tau%%% proteins, which are
the major antigenic components of PHF, are abnormally %%%phosphorylated%%% and two pathological isoforms named %%%Tau%%% 64 and
69 are expressed. We have studied their immunoblot distribution in the cortical gray and white matter from different reginons of normal and Alzheimer brains, to determine if the degenerating process preferentially affects the somatodendritic or the axonal domain. Two categories of antibodies were used. The first category consisted of anti-human native %%%Tau%%%, anti-%%%Tau%%% proteins from different vertebrates, anti-PHF,
%%%monoclonal%%% antibody Alz-50 and an anti-C terminal repeated region
of %%%Tau%%%. In control brains, these antibodies strongly detected normal %%%Tau%%% proteins in the gray matter while %%%Tau%%% immunodetection was weak in the white matter. In Alzheimer brain cortices, each antibody detected %%%Tau%%% 64 and 69 in gray matter extracts but not at all in white matter extracts. The second category of anti-%%%Tau%%% consisted of the anti-PHF saturated with normal brain protein extracts. This antiserum only probed the abnormally %%%phosphorylated%%% %%%Tau%%% proteins. It detected %%%Tau%%% 64 and 69
exclusively in the cortical gray matter of Alzheimer brains. Moreover, a 55-kDa %%%Tau%%% protein was also immunolabelled, which might be an intermediary form between normal %%%Tau%%% and %%%Tau%%% 64 and 69. Our
results demonstrate that %%%Tau%%% proteins are normal and major components of the somatodendritic domain and that %%%Tau%%% pathology,
reflected by the presence of %%%Tau%%% 64 and 69, affects preferentially
this domain during Alzheimer's disease.

4/7/21 (Item 21 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07226418 BIOSIS NO.: 000090006280
IMMUNOCYTOCHEMICAL AND ULTRASTRUCTURAL STUDIES OF PICK'S DISEASE
AUTHOR: MURAYAMA S; MORI H; IHARA Y; TOMONAGA M
AUTHOR ADDRESS: DIV. NEUROPATHOL., DEP. PATHOL. CB NO. 7525, BRINKHOUS-BULLITT BUILDING NO. 409, UNIV. N.C. 27599-7525.
JOURNAL: ANN NEUROL 27 (4). 1990. 394-405. %%%1990%%%
FULL JOURNAL NAME: Annals of Neurology
CODEN: ANNED
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Cerebral cortical changes in 10 cases with Pick's disease were studied immunocytochemically and ultrastructurally. All cases contained Pick's argentophilic bodies and ballooned neurons. The antibodies against %%%phosphorylated%%% %%%tau%%% proteins that intensely stained all Pick
bodies recognized numerous neuronal processes around Pick body-bearing cells and focal portions in the perikarya of ballooned neurons. %%%Monoclonal%%% and polyclonal anti-ubiquitin antibodies stained not only some Pick bodies consisted of accumulation of randomly oriented, approximately 15-nm straight filaments and paired twisted profiles with a minimal diameter of 13 nm, maximal diameter of 26 nm, and twist periodicity of 120 nm. These Pick body-type filaments were also observed in the perikarya of ballooned neurons and neuronal processes around Pick body-bearing cells. Our studies demonstrate, for the first time, the characteristic pathological feature of neuropil in Pick's disease. Pick body-bearing cells and ballooned neurons show unique immunocytochemical and ultrastructural properties that may be a clue to the pathogenesis of Pick's disease.

4/7/22 (Item 22 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07038474 BIOSIS NO.: 000089120029
ALZHEIMER DISEASE PROTEINS A68 SHARE EPITOPES WITH %%%TAU%%% BUT SHOW
DISTINCT BIOCHEMICAL PROPERTIES
AUTHOR: KSIEZAK-REDING H; BINDER L I; YEN S-H
AUTHOR ADDRESS: DEP. PATHOL., ALBERT EINSTEIN COLL. MED., 1300 MORRIS PARK
AVE., BRONX, N.Y. 10461.
JOURNAL: J NEUROSCI RES 25 (3). 1990. 420-430. %%%1990%%%
FULL JOURNAL NAME: Journal of Neuroscience Research
CODEN: JNRED
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Alz 50, a %%%monoclonal%%% antibody raised against Alzheimer
brain homogenate, reacts with neurofibrillary tangles,
microtubule-associated proteins %%%tau%%%, and Alzheimer brain proteins
of molecular weight 70-60 kDa (A68). To study the relationship between A68 and normal human %%%tau%%% we compared the biochemical properties of
these proteins and tested the reactivity of A68 with eight antibodies (Alz 50, %%%Tau%%% 60, %%%Tau%%%-2, %%%Tau%%% 14, %%%Tau%%%-1, Ab 636.7,
NP14, %%%Tau%%% 46) that bind to various regions of %%%tau%%% molecule.
On Western blots, all %%%tau%%%-reactive antibodies, except %%%Tau%%%-1,
recognized A68. Pretreatment with alkaline phosphatase was required for the %%%Tau%%%-1 binding to A68. A68 consisted of three polypeptides of
68, 64, and 60 kDa, while %%%tau%%% contained 4-6 polypeptides of 50-65
kDa. A68 was less heterogenous than %%%tau%%% in the number of pI variants on two-dimensional gels. All A68 variants were more acidic (pI 5.5-6.5) than human %%%tau%%% (pI 6.5-8.5). Phosphatase treatment had only a minor effect on the pI and mobility of A68. Limited proteolysis of A68 with trypsin or chymotrypsin generated large fragments of 56-66 kDa (chymotrypsin) and 40-45 kDa (trypsin). While none of the fragments was recognized by Alz 50, the chymotryptic fragments were reactive with all

the other %%%tau%%% antibodies, and the tryptic fragments were positive
with five of the antibodies (%%%Tau%%% 14, %%%Tau%%%-1, Ab 636.7, NP14,
and %%%Tau%%% 46). The peptide maps of A68 differed from that of %%%tau%%% in the number and the size of the peptide fragments. The differences in biochemical properties of these proteins and the sharing multiple epitopes suggest that A68 is a modified form of %%%tau%%%. The
modification in part may be due to %%%phosphorylation%%%, although other
changes rendering different isoelectrical properties and susceptibility to proteases need to be considered. The removal of the Alz 50 epitope by a cleavage of a 2-3 kDa fragment which does not contain the most C-terminal epitope (%%%Tau%%% 46) indicates that the Alz 50 epitope is located at the N-terminal periphery of the A68 molecule.

4/7/23 (Item 23 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06994695 BIOSIS NO.: 000089095959
IMMUNOCYTOCHEMICAL AND ULTRASTRUCTURAL STUDIES OF LOWER MOTOR NEURONS IN
AMYOTROPHIC LATERAL SCLEROSIS
AUTHOR: MURAYAMA S; MORI H; IHARA Y; BOULDIN T W; SUZUKI K; TOMONAGA M
AUTHOR ADDRESS: DEP. PATHOL., UNIV. N.C. CHAPEL HILL, CB 7525, BRINKHOUS-BULLITT BUILD. 409, CHAPEL HILL, N.C. 27599-7525.
JOURNAL: ANN NEUROL 27 (2). 1990. 137-148. %%%1990%%%
FULL JOURNAL NAME: Annals of Neurology
CODEN: ANNED
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Neuronal inclusions in lower motor neurons in 23 cases of adult-onset sporadic amyotrophic lateral sclerosis were studied immunocytochemically and ultrastructurally. %%%Monoclonal%%% and polyclonal antiubiquitin antibodies recognized four structures in the neuronal perikarya: (1) all Lewy body-like inclusions in 6 cases with a relatively short clinical course, (2) a small percentage of Bunina bodies in 4 cases with abundant Bunina bodies, (3) ill-defined structures closely associated with Bunina bodies (Bunina body-related structures) in 15 cases, and (4) a focally aggregated meshwork of fine filamentous structures not associated with Bunina bodies in all cases. These four structures were not recognized by the antibodies raised against cytoskeletal proteins (neurofilament, tubulin, microtubule-associated protein 2, and %%%phosphorylated%%% %%%tau%%%). Electron microscopy
revealed Lewy body-like inclusions to be accumulations of randomly oriented filaments, approximately 15 nm in diameter, covered by fine granules. Bundles of coated filaments 12 nm in diameter that sometimes formed Bunina body-like structures were also observed in the perikarya. Immunoelectron microscopy showed the reaction product with antiubiquitin to be on the filaments, 15 nm in diameter, of Lewy body-like inclusions. Our study revealed the existence of two types of filaments in lower motor neurons of patients with amyotrophic lateral sclerosis: (1) ubiquitin-positive, granule-associated filaments, approximately 15 nm in diameter, that form Lewy body-like inclusions; and (2) 12 nm coated filaments that may be a candidate for another ubiquitin-positive structure and possibly a precursor or Bunina bodies. These two types of filaments may represent early pathological changes of lower motor neurons in amyotrophic lateral sclerosis.

4/7/24 (Item 24 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06951929 BIOSIS NO.: 000089073934
INCREASED MICROTUBULE ASSEMBLY IN BOVINE BRAIN TUBULIN LACKING THE TYPE III
ISOTYPE OF BETA TUBULIN
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AUTHOR ADDRESS: DEP. BIOCHEMISTRY, UNIV. TEXAS HEALTH SCI. CENTER, SAN
ANTONIO, TEXAS 78284.
JOURNAL: J BIOL CHEM 265 (3). 1990. 1794-1799. %%%1990%%%
FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Tubulin, the major constituent protein of microtubules, is a heterodimer of .alpha. and .beta. subunits. Both .alpha. and .beta. exist in multiple isotypic forms. It is not clear if different isotypes perform different functions. In order to approach this question, we have made a %%%monoclonal%%% antibody specific for the .beta.III isotype of tubulin. This particular isotype is neuron-specific and appears to be %%%phosphorylated%%% near the C terminus. We have used immunoaffinity
depletion chromatography to prepare tubulin lacking the .beta.III subunit. We find that removal of the .beta.III isotype results in a tubulin mixture able to assemble much more rapidly than is unfractionated tubulin when reconstituted with eithe of the two microtubule-associated proteins (MAPs), %%%tau%%% or MAP 2. Our results suggest that the different isotypes of tubulin differ from each other in their ability to polymerize into microtubules. We have also found that the anti-.beta.III antibody can stimulate microtubule assembly when reconstituted with tubulin and either %%%tau%%% or MAP 2. When reconstituted with tubulin
lacking the .beta.III isotype, the antibody causes the tubulin to polymerize into a polymer that is a microtubule in the presence of MAP 2 and a ribbon in the presence of %%%tau%%%.

4/7/25 (Item 25 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06927455 BIOSIS NO.: 000089060848
MOLECULAR MARKERS OF PRIMITIVE NEUROECTODERMAL TUMORS AND OTHER PEDIATRIC
CENTRAL NERVOUS SYSTEM TUMORS %%%MONOCLONAL%%% ANTIBODIES TO NEURONAL AND
GLIAL ANTIGENS DISTINGUISH SUBSETS OF PRIMITIVE NEUROECTODERMAL TUMORS
AUTHOR: MOLENAAR W M; JANSSON D S; GOULD V E; RORKE L B; FRANKE W W; LEE V
M-Y; PACKER R J; TROJANOWSKI J Q
AUTHOR ADDRESS: DEP. PATHOL. LAB. MED., MED. PATHOL. SECT., DIV. ANATOMIC
PATHOL., UNIV. PA. HOSP., BASEMENT MALONEY A009, 34TH AND SPRUCE ST.,
PHILADELPHIA, PA. 19104-4283.
JOURNAL: LAB INVEST 61 (6). 1989. 635-643. %%%1989%%%
FULL JOURNAL NAME: Laboratory Investigation
CODEN: LAINA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Seventy-one tumors of the central nervous system in children were
studied immunohistiologically. Thirty-seven were classified histologically as PNETs, of which 35 were located in the cerebellum (medulloblastomas), one in the cerebrum, and one in the spinal cord. The 34 non-PNETs included five ependymomas, seven gangliogliomas, 15 astrocytomas, and seven tumors of other histology. We used %%%monoclonal%%% antibodies specific for neurofilament (NF) triplet proteins, for microtubule associated protein 2 and .%%%tau%%%. protein and for glial fibrillary acidic protein (GFAP) and myelin basic protein. In addition, a %%%monoclonal%%% antibody to epithelial membrane antigen
was applied. The presence or absence of these antigens defined four major groups of PNETs:1) PNETs not otherwise specified (10 cases), 2) PNETs with neuronal differentiation (eight cases), 3) PNETs with astrocytic differentiation (six cases), and 4) PNETs with both neuronal and astrocytic differentiation (12 cases). One case showed ependymal differentiation. The pattern of expression of NF isoforms in PNETs was reminiscent of that seen during normal mammalian development, such that %%%phosphorylated%%% NF-H was only present in combination with NF-N

and
NF-L. Among the other central nervous system tumors, all astrocytomas and
ganglioglomas were positive for GFAP, and the ganglioglomas also expressed all NF isoforms. Three atypical teratoid tumors and two rhabdoid tumors showed strong positivity for epithelial membrane antigen and also for GFAP. We conclude that the differentiation antigens described here serve to distinguish PNETs from other pediatric central nervous system tumors and to identify subsets of PNETs. Accordingly, PNETs represent a heterogeneous group of pediatric brain tumors capable of neuronal and glial differentiation.

4/7/26 (Item 26 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06885544 BIOSIS NO.: 000089039472
AN IMMUNOHISTOCHEMICAL STUDY OF NEUROPEPTIDES AND NEURONAL CYTOSKELETAL
PROTEINS IN THE NEUROEPITHELIAL COMPONENT OF A SPONTANEOUS MURINE OVARIAN
TERATOMA PRIMITIVE NEUROEPITHELIUM DISPLAYS IMMUNOREACTIVITY FOR
NEUROPEPTIDES AND NEURON-ASSOCIATED BETA TUBULIN ISOTYPE
AUTHOR: CACCAMO D V; HERMAN M M; FRANKFURTER A; KATSETOS C S; COLLINS V P;
RUBINSTEIN L J
AUTHOR ADDRESS: DIV. NEUROPATHOL., DEP. PATHOL., UNIV. VA. SCH. MED.,
CHARLOTTESVILLE, VA. 22908.
JOURNAL: AM J PATHOL 135 (5). 1989. 801-814. %%%1989%%%
FULL JOURNAL NAME: American Journal of Pathology
CODEN: AJPAA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Approximately one thrid of the female mice of the LTXBO strain
develop spontaneous ovarian teratomas. These tumors contain a large neuroepithelial component, which includes primitive neural structures resembling embryonic neural tubes (medulloepithelial rosettes), ependymoblastic and ependymal rosettes, neuroblasts, mature ganglionic neurons, myelinated neurites, and astrocytes. The purpose of this study was to characterize these tumors according to the immunohistochemical location of some well-characterized trophic and regulatory neuropeptides and neurotransmitters, several neuronal-associated cytoskeletal proteins, and other proteins indicative of neuronal and glial differentiation. Medulloepithelial rosettes showed focal serotonin-like opioid peptide-like and .gamma.-amino butyric acid-like immunoreactivity, and displayed immunostaining for the neuron-associated class III .beta.-tubulin isotype. The mature ganglion cells were also immunoreactive for these markers, and, in addition, for somatostatin, cholecystokinin, bombesin, glucagon, vasoactive intestinal peptide, and neuropeptide Y. Mature ganglion cells were also immunoreactive for proteins associated with the neuronal cytoskeleton (including microtubule-associated proteins, MAP2 and %%%tau%%%, and higher molecular
weight %%%phosphorylated%%% and non-%%%phosphorylated%%% neurofilament
subunits), neuron-specific enolase, and synaptophysin. Undifferentiated stem cells, ependymoblastic and ependymal rosettes, and astroglia all stained with a %%%monoclonal%%% antibody that recognizes all mammalian .beta.-tubulin isotypes, but did not react with antibodies to neuronal-associated cytoskeletal proteins or neuropeptides. Neuropeptide-like immunoreactivity and demonstration of the class III .beta.-tubulin isotype indicate early neuronal commitment in neoplastic primitive neuroepithelium. These patterns of immunoreactivity closely follow those encountered in the normal neurocytogenesis of the mammalian and avian forebrain, and increase the precision with which the early stages of progressive neuroepithelial differentiation can be analyzed in human embryonal tumors of the CNS.

4/7/27 (Item 27 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06867202 BIOSIS NO.: 000089016793
ABNORMAL PROCESSING OF MULTIPLE PROTEINS IN ALZHEIMER DISEASE
AUTHOR: ZHANG H; STERNBERGER N H; RUBINSTEIN L J; HERMAN M M; BINDER L I;
STERNBERGER L A
AUTHOR ADDRESS: DEP. NEUROL., UNIV. MARYLAND SCH. MED., BALTIMORE, MD.
21201.
JOURNAL: PROC NATL ACAD SCI U S A 86 (20). 1989. 8045-8049. %%%1989%%%
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Cerebrovascular amyloid is the main constituent of the perivascular and neuritic plaques typical of Alzheimer disease, whereas neurofilaments and microtubule-associated %%%tau%%% protein have been considered primary contributors to the formation of the characteristic Alzheimer tangles. Plaques and tangles and their constituents have at times been ascribed a role in pathogenesis of the disease. Normally, neurofilaments become %%%phosphorylated%%% only upon axonal entry. In many neurologic disorders, neurofilament %%%phosphorylation%%%, as detected by any of the available %%%monoclonal%%% antibodies (mAbs) to neurofilament %%%phosphorylated%%% epitopes is shifted from an axonal to
a cell-body location. An exception is provided by Alzheimer disease, where tangles (which are neuronal cell-body-derived structures) exhibit only one %%%phosphorylated%%% epitope. However, the very presence of neurofilaments in tangles and plaques has been questioned because of a reported cross-reaction of mAbs to %%%phosphorylated%%% neurofilaments
with %%%tau%%% protein. On reinvestigating this cross-reactivity we found
that four of five mAbs to %%%phosphorylated%%% neurofilaments and four of
five mAbs to nonphosphorylated neurofilaments failed to react with %%%tau%%% protein. A fifth %%%mAb%%% (07-5) to %%%phosphorylated%%%
neurofilament cross-reacted with partially denatured %%%tau%%% protein at
an affinity 1/1700th of that for denatured neurofilaments; nondenatured %%%tau%%% protein in tissue sections did not cross-react. A fifth %%%mAb%%% (02-40) to nonphosphorylated neurofilament also cross-reacted
weakly. In Alzheimer disease normal-appearing axons were revealed with all the mAbs to %%%phosphorylated%%% neurofilaments, but tangles were revealed with only one of them (%%%mAb%%% 07-5). %%%mAb%%% to %%%tau%%%
protein did not stain or did so indistinctly. Four of five mAbs to nonphosphorylated neurofilaments failed to reveal axons. Upon dephosphorylation of tissue, staining by mAbs to %%%phosphorylated%%% neurofilaments disappeared, and axons were revealed with the %%%mAb%%% to
%%%tau%%% protein and all mAbs to the nonphosphorylated neurofilaments.
Tangles became stained with %%%tau%%% %%%mAb%%% and one %%%mAb%%% to the
nonphosphorylated neurofilaments (%%%mAb%%% 10-1). Quantitative evaluation of immunocytochemical staining intensities and immunoblot cross-reactivity showed that neurofilaments are, indeed, constituents of tangles-apparently exceeding the concentration of %%%tau%%% protein 17-fold. Contribution of both conformation and primary structure to IgG specificity may explain the lack of any cross-reaction of mAbs to neurofilaments with %%%tau%%% protein in intact tissue and the appearance
of cross-reaction in immunoblots where conformation specificity may be largely lost. The present data extend earlier findings of abnormal processing of neurofilaments and %%%tau%%% protein in Alzheimer disease

and, together with reported abnormal processing of cerebrovascular amyloid .beta.-protein, suggest that inhibition of the processing of multiple proteins is basic to the pathogenesis of Alzheimer disease, whereas formation of plaques and tangles could be merely the most striking histologic results.

4/7/28 (Item 28 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06778057 BIOSIS NO.: 000088087494
IDENTIFICATION AND LOCALIZATION OF A %%%TAU%%% PEPTIDE TO PAIRED HELICAL
FILAMENTS OF ALZHEIMER DISEASE
AUTHOR: IQBAL K; GRUNDKE-IQBAL I; SMITH A J; GEORGE L; TUNG Y-C; ZAIDI T
AUTHOR ADDRESS: NEW YORK STATE INST. BASIC RES. DEVELOPMENTAL DISABILITIES,
1050 FOREST HILL RD., STATEN ISLAND, N.Y. 10314.
JOURNAL: PROC NATL ACAD SCI U S A 86 (14). 1989. 5646-5650. %%%1989%%%
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Amino acid sequencing of a CNBr digest of the .%%%tau%%%. protein
isolated from bovine brain revealed an amino acid sequence of 17 residues,
Pro-Gly-Leu-Lys-Glu-Ser-Pro-Leu-Gln-Ile-Gly-Ala-Ala-Pro-Gly-Leu-Lys, which we call peptide I, with heterogeneity at position 11 of glycine (peptide Ia) and proline (peptide Ib); peptide I showed no homology with the previously reported cDNA-derived mouse and human .%%%tau%%%. sequences. Antisera raised to synthetic peptides corresponding to peptides Ia and Ib labeled all the bovine .%%%tau%%%. polypeptides recognized by other %%%monoclonal%%% and polyclonal antibodies to bovine
.%%%tau%%%.. Antisera to peptide Ib did not label any mouse .%%%tau%%%.
polypeptides; however, an anti-Ia antiserum labeled two of the four mouse .%%%tau%%%. polypeptides. Antisera to both peptides labeled paired helical filaments (PHF) as neurofibrillary tangles, plaque neurites, and neuropil threads in Alzheimer disease brain and PHF polypeptides on immunoblots. Immunostaining with anti-Ia antisera of PHF in tissue sections and PHF polypeptides, but not bovine .%%%tau%%%., on immunoblots
was markedly increased when pretreated with alkaline phosphatase. These studies suggest that (i) the amino acid sequences of some isoforms of . %%%tau%%%. peptide might be different from that predicted from cDNAs,
(ii) a .%%%tau%%%. peptide that is absent in the predicted sequences is present in PHF in Alzheimer disease, and (iii) .%%%tau%%%. in PHF is abnormally %%%phosphorylated%%%.

4/7/29 (Item 29 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06743025 BIOSIS NO.: 000088052455
BIOCHEMISTRY OF PAIRED HELICAL FILAMENTS PHF
AUTHOR: IHARA Y
AUTHOR ADDRESS: TOKYO METROPOLITAN INST. GERONTOL., JPN.
JOURNAL: JPN J GERIATR 25 (4). 1988. 364-367. %%%1988%%%
FULL JOURNAL NAME: Japanese Journal of Geriatrics
CODEN: NIRZA
RECORD TYPE: Abstract
LANGUAGE: JAPANESE

ABSTRACT: Since 1980, the nature of PHF has been heavily focused in several
laboratories. The most unexpected observation was that PHF are insoluble in harsh denaturants or detergents including SDS, urea and guanidine HCl. This unusual insolubility of PHF made possible high grade purification of PHF, but prevented the application of analytical biochemical methods to the identification of the PHF components. Therefore, we took an immunochemical approach using specific antibodies to PHF, which were prepared by immunization of purified PHF. Our strategy was to search for soluble polypeptides reactive with antiPHF, instead of analyzing PHF directly. Polyclonal antibodies to PHF were found to label %%%tau%%%, a neuron-specific microtubule-associated phosphoprotein. The analysis of PHF antisera showed that there are two populations of %%%tau%%% antibodies; one is reactive with both %%%phosphorylated%%% and nonphosphorylated forms of %%%tau%%%, the other is specific for %%%phosphorylated%%% %%%tau%%%. In addition, antibodies specific for
nonphosphorylated %%%tau%%% could not be detected in the PHF antisera.
From these observations, one of the antigenic determinants of PHF has been considered as %%%phosphorylated%%% %%%tau%%%. A hybridoma producing
a %%%monoclonal%%% antibody to PHF (DF2) was obtained by the fusion of
mouse myeloma cells and rat spleen cells immunized with PHF. DF2 was confirmed to specifically bind to PHF. In the blot of the soluble fraction of brain homogenates, DF2 labeled a small polypeptide Mr .apprx. 5 kD, which was identified as ubiquitin by its purification and subsequent protein sequencing. Moreover, five ubiquitin fragments were identified in the PHF digest. Thus ubiquitin is a component of PHF. Two components, %%%tau%%% and ubiquitin, have been identified in PHF immunochemically and protein chemically, respectively. Two lines of evidence suggest that PHF contain the components other than %%%tau%%% or
ubiquitin: first, ghost tangles (extracellular tangles) are not stained with antiPHF or %%%tau%%% antibodies, although they appear to be made of
PHF. Second, the staining activity of antiPHF cannot be absorbed out with excess amount of %%%tau%%%. These strongly suggest that PHF contain as-yet-unidentified components.

4/7/30 (Item 30 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06675461 BIOSIS NO.: 000087117638
SENILE PLAQUE NEURITES FAIL TO DEMONSTRATE ANTI-PAIRED HELICAL FILAMENT AND
ANTI-MICROTUBULE-ASSOCIATED PROTEIN-%%%TAU%%% IMMUNOREACTIVE PROTEINS IN
THE ABSENCE OF NEUROFIBRILLARY TANGLES IN THE NEOCORTEX
AUTHOR: PROBST A; ANDERTON B H; BRION J-P; ULRICH J
AUTHOR ADDRESS: DEP. PATHOL., DIV. NEUROPATHOL., UNIV. BASEL, SWITZERLAND.
JOURNAL: ACTA NEUROPATHOL 77 (4). 1989. 430-436. %%%1989%%%
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Although much work has been directed recently towards unravelling
the protein chemistry of neurofibrillary tangle (NFT) and senile plaque (SP) components in Alzheimer's disease, the pathogeneses of these lesions remains largely unknown and the problem of their relationship is unresolved. In particular, although paired helical filaments (PHF) have long been documented in SP neurites, we do not know if they are of pathogenetic relevance for the formation of the SP. To investigate the relationship between NFT and SP, we examined antigenic properties of proteins in SP neurites in neocortical tissues of patients with senile dementia of Alzheimer type, in the presence or absence of NFT in the same cortical area. We used two polyclonal antibodies directed against PHF and microtubule-associated protein (MAP)-%%%tau%%% and three %%%monoclonal%%%
antibodies (MAbs) (RT97, BF10, 147) to %%%phosphorylated%%% epitopes of
human neurofilament polypeptides, as well as the Gallyas silver impregnation method which specifically stains PHF in NFT and neurites.

The main finding of our investigations consists in a differential pattern of immunoreactivity of SP neurites depending on the presence or absence of NFT in the neocortex. In the presence of NFT, there were numerous neuropil threads and SP neurites containing Gallyas-positive, as well as anti-PHF- and anti-%%%tau%%%-labelled material. In the absence of NFT in the neocortex there was a striking absence of any GAllyas-positive or PHF- and %%%tau%%%-immunoreactive structure in the cortical neuropil and in SP neurites, irrespective of the maturation stage of the SP. In contrast with these results, the number of neurites labelled by MAbs RT97, BF10 and 147 in SP and in the neuropil was apparently unaffected by the presence or absence of NFT. Amyloid in SP, remained consistently unstained by all antibodies of the panel as well as by the Gallyas stain. Our findings indicate that PHF and %%%tau%%% polypeptides are facultative components of SP neurites and suggest that the development of SP may occur independently of PHF pathology in neocortical neurons.

4/7/31 (Item 31 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06664050 BIOSIS NO.: 000087106227
IMMUNOCYTOCHEMICAL CHARACTERIZATION OF NEUROFIBRILLARY TANGLES IN AMYOTROPIC LATERAL SCLEROSIS AND PARKINSONISM-DEMENTIA OF GUAM WEST PACIFIC OCEAN
AUTHOR: SHANKAR S K; YANAGIHARA R; GARRUTO R M; GRUNDKE-IQBAL I; KOSIK K S; GAJDUSEK D C
AUTHOR ADDRESS: NATL. INST. HEALTH, BUILD. 36, ROOM 5B-21, BETHESDA, MD 20892.
JOURNAL: ANN NEUROL 25 (2). 1989. 146-151. %%%1989%%%
FULL JOURNAL NAME: Annals of Neurology
CODEN: ANNED
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Cryostat-cut sections of formalin-fixed and unfixed hippocampus from 23 Guamanian Chamorros with clinically and neuropathologically verified amyotrophic lateral sclerosis (ALS) (8 cases) and parkinsonism-dementia (PD) (15 cases) and from 12 neurologically normal Guamanians (5 with and 7 without neurofibrillary degeneration) were evaluated by the immunoperoxidase technique, using %%%monoclonal%%% antibodies against %%%phosphorylated%%% neurofilament, human fetal microtubule-associated protein %%%tau%%%, and paired helical filaments. On immunostaining, all three antibodies showed intracellular tangles in the hippocampal neurons of patients with ALS, patients with PD, and in neurologically normal Guamanians with neurofibrillary pathology, but the correlation of immunostaining between these antibodies was not absolute. Extracellular or ghost tangles were immunostained only with the antibody against paired helical filaments. Our immunocytochemical data indicate that the antigenic composition of neurofibrillary tangles in Guamanian ALS and PD is similar to that of Alzheimer's disease, suggesting a common pathogenetic pathway for neurofibrillary tangle formation in these neurodegenerative disorders.

4/7/32 (Item 32 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06644905 BIOSIS NO.: 000087087082
ACCUMULATION OF ABNORMALLY %%%PHOSPHORYLATED%%% %%%TAU%%% PRECEDES THE FORMATION OF NEUROFIBRILLARY TANGLES IN ALZHEIMER'S DISEASE
AUTHOR: BANCHER C; BRUNNER C; LASSMANN H; BUDKA H; JELLINGER K; WICHE G; SEITELBERGER F; GRUNDKE-IQBAL I; IQBAL K; WISNIEWSKI H M
AUTHOR ADDRESS: INST. BASIC RES. DEVELOPMENTAL DISABILITIES, 1050 FOREST HILL RD., STATEN ISLAND, N.Y. 10314, USA.
JOURNAL: BRAIN RES 477 (1-2). 1989. 90-99. %%%1989%%%
FULL JOURNAL NAME: Brain Research
CODEN: BRREA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The intraneuronal accumulation of paired helical filaments in the form of neurofibrillary tangles is one hallmark of the brain pathology in Alzheimer's disease. At certain predilection sites, a small number of similar lesions are also present in the brains of the majority of aged non-demented individuals. As suggested by several studies before, these abnormal cytoskeletal structures contain determinants of microtubule-associated protein .%%%tau%%%. and ubiquitin. The present study uses a morphological classification of neurofibrillary tangles into different stages of maturation, as suggested by Alzheimer in 1911, and shows by quantitative immunocytochemistry that early stages of neurofibrillary degeneration contain abnormally %%%phosphorylated%%% . %%%tau%%%.. Immunoreactivity for the altered .%%%tau%%%. is seen not only in tangles but also in the cytoplasm of some nerve cells lacking neurons without tangles are present in age-matched non-demented individuals as in Alzheimer cases, but are absent in young controls. In contrast, incorporation of an epitope, recognized by a %%%monoclonal%%% antibody (3-39) raised to paired helical filaments, which is directed against a determinant residing in the 50-65 amino acid residue region of ubiquitin occurs late in the process of tangle maturation and is most pronounced in extracellular 'ghost tangles'. It is suggested that the accumulation of abnormally %%%phosphorylated%%% .%%%tau%%%. is one of the earliest cytoskeletal changes in the process of tangle formation. Exposure of certain ubiquitin epitopes in the pathological fibers may reflect an unsuccessful attempt of proteolytic degradation.

4/7/33 (Item 33 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06631242 BIOSIS NO.: 000087073404
PROGRESSIVE SUPRANUCLEAR PALSY EXTENSIVE NEUROPIL THREADS IN ADDITION TO NEUROFIBRILLARY TANGLES VERY SIMILAR ANTIGENICITY OF SUBCORTICAL NEURONAL PATHOLOGY IN PROGRESSIVE SUPRANUCLEAR PALSY AND ALZHEIMER'S DISEASE
AUTHOR: PROBST A; LANGUI D; LAUTENSCHLAGER C; ULRICH J; BRION J P; ANDERTON B H
AUTHOR ADDRESS: DEP NEUROPATHOL., INST. PATHOL., UNIV. BASEL, SCHOEBEINSTRASSE 40, CH-4003 BASEL, SWITZ.
JOURNAL: ACTA NEUROPATHOL 77 (1). 1988. 61-68. %%%1988%%%
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Light microscopic immunohistochemical investigations were performed on neurofibrillary tangles (NFT) in four histologically confirmed cases of Alzheimer's disease (AD) and in five patients with a progressive supranuclear palsy (PSP). The antibody panel included antisera to the neuronal mirotubule-associated protein, %%%tau%%%, and to isolated paired helical filaments (PHF), as well as mouse %%%monoclonal%%% antibodies (MAbs) to %%%phosphorylated%%% epitopes on high and medium molecular weight neurofilament subunits (RT97 and BF10, respectively). Paraffin sections were also impregnated with the Gallyas silver method, which specifically stains tangles and cortical neuropil threads in AD, but does not stain normal neurofilaments. All tangles in PSP and AD showed consistent immunostaining with antibodies to %%%tau%%% protein and isolated PHF, regardless of their localization. MAbs RT97 and BF10, however, did not stain or only weakly stained, subcortical tangles in PSP and AD, whereas most cortical NFT in AD were intensely

immunostained. All tangles In PSP were as heavily impregnated with Gallyas as they were in AD. Furthermore there were extensive networks of Gallyas-positive, %%%tau%%%- and PHF-immunoreactive neurites in subcortical gray areas containing NFT, and bundles of positive axons in white matter tracts interconnecting subcortical nuclei of PSP. Our studies indicate a much more extensive disruption of fibrillar proteins in PSP subcortical neurons than previously reported. They furthermore indicate a very similar antigenic profile of NFT in PSP and AD, as far as subcortical neurons are concerned.

4/7/34 (Item 34 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06619784 BIOSIS NO.: 000087061946
AN ANTIGENIC PROFILE OF LEWY BODIES IMMUNOCYTOCHEMICAL INDICATION FOR
PROTEIN %%%PHOSPHORYLATION%%% AND UBIQUITINATION
AUTHOR: BANCHER C; LASSMANN H; BUDKA H; JELLINGER K; GRUNDKE-IQBAL I; IQBAL
K; WICHE G; SEITELBERGER F; WISNIEWSKI H M
AUTHOR ADDRESS: NEUROLOGICAL INST. UNIV. VIENNA, SCHWARZSPANIERSTRASSE 17,
1090 WIEN, AUSTRIA.
JOURNAL: J NEUROPATHOL EXP NEUROL 48 (1). 1989. 81-93. %%%1989%%%
FULL JOURNAL NAME: Journal of Neuropathology & Experimental Neurology
CODEN: JNENA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: An antigenic profile of subcortical and cortical Lewy bodies was determined in the presence or absence of neurofibrillary tangles in the same brain using antisera and %%%monoclonal%%% antibodies to various cytoskeletal elements as well as to determinants not present in the normal cytoskeleton. The cores of many Lewy bodies were strongly reactive with a %%%monoclonal%%% antibody to paried helical filaments which has been shown to recognize ubiquitin. This antibody also stained Marinesco bodies in the same tissue sections. Two %%%monoclonal%%% antibodies to %%%phosphorylated%%% epitopes of neurofilament proteins (SM I 31, SM I
34) stained the peripheries of about 40% of all discernable Lewy bodies on untreated paraffin sections. Reactivity with a %%%monoclonal%%% antibody to neurofilaments (SM I 33) appeared only after pretreatment of the sections with phosphatase. Lewy bodies did not bind antibodies to %%%tau%%% protein. Our results show that, as previously shown for neurofibrillary tangles, Lewy bodies also contain ubiquitin. The uncovering of neurofilament epitopes by treatment with phosphatase indicates that abnormal %%%phosphorylation%%% of cytoskeletal elements
may play a role in the pathogenesis of the Lewy body.

4/7/35 (Item 35 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06565581 BIOSIS NO.: 000087007742
ALZHEIMER DISEASE TANGLES SHARE IMMUNOLOGICAL SIMILARITIES WITH
MULTIPHOSPHORYLATION REPEATS IN THE TWO LARGE NEUROFILAMENT PROTEINS
AUTHOR: LEE V M-Y; OTVOS L JR; SCHMIDT M L; TROJANOWSKI J Q
AUTHOR ADDRESS: DEP. PATHOL., LAB. MED., UNIV. PENNSYLVANIA SCH. MED.,
PHILADELPHIA, PA. 10104.
JOURNAL: PROC NATL ACAD SCI U S A 85 (19). 1988. 7384-7388. %%%1988%%%
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Immunological and structural analyses of neurofilament (NF) proteins with > 500 anti-NF %%%monoclonal%%% antibodies (mAbs) enumerated
epitopes shared by NF proteins and Alzheimer neurofibrillary tangles. We identified the multiphosphorylation domain of the rat heaviest NF subunit-tandem repeats of Lys-Ser-Pro-Xaa (where Xaa is a small uncharged
amino acid and serine is %%%phosphorylated%%%)-as the determinant recognized by 15 of the 16 mAbs from this collection of > 500 mAbs that detected neurofibrillary tangles. Most (11) of these 16 mAbs also recognized the previously characterized multiphosphorylation repeat in the human middle sized NF subunit. However, although these mAbs shared the ability to recognize NFTs, the antigen-binding domains of these 16 mAbs represented 13 separate classes based on their differential recognition of 12 synthetic peptides derived from the rat heaviest NF subunit and the human middle-sized NF subunit multiphosphorylation sites, NF subunits of 10 diverse species, and normal human .%%%tau%%%. protein.
We conclude that NFTs share highly specific immunological and structural properties with specific rat heaviest NF subunit and human middle-sized NF subunit multiphosphorylation repeats.

4/7/36 (Item 36 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06244054 BIOSIS NO.: 000086078236
MORPHOLOGICAL DIFFERENTIATION OF EMBRYONIC RAT SYMPATHETIC NEURONS IN
TISSUE CULTURE I. CONDITIONS UNDER WHICH NEURONS FORM AXONS BUT NOT
DENDRITES
AUTHOR: BRUCKENSTEIN D A; HIGGINS D
AUTHOR ADDRESS: DEP. PHARMACOL. THER., FARBER 127, SCH. MED., STATE UNIV.
NEW YORK, BUFFALO, N.Y. 14214.
JOURNAL: DEV BIOL 128 (2). 1988. 324-336. %%%1988%%%
FULL JOURNAL NAME: Developmental Biology
CODEN: DEBIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have examined the morphology of fetal rat sympathetic neurons
grown in serum-free medium in the absence of nonneuronal cells. Because cell density can affect phenotypic expression in vitro, the morphological analysis was subdivided into the study of isolated neurons (neurons whose somata were at least 150 .mu.m from their nearest neighbor) and of more highly aggregated neurons. When isolated neurons were injected with intracellular markers, it was found that most (79%) had a single process emanating from their somata and that this unipolar state persisted for at least 8 weeks in vitro. The processes of unipolar sympathetic neurons had the appearance of axons in that they were thin and long, had a constant diameter, and were relatively unbranched. Cytochemical methods revealed that such processes had other axonal characteristics: (1) they were more reactive with a %%%monoclonal%%% antibody against %%%phosphorylated%%%
forms of the M and H neurofilament subunits than with an antibody to nonphosphorylated forms of these proteins; (2) they also reacted with antibodies to the .%%%tau%%%. microtubule-associated protein and to the %%%phosphorylated%%% forms of the H neurofilament subunit; and (3) they
contained only small amounts of RNA as determiend by [3H]uridine autoradiography. These data indicate that neurons which normally form dendrites in vivo need not express this capacity in vitro and that axonal and dendritic growth can be dissociated under some conditions in culture. While most isolated neurons were unipolar, neurons in regions of high neuronal cell density were usually multipolar. In addition to axons, multipolar neurons had processes with some of the characteristics expected of rudimentry dendrites: they ended locally (usually within 100 .mu.m), were often highly branched, and reacted with an antibody to nonphosphorylated forms of the M and H neurofilament subunits. The effects of density were most prominent when neurons were within aggregates in which the somata were in close apposition. Density-dependent changes in morphology were less frequently observed

when neuronal somata were separated by greater distances (30-100 .mu.m). These data indicate that the morphology of sympathetic neurons is subject to environmental regulation and that neuron-neuron interactions can promote the extension of rudimentary dendrites in vitro.

4/7/37 (Item 37 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06151013 BIOSIS NO.: 000085114165
IDENTIFICATION OF THE MAJOR MULTIPHOSPHORYLATION SITE IN MAMMALIAN
NEUROFILAMENTS
AUTHOR: LEE V M-Y; OTVOS L JR; CARDEN M J; HOLLOSI M; DIETZSCHOLD B;
LAZZARINI R A
AUTHOR ADDRESS: DIV. NEUROPATHOL., DEP. PATHOL. LAB. MED., UNIV. PA. SCH.
MED., PHILADELPHIA, PA. 19104.
JOURNAL: PROC NATL ACAD SCI U S A 85 (6). 1988. 1998-2002. %%%1988%%%
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The sequence
Lys-Ser-Pro-Val-Pro-Lys-Ser-Pro-Val-Glu-Glu-Lys-Gly
repeats six times serially in the human midsized neurofilament (NF) protein (NF-M). To establish whether Lys-Ser-Pro-Val(Ala) is the major site for in vivo NF %%%phosphorylation%%%, peptides based on the human NF-M repeat were synthesized and chemically %%%phosphorylated%%%. These
synthetic peptides were probed with 515 %%%monoclonal%%% antibodies (mAbs) that wereraised to, and distinguished, several differentially %%%phosphorylated%%% forms of NF proteins. Studies with 95 of those mAbs
that recognized the peptides before and after chemical %%%phosphorylation%%% demonstrated that a highly immunogenic epitope shared by the peptides is present in NFs from all species tested, including invertebrates. This suggests the phylogenetic conservation of a major NF %%%phosphorylation%%% site. Lastly, a cross-reactive antigenic determinant shared by the petpides and the major NF %%%phosphorylation%%%
site was shown to exist in neurofibrillary tangles of patients with Alzheimer disease as well as in two neuron-specific microtubule-associated proteins (MAPs).sbd.i.e., MAP2 and %%%tau%%%.

4/7/38 (Item 38 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06097134 BIOSIS NO.: 000085060283
ACCUMULATION OF %%%PHOSPHORYLATED%%% NEUROFILAMENTS IN ANTERIOR HORN
MOTONEURONS OF AMYOTROPHIC LATERAL SCLEROSIS PATIENTS
AUTHOR: MUNOZ D G; GREENE C; PERL D P; SELKOE D J
AUTHOR ADDRESS: DEP. PATHOL., COLL. MED., UNIV. SASKATCHEWAN, SASKATOON,
SASKATCHEWAN S7N 0W0, CANADA.
JOURNAL: J NEUROPATHOL EXP NEUROL 47 (1). 1988. 9-18. %%%1988%%%
FULL JOURNAL NAME: Journal of Neuropathology & Experimental Neurology
CODEN: JNENA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Perikaryal collections of intermediate filaments have been described in the anterior horn motoneurons of patients with amyotrophic lateral sclerosis (ALS), but these inclusions have generally been considered rare and mainly associated with the familial form of ALS. Using the %%%monoclonal%%% antibody NF2F11, which recognizes %%%phosphorylated%%% neurofilament epitopes, we showed that focal collections of neurofilaments in anterior horn motoneurons were a characteristic finding in sporadic as well as in familial ALS; they were present in seven of nine ALS patients, but in none of nine control spinal cords. These neurofilamentous collections are not cross-reactive with antibodies directed against paired helical filaments anbd the microtubule associated protein %%%tau%%%. In addition, diffuse staining for %%%phosphorylated%%% neurofilament epitopes in chromatolytic anterior horn perikarya was significantly more frequent in ALS patients than in controls.

4/7/39 (Item 39 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06086926 BIOSIS NO.: 000085050075
%%%PHOSPHORYLATION%%% DETERMINES TWO DISTINCT SPECIES OF %%%TAU%%% IN THE
CENTRAL NERVOUS SYSTEM
AUTHOR: PAPASOZOMENOS S C; BINDER L I
AUTHOR ADDRESS: DEP. PATHOL., LAB. MED., UNIV. TEX. MED. SCH., PO BOX
20708, HOUSTON, TEX. 77225, USA.
JOURNAL: CELL MOTIL CYTOSKELETON 8 (3). 1987. 210-226. %%%1987%%%
FULL JOURNAL NAME: Cell Motility and the Cytoskeleton
CODEN: CMCYE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The %%%monoclonal%%% antibody, %%%Tau%%%-1, which had previously
been used to localize %%%tau%%% to the axonal compartment in brain has been reutilized for light and electron microscopic immunohistochemistry following phosphatase treatment of tissue. We report here that a signficiant quantity of %%%tau%%% in the central nervous system is %%%phosphorylated%%% in situ at or near the %%%Tau%%%-1 epitope, preventing the binding of the %%%Tau%%%-1 antibody. Upon removal of this/these phosphate group(s), however, %%%Tau%%%-1 was observed in the
somatodendritic compartment of neurons as well as in axons. Furthermore, intense staining was also observed in astrocytes and in perineuronal glial cells. This immunoreactivity was present along the lengths of microtubules and on ribosomes (polysomes). Treatment of immunoblots of extracts of whole cerebral cortex with phosphatase confirmed the immunohistochemical results in that a 50-65% increase in %%%Tau%%%-1 binding to the %%%tau%%% region of the blot was noted. Moreover, a novel
%%%monoclonal%%% antibody, %%%Tau%%%-2, was also used in these experiments. This antibody binds only to %%%tau%%% and localizes along microtubules in axons, somata, dendrites, and astrocytes and on ribosomes (polysomes) without phosphatase pretreatment.

4/7/40 (Item 40 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06076967 BIOSIS NO.: 000085040116
PHOSPHATASE AND CARBOCYANINE DYE BINDING DEFINE DIFFERENT TYPES OF
PHOSPHATE GROUPS IN MAMMALIAN NEUROFILAMENTS
AUTHOR: KSIEZAK-REDING H; YEN S-H
AUTHOR ADDRESS: DEP. PATHOL., ALBERT EINSTEIN COLL. MED., 1300 MORRIS PARK
AVE., BRONX, N.Y. 10461.
JOURNAL: J NEUROSCI 7 (11). 1987. 3554-3560. %%%1987%%%
FULL JOURNAL NAME: Journal of Neuroscience
CODEN: JNRSD
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The %%%phosphorylation%%% state of human and bovine spinal cord

neurofilaments (NF) was studied by direct phosphate analysis and carbocyanine dye ("Stains-all") binding to NF polypeptides resolved on SDS-polyacrylamide gels. Electrophoretically purified NF-H (200 kDa), NF-M (160 kDa), and NF-L (68 kDa) of human origin contained 24, 18, and 4 mol phosphate/mol protein, whereas bovine NF contained 53, 23, and 5 mol phosphate/mol protein, respectively. Incubation of NF preparations with E. coli alkaline phosphatase removed about 55% of the phosphate from NF-H, about 30% of the phosphate from both human and bovine NF-M, but did not change the phosphate content of NF-L. This treatment also inhibited or substantially reduced the binding of electroblotted NF-H and NF-M to 2 anti-NF %%%monoclonal%%% antibodies known to recognize %%%phosphorylated%%% sites on projection side arms. "Stainsall" was found to be a very sensitive probe for detection of %%%phosphorylated%%% cytoskeletal proteins. Without the phosphatase treatment, NF and other phosphoproteins, MAP1, MAP2, tubulin, and %%%tau%%%, all bound the carbocyanine dye on SDS gels, forming blue dye-protein complexes. Measured densitometrically at 615 nm, the staining intensity (relative units/mol protein) was 9, 9, and 3 for human and 10, 13, and 6 for bovine NF-H, NF-M, and NF-L, respectively. NF-H bound the dye less efficiently than was expected from its phosphate content. After phosphatase treatment, NF-H, with half of its phosphate residues remaining, no longer formed blue complex with "Stains-all", the staining intensity of NF-M decreased by 20-40%, and the staining of NF-L was not changed. The results of dye binding, phosphate analysis, and immunostaining showed that there are at least 2 sets of phosphate groups in mammalian NF, which react differently with the phosphatase.

4/7/41 (Item 41 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05810170 BIOSIS NO.: 000034033319
%%%PHOSPHORYLATION%%% OF MICROTUBULE-ASSOCIATED PROTEINS MAP2 AND %%%TAU%%%
BY NEURAL PP60C-S-R-C IN-VITRO
AUTHOR: KIM H
AUTHOR ADDRESS: DEP. CELL BIOL. ANAT., UNIV. ALA., BIRMINGHAM, ALA. 35294, USA.
JOURNAL: TWENTY-SEVENTH ANNUAL MEETING OF THE AMERICAN SOCIETY FOR CELL BIOLOGY, ST. LOUIS, MISSOURI, USA, NOVEMBER 16-20, 1987. J CELL BIOL 105 (4 PART 2). 1987. 108A. %%%1987%%%
CODEN: JCLBA
DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH

4/7/42 (Item 42 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05733122 BIOSIS NO.: 000084081528
NEUROFIBRILLARY TANGLES IN ALZHEIMER'S DISEASE AND PROGRESSIVE SUPRANUCLEAR PALSY ANTIGENIC SIMILARITIES AND DIFFERENCES MICROTUBULE-ASSOCIATED PROTEIN %%%TAU%%% ANTIGENICITY IS PROMINENT IN ALL TYPES OF TANGLES
AUTHOR: BANCHER C; LASSMANN H; BUDKA H; GRUNDKE-IQBAL I; IQBAL K; WICHE G; SEITELBERGER F; WISNIEWSKI H M
AUTHOR ADDRESS: NEUROL. INST., UNIV. VIENNA, SCHWARZSPANIERSTRASSE 17, A-1090 WIEN, AUSTRIA.
JOURNAL: ACTA NEUROPATHOL 74 (1). 1987. 39-46. %%%1987%%%
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The antigenic profile of neurofibrillary tangles (NFT) in Alzheimer's disease (AD), senile dementia of Alzheimer type (SDAT), progressive supranuclear palsy (PSP) and in non-demented aged humans was investigated by light and electron microscopic immunocytochemistry using antisera and %%%monoclonal%%% antibodies to tubulin, microtobule-associated proteins (MAP1, MAP2 and %%%tau%%%), neurofilament proteins and determinants unique to Alzheimer paired helical filaments (PHF). Antibodies to %%%tau%%% proteins labeled NFT in all cases investigated (AD, SDAT, PSP and non-demented aged humans). However, one %%%monoclonal%%% antibody to PHF recognized numerous tangles in AD/SDAT, but only a small minority of the PSP tangles. Antibodies to tubulin, MAP1, MAP2 and neurofilament proteins did not selectively stain NFT. Whereas pretreatment of sections with phosphatase was required for the detection of tangles with %%%Tau%%%-1 %%%monoclonal%%% antibody, digestion of sections with either phosphatase or pronase had no significant effect on the staining pattern obtained with the other antibodies. Our studies show that, as previously described for AD/SDAT, %%%phosphorylated%%% %%%tau%%% polypeptides are also a major antigenic determinant of tangles in PSP, indicating that tangle formation may follow a common pathogenetic pathway in neurofibrillary degenerations. There is, however at least one epitope in AD/SDAT tangles which seems to be absent on, or at least inaccessible in the 15-nm straight fibrils of PSP.

4/7/43 (Item 43 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05702307 BIOSIS NO.: 000084050712
A %%%MONOCLONAL%%% ANTIBODY THAT RECOGNIZES A %%%PHOSPHORYLATED%%% EPITOPE IN ALZHEIMER NEUROFIBRILLARY TANGLES NEUROFILAMENTS AND %%%TAU%%% PROTEINS IMMUNOSTAINS GRANULOVACUOLAR DEGENERATION
AUTHOR: DICKSON D W; KSIEZAK-REDING H; DAVIES P; YEN S-H
AUTHOR ADDRESS: DEP. PATHOL., ALBERT EINSTEIN COLL. MED., 1300 MORRIS PARK AVE., K-438, BRONX, NY 10461, USA.
JOURNAL: ACTA NEUROPATHOL 73 (3). 1987. 254-258. %%%1987%%%
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A %%%monoclonal%%% antibody, raised against extracts from Alzheimer brain, that recognizes a %%%phosphorylated%%% epitope in high molecular weight neurofilament proteins and %%%tau%%% proteins also immunostains Alzheimer neurofibrillary tangles, neurites in senile plaques and granulovacuolar degeneration. This result suggests that granulovacuolar degeneration may contain %%%phosphorylated%%% proteins, possibly due to autophagy of %%%phosphorylated%%% perikaryal proteins that appear to be increased in Alzheimer's disease.

4/7/44 (Item 44 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05700178 BIOSIS NO.: 000084048583
RECOGNITION OF ALZHEIMER PAIRED HELICAL FILAMENTS BY %%%MONOCLONAL%%% NEUROFILAMENT ANTIBODIES IS DUE TO CROSSREACTION WITH %%%TAU%%% PROTEIN
AUTHOR: NUKINA N; KOSIK K S; SELKOE D J
AUTHOR ADDRESS: HARVARD MED. SCH., CENT. NEUROL. DISEASES, DEP. MED., 75 FRANCIS ST., BOSTON, MASS. 02115.
JOURNAL: PROC NATL ACAD SCI U S A 84 (10). 1987. 3415-3419. %%%1987%%%

FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Neurofibrillary tangles and senile plaques are the principal pathological features of Alzheimer disease. Neurofibrillary tangles and the neurites of senile plaques contain paired helical filaments (PHF) that consist of two 10-nm filaments twisted into a double helix. The precursor proteins of PHF are not fully known. To identify these precursors, numerous immunochemical studies have been carried out during the past decade. Two apparently conflicting results have been reported. (i) Some, but not all, %%%monoclonal%%% antibodies to neurofilaments stained neurofibrillary tangle. (ii) Polyclonal antibodies prepared to PHF purified in NaDodSO4 because of their unusual insolubility did not recognize normal proteins, including neurofilaments, on electrophoretic transfer blots of human brain homogenates. These results have been confirmed in several laboratories, including by the use of electron microscopic labeling. Recently, we reported that polyclonal PHF antibodies include antibodies to %%%tau%%% proteins, a family of heat-stable microtubule-associated phosphoproteins, and that antibodies to %%%tau%%% stain Alzheimer neurofibrillary tangles. Those %%%monoclonal%%% neurofilament antibodies that recognize tangles are reported to be directed against %%%phosphorylated%%% epitopes. These facts prompted us to reexamine certain neurofilament %%%monoclonal%%% antibodies that stain neurofibrillary tangles. All %%%monoclonal%%% neurofilament antibodies that stain tangles that we examined, including those initially reported, reacted with %%%tau%%% proteins. Our results suggest that these antibodies react with %%%phosphorylated%%% %%%tau%%% proteins in PHF, not neurofilament proteins, highlighting the problem of using antibodies to %%%phosphorylated%%% protein epitopes in immunochemical studies. Independent evidence for the presence of neurofilament proteins in human paired helical filaments is now required.

4/7/45 (Item 45 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05604691 BIOSIS NO.: 000083077831
TWO %%%MONOCLONAL%%% ANTIBODIES RECOGNIZE ALZHEIMER'S NEUROFIBRILLARY TANGLES NEUROFILAMENT AND MICROTUBULE-ASSOCIATED PROTEINS
AUTHOR: KSIEZAK-REDING H; YEN S-H
AUTHOR ADDRESS: DEP. OF PATHOL. FORCH. 538 , ALBERT EINSTEIN COLL. OF MED., 1300 MORRIS PARK AVE., BRONX, NY 10461, USA.
JOURNAL: J NEUROCHEM 48 (2). 1987. 455-462. %%%1987%%%
FULL JOURNAL NAME: Journal of Neurochemistry
CODEN: JONRA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Two %%%monoclonal%%% antibodies that recognize Alzheimer's neurofibrillary tangles (ANTs), AD10 and AB18, have been characterized by immunoblotting against human and calf spinal cord neurofilament (NF) and calf brain microtubule preparations. Both antibodies bind to the 200-kilodalton (kd) (NF-H) and 160-kd (NF-M) but not to the 68-kd (NF-L) NF triplet proteins. They also bind to high-molecular-weight microtubule-associated proteins (MAPs) and .%%%tau%%%..AD10 immunostains MAP2 and MAP1 families, whereas AB18 stains mainly MAP1 bands. Preincubation of intact filament preparation or nitrocellulose strips containing electroblotted NF proteins with Escherichia coli alkaline phosphatase completely blocks AD10 binding and partially blocks binding of AB18. These results suggest that the determinants recognized by these antibodies are %%%phosphorylated%%%. Immunoblotting of peptide fragments generated by limited proteolysis of NF proteins with .alpha.-chymotrypsin and Staphylococcus aureus V8 protease shows that the localization of the antigenic determinants to AD10 and AB18 in NF-H is .apprx. 100 and 60 kd, respectively, away from the carboxy terminal, a region previously shown to form the NF projection side arm. In NF-M, the antigenic determinants to both antibodies are located also in the projection side arm, in a 60-kd polypeptide adjacent to the .alpha.-helical filament core. The results show that ANTs contain at least two %%%phosphorylated%%% antigenic sites that are present in NF and MAPs, a finding suggesting that ANTs may be composed of proteins or their fragments with epitopes shared by cytoskeletal proteins.

4/7/46 (Item 46 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05553214 BIOSIS NO.: 000083026354
MICROHETEROGENEITY OF MICROTUBULE-ASSOCIATED %%%TAU%%% PROTEINS IS DUE TO DIFFERENCES IN %%%PHOSPHORYLATION%%%
AUTHOR: BUTLER M; SHELANSKI M L
AUTHOR ADDRESS: DEP. PHARMACOLOGY, NEW YORK UNIV. SCH. MED., NEW YORK, NY 10016.
JOURNAL: J NEUROCHEM 47 (5). 1986. 1517-1522. %%%1986%%%
FULL JOURNAL NAME: Journal of Neurochemistry
CODEN: JONRA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have studied the heterogeneity of the microtubule-associated .%%%tau%%%. proteins using .%%%tau%%%.-specific antibodies and two-dimensional electrophoresis. Both %%%monoclonal%%% and polyclonal antibodies to .%%%tau%%%. proteins recognize five bands in cow brain microtubule proteins run on sodium dodecyl sulfate (SDS)-polyacrylamide gels, with apparent molecular weights between 56,000 and 66,000. Immunoblots of cow brain microtubules separated on two-dimensional gels, using nonequilibrium pH gradient electrophoresis in the first dimension and SDS-gel electrophoresis in the second, reveal that > 30 isoforms of .%%%tau%%%. exist. The .%%%tau%%%. proteins vary in pI from 6.5 to 8.5, with the higher-molecular weight forms being more acidic. The microheterogeneity of .%%%tau%%%. is not induced by cycling of microtubules, because two-dimensional immunoblots of .%%%tau%%%. from total brain are almost identical to those of .%%%tau%%%. from cycled tubules. Adult rat brain .%%%tau%%%., which appears as three doublet bands on SDS gels, also exhibits considerable isoelectric heterogeneity, as does .%%%tau%%%. from 7-day-old rats, which appears as only one band on SDS gels. After dephosphorylation of cow brain .%%%tau%%%. with alkaline phosphatase, the highest-molecular-weight band disappears on SDS gels. On two-dimensional gels, the number of .%%%tau%%%. variants decreases by more than half after dephosphorylation, and the more basic species increase greatly in intensity. Preliminary experiments with .%%%tau%%%. labeled in vivo with 32PO4 also indicate that the more acidic .%%%tau%%%. proteins are the more highly %%%phosphorylated%%% forms. Thus, isoelectric heterogeneity of .%%%tau%%%. proteins exists at all ages and is due, at least in part, to differences in the state of %%%phosphorylation%%% of .%%%tau%%%. isoforms.

4/7/47 (Item 47 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05484350 BIOSIS NO.: 000033085203
MICROTUBULE ASSOCIATED PROTEIN %%%TAU%%% IN ALZHEIMER PAIRED HELICAL FILAMENTS PHF
AUTHOR: IQBAL K; GRUNDKE-IQBAL I; WISNIEWSKI H M
AUTHOR ADDRESS: INST. BASIC RES. DEV. DISABILITIES, STATEN ISLAND, N.Y. 10314, USA.
JOURNAL: ELEVENTH MEETING OF THE INTERNATIONAL SOCIETY

FOR NEUROCHEMISTRY
AND THE EIGHTEENTH MEETING OF THE AMERICAN SOCIETY FOR NEUROCHEMISTRY, LA
GUAIRA, VENEZUELA, MAY 31-JUNE 5, 1987. J NEUROCHEM 48 (SUPPL.). 1987.
S157. %%%1987%%%
CODEN: JONRA
DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH

4/7/48 (Item 48 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05263909 BIOSIS NO.: 000082104534
DEFECTIVE BRAIN MICROTUBULE ASSEMBLY IN ALZHEIMER'S DISEASE
AUTHOR: IQBAL K; GRUNDKE-IQBAL I; ZAIDI T; MERZ P A; WEN G Y; SHAIKH S S;
WISNIEWSKI H M; ALAFUZOFF I; WINBLAD B
AUTHOR ADDRESS: NYS INST. BASIC RES. DEV. DISABILITIES, 1050 FOREST HILL
ROAD, STATEN ISLAND, NEW YORK 10314, USA.
JOURNAL: LANCET 2 (8504). 1986. 421-426. %%%1986%%%
FULL JOURNAL NAME: Lancet
CODEN: LANCA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Brains obtained within 2-4 hours post mortem and histopathologically confirmed for Alzheimer's disease and non-Alzheimer brains from age-matched controls were examined for in-vitro assembly of microtubules and neurofilaments. Microtubule assembly was observed only in control but not in Alzheimer brains, and neurofilaments were obained from both types of brain. The microtubule-associated protein %%%tau%%%, which stimulates assembly for microtubules from tubulin, was abnormally %%%phosphorylated%%% in Alzheimer but not in control brain microtubule preparations. Alzheimer brains did not show the presence of any inhibitor of microtubule assembly or any abnormality of tubulin. DEAE-dextran, a polycation which mimics %%%tau%%% in stimulating microtubule assembly, induced the assembly of microtubules in Alzheimer brain. Tubulin from both normal and Alzheimer brains was labelled on western blots by a %%%monoclonal%%% antibody to the tyrosinylated carboxy-terminal epitope of .alpha. tubulin. These studies suggest that in Alzheimer's disease tubulin can be assembled into brain microtubules, but the process is defective, probably because of abnormal %%%phosphorylation%%% of %%%tau%%%. This post-translational alteration of %%%tau%%% might be the cause of the neurofibrillary abnormality in Alzheimer's disease.

4/7/49 (Item 49 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05234674 BIOSIS NO.: 000082075296
ABNORMAL %%%PHOSPHORYLATION%%% OF THE MICROTUBULE-ASSOCIATED PROTEIN
%%%TAU%%% IN ALZHEIMER CYTOSKELETAL PATHOLOGY
AUTHOR: GRUNDKE-IQBAL I; IQBAL K; TUNG Y-C; QUINLAN M; WISNIEWSKI H M;
BINDER L I
AUTHOR ADDRESS: N.Y. STATE UNIV. BASIC RES. DEV. DISABILITIES, 1050 FOREST
HILL ROAD, STATEN ISLAND, N.Y. 10314.
JOURNAL: PROC NATL ACAD SCI U S A 83 (13). 1986. 4913-4917. %%%1986%%%
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A %%%monoclonal%%% antibody to the microtubule-associated protein
.%%%tau%%%. (%%%tau%%%) labeled some neurofibrillary tangles and plaque
neurites, the two major locations of paired-helical filaments (PHF), in Alzheimer disease brain. The antibody also labeled isolated PHF that had been repeatedly washed with NaDodSO4. Dephosphorylation of the tissue sections with alkaline phosphatase prior to immunolabeling dramatically increased the number of tangles and plaques recognized by the antibody. The plaque core amyloid was not stained in either dephosphorylated or nondephosphorylated tissue sections. On immunoblots PHF polypeptides were labeled readily only when dephosphorylated. In contrast, a commercially available %%%monoclonal%%% antibody to a %%%phosphorylated%%% epitope of neurofilaments that labeled the tangles and the plaque neurites in tissue did not label any PHF polypeptides on immunoblots. The PHF polypeptides, labeled with the %%%monoclonal%%% antibody to .%%%tau%%%., electrophoresed with those polypeptides recognized by antibodies to isolated PHF. The antibody to .%%%tau%%%.-labeled microtubules from normal human brains assembled in vitro but identically treated Alzheimer brain preparations had to be dephosphorylated to be completely recognized by this antibody. These findings suggest that .%%%tau%%%. in Alzheimer brain is an abnormally %%%phosphorylated%%% protein component of PHF.

4/7/50 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

02130742 Genuine Article#: KD144 Number of References: 42
Title: COMPARISON OF METHODS FOR THE INVITRO ASSEMBLY OF POSTMORTEM HUMAN
BRAIN MICROTUBULES THAT RETAIN THE MICROTUBULE-ASSOCIATED PROTEIN
%%%TAU%%%
Author(s): SPARKMAN DR
Corporate Source: UNIV TEXAS,SW MED CTR,DEPT PATHOL,5323 HARRY HINES
BLVD/DALLAS//TX/75235
Journal: JOURNAL OF NEUROSCIENCE METHODS, %%%1992%%%, V45, N1-2 (OCT-NOV)
, P41-53
ISSN: 0165-0270
Language: ENGLISH Document Type: ARTICLE
Abstract: Several methods for the in vitro assembly of microtubules from postmortem human brain were compared for the purpose of obtaining microtubule preparations that best retained their microtubule-associated proteins. The polymerized microtubules from the preparations were examined by negative staining and electron microscopy and shown to consist of well-formed microtubules with varying amounts of abnormal assembly products that differed between methods. The microtubule protein was analyzed by SDS-polyacrylamide gel electrophoresis, quantitative densitometry, as well as trans-blotted onto membranes which were reacted with %%%monoclonal%%% antibodies to tubulin subunits and microtubule-associated proteins. All the preparations were found to contain both the alpha- and beta-tubulin subunits with quantitative differences, but they varied most, both quantitatively and qualitatively, in their content of microtubule-associated proteins. The optimal method for the assembly of soluble tubulin from postmortem human brain cytosol into intact microtubules which specifically retained most of their MAPs, especially %%%tau%%%, employed 4 M glycerol assembly buffer in the presence of 10 muM taxol and 1 mM GTP. The isolation methods were used to compare young and aged brains, and there were fewer microtubule-associated proteins, especially %%%tau%%%, associated with the microtubules in advanced age, in all preparations.

4/7/51 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

02066136 Genuine Article#: JY197 Number of References: 51
Title: IMMUNOCYTOCHEMISTRY OF NEUROFIBRILLARY TANGLES WITH ANTIBODIES TO
SUBREGIONS OF %%%TAU%%%-PROTEIN - IDENTIFICATION OF HIDDEN AND CLEAVED
%%%TAU%%% EPITOPES AND A NEW %%%PHOSPHORYLATION%%% SITE
Author(s): DICKSON DW; KSIEZAKREDING H; LIU WK; DAVIES P; CROWE A; YEN SHC
Corporate Source: YESHIVA UNIV ALBERT EINSTEIN COLL MED,DEPT PATHOL
NEUROPATHOL,1300 MORRIS PK AVE/BRONX//NY/10461; YESHIVA UNIV ALBERT
EINSTEIN COLL MED,ROSE F KENNEDY CTR RES MENTAL RETARDAT & HUMAN
DEV/BRONX//NY/10461
Journal: ACTA NEUROPATHOLOGICA, %%%1992%%%, V84, N6 (NOV), P596-605
ISSN: 0001-6322
Language: ENGLISH Document Type: ARTICLE
Abstract: Antibodies to multiple epitopes spanning the length of the %%%tau%%% molecule were used to study Alzheimer neurofibrillary tangles
(NFT) using immunocytochemical methods and several different methods of
fixation and tissue processing, including staining of vibratome sections, hydrated autoclaving of paraffin sections and immunofluorescence of NFT isolated from fresh brain tissue. Smears and sections were pretreated with trypsin and/or phosphatase to further characterize antibody binding. In tissue fixed briefly in periodate-lysine-paraformaldehyde, %%%tau%%% immunoreactivity was detected in astrocytes, but only a few %%%tau%%% epitopes were detected
in NFT with this fixation method. In contrast, all %%%tau%%% epitopes were detected in NFT in tissue fixed in formaldehyde for prolonged periods of time. In the hippocampus, the number of NFT detected in the dentate fascia was in proportion to the duration of dementia, as we previously noted. Dentate fascia NFT were intracellular (i-NFT) and were reactive with antibodies recognizing epitopes in both the carboxy- and amino-terminal regions of %%%tau%%%, but not the microtubule-binding domain of %%%tau%%%, suggesting that microtubule-binding domain epitopes are hidden in i-NFT. In contrast, NFT in the subiculum and layer II of the parahippocampal cortex were mostly extracellular (e-NFT), especially in severe cases of long duration. e-NFT were immunoreactive with antibodies to the microtubule-binding domain, but only weakly reactive with antibodies to carboxy- or amino-terminal epitopes, suggesting that e-NFT may contain fragments of %%%tau%%%. In both isolated NFT and NFT in sections, amino-terminal epitopes, including the Alz-50 epitope, were sensitive to trypsin proteolysis, which suggests that the lack of staining of e-NFT by antibodies to the amino-terminal regions of %%%tau%%% is due to proteolysis. Antibodies reactive with amino-terminal epitopes also stained fewer NFT following hydrated autoclaving, while those reacting with the carboxy half of %%%tau%%% stained more NFT after hydrated autoclaving. Thus, although carboxy-terminal regions are not detected in e-NFT, they are probably masked, rather than proteolytically cleaved, since they can be revealed by hydrated autoclaving. Finally, phosphatase treatment of isolated NFT revealed enhanced immunostaining not only with %%%Tau%%%-1, as in previous studies demonstrating abnormal %%%phosphorylation%%% of %%%tau%%% proteins in NFT, but also
with an antibody to exon 2, which reveals yet another %%%phosphorylation%%% site in %%%tau%%% of NFT.

4/7/52 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01955811 Genuine Article#: JP530 Number of References: 40
Title: IMMUNOHISTOCHEMICAL STUDIES ON THE NEW TYPE OF ASTROCYTIC INCLUSIONS
IDENTIFIED IN A PATIENT WITH BRAIN MALFORMATION
Author(s): KATO S; HIRANO A; UMAHARA T; HERZ F; SHIODA K; MINAGAWA M
Corporate Source: MONTEFIORE MED CTR,DIV NEUROPATHOL,111 E 210TH
ST/BRONX//NY/10467; MONTEFIORE MED CTR,DIV NEUROPATHOL,111 E 210TH
ST/BRONX//NY/10467; MONTEFIORE MED CTR,DEPT PATHOL/BRONX//NY/10467;
SAITAMA MED SCH,DEPT PATHOL/MOROYAMA/SAITAMA 35004/JAPAN/; SAITAMA MED
SCH,DEPT NEUROPSYCHIAT/MOROYAMA/SAITAMA 35004/JAPAN/
Journal: ACTA NEUROPATHOLOGICA, %%%1992%%%, V84, N4 (SEP), P449-452
ISSN: 0001-6322
Language: ENGLISH Document Type: NOTE
Abstract: Immunohistochemical studies were carried out on the new type of cerebral cortical astrocytic inclusions recently discovered in a 20-year-old patient with maldeveloped brain and micropolygyria. The inclusions appeared as eosinophilic structures (hematoxylin and eosin stain) and did not exhibit argyrophilia (modified Bielschowsky method). The inclusions were strongly stained by the antibody against S-100 protein (S 100) and to a lesser extent by the antibody to microtubule-associated protein 1B (MAP 1B). In contrast to Rosenthal fibers, the astrocytic inclusions did not react with antibodies to alpha-B-crystallin, glial fibrillary acidic protein and ubiquitin. No positive reactions were obtained with antibodies against heat-shock protein 27 (HSP 27), HSP 72, actin, vimentin, desmin, cytokeratin, myelin basic protein, beta-tubulin, MAP 2, %%%tau%%% protein, paired helical filament, %%%phosphorylated%%% neurofilament protein (NFP), nonphosphorylated NFP, synaptophysin, cathepsin D, alpha-1-antichymotrypsin, alpha-1-antitrypsin and basic fibroblast growth factor. By immunoelectron microscopy, the products of the reaction with the anti-S 100 antibody appeared as heterogeneous granular deposits and with the antibody to MAP 1B they were randomly scattered throughout the astrocytic inclusions. Our results demonstrate that the immunohistochemical profile of the recently described inclusions differs from that of Rosenthal fibers. Whether the novel inclusions are involved in congenital astrocyte dysfunction and cerebral malformation remains to be established.

4/7/53 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01952677 Genuine Article#: JN807 Number of References: 74
Title: APPROPRIATE TARGET INTERACTIONS PREVENT ABNORMAL CYTOSKELETAL
CHANGES IN NEURONS - A STUDY WITH INTRASCIATIC GRAFTS OF THE SEPTUM AND
THE HIPPOCAMPUS
Author(s): DOERING LC
Corporate Source: MCMASTER UNIV,DIV ANAT,HSC 1R1,1200 MAIN ST W/HAMILTON
L8N 3Z5/ONTARIO/CANADA/
Journal: JOURNAL OF NEUROSCIENCE, %%%1992%%%, V12, N9 (SEP), P3399-3413
ISSN: 0270-6474
Language: ENGLISH Document Type: ARTICLE
Abstract: Transplantation of embryonic CNS regions into the PNS provides an
opportunity to study temporal and spatial changes in the cytoskeleton that are associated with aging and neurodegenerative diseases. In this study, the fetal septum was transplanted alone or with the hippocampus into the sciatic nerves of young adult rats to determine whether the proper central neural target could prevent the expression of abnormal cytoskeletal changes. The substantia nigra, a nontarget area of the septum, served as control co-grafts. After 1, 3, 6, 12, and 18 months of survival, the grafts were examined by immunocytochemistry with antibodies to %%%phosphorylated%%% and nonphosphorylated neurofilaments, microtubule-associated proteins (MAPs), and glial fibrillary acidic protein (GFAP).

Subpopulations of neurons in the septal transplants expressed CAT and the NGF receptor (192-IgG). Long-term (12-18 months) expression of these two markers was only observed when the septum was combined with the hippocampus.

Although isolated single grafts of septum survived within the PNS

substratum, significant neuronal loss, extensive graft shrinkage, and aberrant cytoskeletal immunoreactivity were prominent in the long-term group. Changes that reflected an aging process included the ectopic expression of %%%phosphorylated%%% neurofilaments in neuronal perikarya, swollen axons, and a loss of MAP2 immunoreactivity that paralleled dendrite regression. In addition, abnormal "curly" fibers in the neuropil were also immunolabeled with an antibody directed against %%%tau%%% (5E2). Introduction of hippocampal co-grafts increased the final size of the septal transplants and prevented the cytoskeletal changes that accompanied the degeneration in the single septal grafts. The degree of GFAP immunostaining in the septum corresponded with advancing graft age and was minimized when grafted with the hippocampal formation. When the septum was combined with the substantia nigra, the grafts also underwent shrinkage and no protective influence from aberrant cytoskeletal staining was observed.

These experiments exemplify the importance of an appropriate CNS neural target on the maintenance of long-term cholinergic neuron survival and normal morphology at the cytoskeletal level and illustrate the usefulness of these CNS-PNS constructs to examine conditions that influence the cytoskeleton.

4/7/54 (Item 5 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01939271 Genuine Article#: JM812 Number of References: 37
Title: PATHOLOGICAL-CHANGES IN OLFACTORY NEURONS IN ALZHEIMERS-DISEASE
Author(s): TALAMO BR; FENG WH; PEREZCRUET M; ADELMAN L; KOSIK K; LEE VMY;
CORK LC; KAUER JS
Corporate Source: TUFTS UNIV,SCH MED,DIV NEUROSCI/BOSTON//MA/02111; NEW
ENGLAND MED CTR/BOSTON//MA/02111; HARVARD UNIV,SCH MED/BOSTON//MA/02115
; UNIV PENN,SCH MED/PHILADELPHIA//PA/19104; JOHNS HOPKINS UNIV,SCH
MED/BALTIMORE//MD/21205
Journal: ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, %%%1991%%%, V640, DEC
(DEC 3), P1-7
ISSN: 0077-8923
Language: ENGLISH Document Type: ARTICLE

4/7/55 (Item 6 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01873790 Genuine Article#: JH625 Number of References: 57
Title: IMMUNE ELECTRON-MICROSCOPIC CHARACTERIZATION OF %%%MONOCLONAL%%%
-ANTIBODIES TO ALZHEIMER NEUROFIBRILLARY TANGLES
Author(s): WRZOLEK MA; MERZ PA; KASCSAK R; GRUNDKEIQBAL I; IQBAL K;
RUBENSTEIN R; TONNADEMASI M; GOLLER NL; MEHTA P; WISNIEWSKI HM
Corporate Source: NEW YORK STATE INST BASIC RES DEV DISABILITIES,1050
FOREST HILL RD/STATEN ISL//NY/10301; NEW YORK STATE INST BASIC RES DEV
DISABILITIES,1050 FOREST HILL RD/STATEN ISL//NY/10301
Journal: AMERICAN JOURNAL OF PATHOLOGY, %%%1992%%%, V141, N2 (AUG), P
343-355
Language: ENGLISH Document Type: ARTICLE
Abstract: Characterization of eleven %%%monoclonal%%% antibodies (MAbs),
raised to isolated sodium dodecyl sulfate (SDS)-treated Alzheimer's neurofibrillary tangles (ANT), has revealed the presence of at least two different epitopes. MAbs were tested for reactivity to ubiquitin and paired helical filaments (PHF) isolated by three different procedures. The effect of protease and/or alkaline phosphatase pretreatment on the reactivity of the MAbs with isolated PHF was also examined All MAbs that bad reacted strongly in the ELISA with sonicated
SDS-treated ANT also immune decorated isolated PHF to varying degrees.
Two MAbs exhibited a high reactivity to PHF: 3-39 and 5-25. %%%MAb%%%
3-39 was found to recognize a protease sensitive epitope, In contrast %%%MAb%%% 5-25 was found to consistently decorate isolated PHF in all
preparations and exhibited a strong reactivity to ubiquitin, and the epitope in isolated PHF was not protease sensitive. Thus structural PHF after protease treatment and detergent treatment contain an antigenic site that is present in ubiquitin.

4/7/56 (Item 7 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01717048 Genuine Article#: HV352 Number of References: 87
Title: UBIQUITINATION AND ABNORMAL %%%PHOSPHORYLATION%%% OF PAIRED HELICAL
FILAMENTS IN ALZHEIMERS-DISEASE
Author(s): IQBAL K; GRUNDKEIQBAL I
Corporate Source: NEW YORK STATE INST BASIC RES DEV DISABILITIES,1050
FOREST HILL RD/STATEN ISL//NY/10314
Journal: MOLECULAR NEUROBIOLOGY, %%%1991%%%, V5, N2-4, P399-410
Language: ENGLISH Document Type: ARTICLE
Abstract: The most characteristic cellular change in Alzheimer's disease is the accumulation of aberrant filaments, the paired helical filaments (PHF), in the affected neurons. There is growing evidence from a number of laboratories that dementia correlates better with the accumulation of PHF than of the extracellular amyloid, the second major lesion of Alzheimer's disease. PHF are both morphologically and biochemically unlike any of the normal neurofibrils. The major polypeptides in isolated PHF are microtubule-associated protein %%%tau%%%. %%%Tau%%% in
PHF is %%%phosphorylated%%% differently from %%%tau%%% in microtubules.
This abnormal %%%phosphorylation%%% of %%%tau%%% in PHF occurs at
several sites. The accumulation of abnormally %%%phosphorylated%%% %%%tau%%% in the affected neurons in Alzheimer's disease brain precedes
both the formation and the ubiquitination of the neurofibrillary tangles. In Alzheimer's disease brain, tubulin is assembly competent, but the in vitro assembly of microtubules is not observed. In vitro, the phosphate groups in PHF are less accessible than those of %%%tau%%%
to alkaline phosphatase. The in vitro dephosphorylated PHF polypeptides stimulate microtubule assembly from bovine tubulin. It is hypothesized that a defect in the protein %%%phosphorylation%%%/dephosphorylation system is one of the earliest events in the cytoskeletal pathology in Alzheimer's disease. Production of nonfunctional %%%tau%%% by its %%%phosphorylation%%% and its polymerization into PHF most probably contributes to a microtubule assembly defect, and consequently, to a compromise in both axoplasmic flow and neuronal function.

4/7/57 (Item 8 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01712492 Genuine Article#: HV090 Number of References: 40
Title: THE JUVENILE MICROTUBULE-ASSOCIATED PROTEIN MAP2C IS A ROD-LIKE
MOLECULE THAT FORMS ANTIPARALLEL DIMERS
Author(s): WILLE H; MANDELKOW EM; MANDELKOW E
Corporate Source: DESY,MAX PLANCK UNIT STRUCT MOLEC BIOL,NOTKESTR85/W-2000
HAMBURG 52//GERMANY/; DESY,MAX PLANCK UNIT STRUCT MOLEC BIOL,NOTKESTR85/W-2000 HAMBURG 52//GERMANY/
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, %%%1992%%%, V267, N15 (MAY 25), P

10737-10742
Language: ENGLISH Document Type: ARTICLE
Abstract: We have developed a procedure to isolate the microtubule-associated protein 2c (MAP2c), a juvenile form of MAP2 occurring in mammalian brain. The shape, size, self-association, and antibody interactions of MAP2c were studied. Monomeric MAP2c is an elongated molecule with a length approximately 48 nm, considerably shorter than the higher molecular weight forms MAP2a or b of adult brain. Two %%%monoclonal%%% antibodies whose epitopes are near the N or C terminus, respectively, are located close to the opposite ends of the MAP2c rods. This places constraints on the types of internal folding of the molecule.

MAP2c self-associates into dimers and fibrous aggregates. The dimers are predominantly antiparallel and nearly in register, as judged by antibody labeling.

4/7/58 (Item 9 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01634193 Genuine Article#: HN274 Number of References: 20
Title: DETERGENT-INSOLUBLE CORTICAL LEWY BODY FIBRILS SHARE EPITOPES WITH NEUROFILAMENT AND %%%TAU%%%
Author(s): POLLANEN MS; BERGERON C; WEYER L
Corporate Source: UNIV TORONTO,CTR RES NEURODEGENERAT DIS,TANZ NEUROSCI BLDG,ROOM 121/TORONTO M5S 1A8/ONTARIO/CANADA/; UNIV TORONTO,CTR RES NEURODEGENERAT DIS,TANZ NEUROSCI BLDG,ROOM 121/TORONTO M5S 1A8/ONTARIO/CANADA/; TORONTO HOSP,TORONTO GEN DIV/TORONTO/ONTARIO/CANADA/
Journal: JOURNAL OF NEUROCHEMISTRY, %%%1992%%%, V58, N5 (MAY), P1953-1956
Language: ENGLISH Document Type: NOTE
Abstract: Lewy bodies are cytoskeletal inclusions associated with neuronal injury and death in idiopathic Parkinson's disease and other neurodegenerative disorders. The chemical composition of the 8-10-nm fibrils of the Lewy body is unknown, although they are related to both normal cytoskeletal elements and paired helical filaments of Alzheimer neurofibrillary tangles. From the Lewy body-rich cerebral cortex of patients with diffuse Lewy body disease we have isolated intact Lewy bodies using a high salt buffer/nonionic detergent gradient centrifugation procedure and extracted the constitutive fibrils with urea and sodium dodecyl sulfate. Urea/detergent-resistant Lewy body fibrils were solubilized with formic acid and found to contain a single protein band of 68 kDa, which was not found in identically prepared normal brain homogenates. The Lewy body derived-polypeptide was recognized on immunoblots by a polyclonal antibody that reacted with both the 68-kDa neurofilament subunit and the microtubule-associated protein %%%tau%%%. The 68-kDa Lewy body protein was not labeled by the %%%monoclonal%%% antibody %%%tau%%%-1 despite prior in vitro enzymatic dephosphorylation. We conclude that the detergent-insoluble component of the cortical Lewy body fibril shares epitopes with neurofilament and %%%tau%%% and may be a posttranslationally modified derivative of either neurofilament or %%%tau%%% with substantially altered biochemical and immunologic properties.

4/7/59 (Item 10 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01584230 Genuine Article#: HK061 Number of References: 37
Title: THE 72-KDA MICROTUBULE-ASSOCIATED PROTEIN FROM PORCINE BRAIN
Author(s): TAKEUCHI M; HISANAGA S; UMEYAMA T; HIROKAWA N
Corporate Source: UNIV TOKYO,FAC MED,DEPT ANAT & CELL BIOL,HONGO,BUNKYO KU/TOKYO 113//JAPAN/; UNIV TOKYO,FAC MED,DEPT ANAT & CELL BIOL,HONGO,BUNKYO KU/TOKYO 113//JAPAN/
Journal: JOURNAL OF NEUROCHEMISTRY, %%%1992%%%, V58, N4 (APR), P1510-1516
Language: ENGLISH Document Type: ARTICLE
Abstract: A microtubule-associated protein (MAP) with a molecular mass of 72-kDa that was purified from porcine brain by using its property of heat stability in a low pH buffer was characterized. Low-angle rotary shadowing revealed that the 72-kDa protein was a rodlike protein approximately 55-75 nm long. The 72-kDa protein bound to microtubules polymerized from phosphocellulose column-purified tubulin (PC-tubulin) with taxol and promoted the polymerization of PC-tubulin in the absence of taxol. Microtubules polymerized by the 72-kDa protein showed a tendency to form bundles of several microtubules. Quick-freeze, deep-etch electron microscopy revealed that the 72-kDa protein formed short crossbridges between microtubules. We performed peptide mapping to analyze the relationship of the 72-kDa protein to other heatstable MAPs, and the results showed some resemblance of the 72-kDa protein to MAP2. Cross-reactivity with a %%%monoclonal%%% anti-MAP2 antibody further suggested that the 72-kDa protein and MAP2 are immunologically related. To study the relationship between the 72-kDa protein and MAP2C, a smaller molecular form of MAP2 identified in juvenile rat brain, we prepared the 72-kDa protein from rat brain by the same method as that used for porcine brain. The fact that the 72-kDa protein from juvenile rat brain was also stained with our %%%monoclonal%%% anti-MAP2 antibody also suggested that the 72-kDa protein is an MAP2C homologue of the porcine brain.

4/7/60 (Item 11 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01512952 Genuine Article#: HE275 Number of References: 35
Title: %%%TAU%%%-2 - A PROBE FOR A SER CONFORMATION IN THE AMINO TERMINUS OF %%%TAU%%%
Author(s): WATANABE N; TAKIO K; HASEGAWA M; ARAI T; TITANI K; IHARA Y
Corporate Source: UNIV TOKYO,FAC MED,INST BRAIN RES,DEPT NEUROPATHOL,7-3-1 HONGO,BUNKYO KU/TOKYO 113//JAPAN/; UNIV TOKYO,FAC MED,INST BRAIN RES,DEPT NEUROPATHOL,7-3-1 HONGO,BUNKYO KU/TOKYO 113//JAPAN/; SCI UNIV TOKYO,FAC SCI & TECHNOL,DEPT APPL BIOLSCI/NODA/CHIBA 278/JAPAN/; RIKEN,AGING PROC RES LAB,FRONTIER RES PROGRAM/WAKO//JAPAN/; FUJITA HLTH UNIV,SCH MED,INST COMPREHENS MED SCI,DIV BIOMED POLYMER SCI/TOYOAKE//JAPAN/; TOKYO METROPOLITAN GERIATR HOSP & INST GERONTOL,DEPT NEUROPHYSIOL/TOKYO 173//JAPAN/
Journal: JOURNAL OF NEUROCHEMISTRY, %%%1992%%%, V58, N3 (MAR), P960-966
Language: ENGLISH Document Type: ARTICLE
Abstract: We have determined the epitope for %%%Tau%%% 2, a %%%monoclonal%%% antibody that intensely stained tangles, plaque neurites, and curly fibers in the tissue section, and strongly labeled bovine %%%tau%%%, but only very weakly labeled human %%%tau%%% on the blot. The epitope has been localized to Ala95 through Ala108 of bovine %%%tau%%%. Ser101 is critical for %%%Tau%%% 2 reactivities; the replacement of Ser by Pro, which is found in rat, mouse, and human %%%tau%%%, brings about very weak %%%Tau%%% 2 reactivities. The strong %%%Tau%%% 2 staining of tangles and its effective absorption with a synthetic Ser peptide (Ala95 through Ala108) suggest that the %%%tau%%% in paired helical filaments takes a Ser conformation, rather than a Pro conformation, in its amino-terminal portion.

4/7/61 (Item 12 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01501607 Genuine Article#: HE042 Number of References: 37
Title: COMMON EPITOPES OF HUMAN AND MURINE MALLORY BODIES AND LEWY BODIES
AS REVEALED BY A NEUROFILAMENT ANTIBODY
Author(s): PREISEGGER KH; ZATLOUKAL K; SPUREJ G; RIEGELNEGG D; DENK H
Corporate Source: GRAZ UNIV,SCH MED,INST PATHOL,DIV MOLEC PATHOL,MOLEC PATHOL LAB,AUENBRUGGERPL 25/A-8036 GRAZ//AUSTRIA/; GRAZ UNIV,SCH MED,INST PATHOL,DIV MOLEC PATHOL,MOLEC PATHOL LAB,AUENBRUGGERPL 25/A-8036 GRAZ//AUSTRIA/
Journal: LABORATORY INVESTIGATION, %%%1992%%%, V66, N2 (FEB), P193-199
Language: ENGLISH Document Type: ARTICLE
Abstract: The antibody SMI 31, which is directed against a %%%phosphorylated%%% epitope, associated with neurofilaments and recognizes Lewy bodies in brains of patients with Parkinson's disease (Bancher C, Lassmann H, Budka H, Jellinger K, Grundgke-Iqbal I, Iqbal K, Wiche G, Seitelberger F, Wisniewski H: J Neuropathol Exp Neurol 1:81, 1989), decorated in immunofluorescence microscopy Mallory bodies (MBs) present in livers of mice chronically treated with griseofulvin and 3,5-diethoxycarbonyl-1,4-dihydrocollidine. In immunoblots it recognized very acidic MB components in a molecular weight range between 55 and 69.5 kilodaltons in addition to poorly soluble high molecular weight material. Moreover, an antibody to %%%tau%%% protein showed similar reactivities in immunofluorescence microscopy and immunoblotting experiments. Both antibodies also stained MBs in human liver with alcoholic hepatitis. These observations support and extend earlier findings which indicate that several intermediate filament-related cellular inclusion bodies, including MBs, share a variety of morphologic, structural and antigenic features. They also suggest the involvement of %%%tau%%% or %%%tau%%%-like proteins in MB formation.

4/7/62 (Item 13 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01483122 Genuine Article#: HC201 Number of References: 49
Title: IMMUNOCYTOCHEMICAL STUDY OF BALLOONED NEURONS IN CORTICAL DEGENERATION WITH NEURONAL ACHROMASIA
Author(s): SMITH TW; LIPPA CF; DEGIROLAMI U
Corporate Source: UNIV MASSACHUSETTS,MED CTR,DEPT PATHOL NEUROPATHOL,55 LAKE AVE N/WORCESTER//MA/01655; UNIV MASSACHUSETTS,MED CTR,DEPT NEUROL/WORCESTER//MA/01605
Journal: CLINICAL NEUROPATHOLOGY, %%%1992%%%, V11, N1 (JAN-FEB), P28-35
Language: ENGLISH Document Type: ARTICLE
Abstract: We studied the immunocytochemical characteristics of the ballooned neurons (BN) in three patients with cortical degeneration with neuronal achromasia (CDNA) using antibodies to %%%phosphorylated%%% neurofilaments (PNF), %%%tau%%%, Alz-50, ubiquitin, beta (A4) amyloid, and glial fibrillary acidic protein. All BN exhibited intense perikaryal staining for PNF protein. Most BN and some normal-appearing neurons also stained for ubiquitin and Alz-50. The BN did not immunostain for %%%tau%%% protein, and none of the cases had %%%tau%%%-reactive neocortical neurofibrillary tangles or Pick bodies. One case had occasional senile plaques that stained for beta amyloid; no case had amyloid angiopathy. Our findings suggest that the pathophysiologic basis of the cortical degeneration in CDNA involves an alteration of neuronal cytoskeletal metabolism affecting neurofilament and possibly microtubular proteins in conjunction with activation of the ubiquitin proteolytic system.

4/7/63 (Item 14 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01428655 Genuine Article#: GY439 Number of References: 46
Title: HYDROFLUORIC ACID-TREATED %%%TAU%%%-PHF PROTEINS DISPLAY THE SAME BIOCHEMICAL-PROPERTIES AS NORMAL %%%TAU%%%
Author(s): GREENBERG SG; DAVIES P; SCHEIN JD; BINDER LI
Corporate Source: WM BURKE MED RES INST,785 MAMARONECK AVE/WHITE PLAINS//NY/10605; YESHIVA UNIV ALBERT EINSTEIN COLL MED,DEPT PATHOL/BRONX//NY/10461; UNIV ALABAMA,SCH MED & DENT,DEPT CELL BIOL/BIRMINGHAM//AL/35294
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, %%%1992%%%, V267, N1 (JAN 5), P 564-569
Language: ENGLISH Document Type: ARTICLE
Abstract: %%%Tau%%% (%%%tau%%%) is a major constituent of paired helical filaments (PHF) found in Alzheimer's disease. The current study examines the possibility that the distinct properties of PHF-associated %%%tau%%%-proteins (%%%tau%%%(PHF)) result from post-translational modifications of normal soluble-%%%tau%%% (%%%tau%%%(s)). Following hydrofluoric acid (HF) treatment, %%%tau%%%(PHF) proteins are heat- and acid-stable, soluble in 2-(N-morpholino)ethanesulfonic acid buffers and display the same molecular weight, pI, and immunochemical properties as normal %%%tau%%%(s). Alkaline phosphatase treatment of dissociated PHF results in similar, although less extensive, electrophoretic changes and a reduction in PHF-1 immunoreactivity. Therefore, %%%phosphorylation%%% of normal %%%tau%%%(s). appears to be responsible for the distinct properties of %%%tau%%%(PHF). Although our results suggest that all of the normal %%%tau%%%-isoforms are in PHF, the relative abundance of individual %%%tau%%%-species differs in HF-treated PHF and %%%tau%%%(s) samples. Moreover, the loss of PHF following HF treatment suggests that post-translational modifications contribute to the structural stability of PHF.

4/7/64 (Item 15 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01332783 Genuine Article#: GP898 Number of References: 71
Title: 2 NOVEL KINASES %%%PHOSPHORYLATE%%%-%%%TAU%%% AND THE KSP SITE OF HEAVY NEUROFILAMENT SUBUNITS IN HIGH STOICHIOMETRIC RATIOS
Author(s): RODER HM; INGRAM VM
Corporate Source: MIT,DEPT BIOL,ROOM 56-601/CAMBRIDGE//MA/02139; MIT,DEPT BIOL,ROOM 56-601/CAMBRIDGE//MA/02139
Journal: JOURNAL OF NEUROSCIENCE, %%%1991%%%, V11, N11, P3325-3343
Language: ENGLISH Document Type: ARTICLE
Abstract: We have identified, purified, and characterized two neurofilament/%%%tau%%% kinases from bovine brain, PK36 and PK40, with apparent M(r) of 36,000 and 40,000 and with novel biochemical properties. A specially designed immunoassay for %%%phosphorylated%%% epitopes in neurofilament (NF) proteins was used in the early stages of the purification. Neither kinase is closely associated with the cytoskeleton. Both kinases %%%phosphorylate%%% bovine intermediate (NF-M) and heavy (NF-H) NF subunits and also bovine %%%tau%%% at the expected KSP sequences, though other sites cannot be ruled out. In human paired helical filaments, %%%tau%%%, %%%phosphorylated%%% at

these same KSP sites, is a major characterized constituent. Neither kinase is activated by the usual second messengers. %%%Tau%%% and the above NF subunits are %%%phosphorylated%%% in high stoichiometric ratios. In the intermediate NF subunit, all the expected sites appear to be %%%phosphorylated%%%, but in the heavy NF subunit only 7 out of the > 40 expected sites can be %%%phosphorylated%%% by our kinases. We
demonstrate that both kinases can induce considerable shifts of apparent M(r) with SDS-PAGE for %%%tau%%% and, for the first time in vitro, also for the intermediate NF subunit.

Interestingly, PK36 and particularly PK40 are strongly inhibited by an excess of free ATP. We propose that during normal aging, and in Alzheimer's disease, age-related mitochondrial dysfunction would reduce ATP levels, which in turn might release the neurofilament/%%%tau%%% kinase from inhibition with consequent paired helical filament formation.

4/7/65 (Item 16 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01261754 Genuine Article#: GK042 Number of References: 51
Title: EVIDENCE FOR DIRECT COUPLING OF PRIMARY AGONIST RECEPTOR INTERACTION
TO THE EXPOSURE OF FUNCTIONAL IIB-IIIA COMPLEXES IN HUMAN
BLOOD-PLATELETS - RESULTS FROM STUDIES WITH THE ANTIPLATELET COMPOUND
AJOENE
Author(s): APITZCASTRO R; JAIN MK; BARTOLI F; LEDEZMA E; RUIZ MC; SALAS R
Corporate Source: INST VENEZOLANO INVEST CIENT,CTR BIOFIS & BIOQUIM,TROMBOSIS EXPTL LAB,APARTADO 21827/CARACAS 1020A//VENEZUELA/;
UNIV DELAWARE,DEPT CHEM/NEWARK//DE/19711
Journal: BIOCHIMICA ET BIOPHYSICA ACTA, %%%1991%%%, V1094, N3, P269-280
Language: ENGLISH Document Type: ARTICLE
Abstract: Ajoene, (E,Z)-4,5,9-trithiadodeca-1,6,11-triene 9-oxide, is a potent antiplatelet compound isolated from alcoholic extracts of garlic. In vitro, ajoene reversibly inhibits platelet aggregation as well as the release reaction induced by all known agonists. In this paper we show that ajoene has a unique locus of action, that is not shared by any other known antiplatelet compound. For example, ajoene inhibits agonist-induced exposure of fibrinogen receptors, as well as intracellular responses such as activation of protein kinase C and the increase in cytoplasmic free calcium induced by receptor-dependent agonists (collagen, ADP, PAF, low-dose thrombin). On the other hand, with agonists that can by-pass (at least partially) the receptor-transductor-effector sequence, such as high-dose thrombin, PMA, NaF, only the exposure of fibrinogen receptors is blocked by ajoene. Binding of fibrinogen to chymotrypsin-treated platelets is only slightly inhibited by ajoene. The results reported here also show that: (a) ajoene does not act as a calcium chelator, does not impair the initial agonist-receptor interaction and does not influence the basal levels of intracellular inhibitors of platelet activation such as cyclic GMP; (b) the locus of action of ajoene is a yet unknown molecular step that links, in the case of physiological agonists, specific agonist-receptor complexes to the sequence of the signal transduction system on the plasma membrane of platelets. In the case of the non-physiological, receptor-independent agonists (PMA, NaF), we can only speculate on the hypothesis that they somehow mimic the effect of the agonist-receptor complexes on the signal transduction system; and (c) the exposure of fibrinogen receptors is not a direct consequence of other intracellular processes. These observations clearly show, for the first time, that the exposure of fibrinogen receptors is a membrane event proximally and obligatorily coupled to the occupancy of other membrane receptors by their agonists without any intervention by the cytoplasmic biochemical processes. Additional results support the involvement of G-proteins in these early events of platelet activation. Furthermore, a role of the beta-%%%tau%%% -subunits of G-proteins in the exposure of fibrinogen receptors is proposed.

4/7/66 (Item 17 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

01212160 Genuine Article#: GE895 Number of References: 46
Title: DEMONSTRATION OF A NOVEL NEUROFILAMENT ASSOCIATED ANTIGEN WITH THE
NEUROFIBRILLARY PATHOLOGY OF ALZHEIMER AND RELATED DISEASES
Author(s): GHEUENS J; CRAS P; PERRY G; BOONS J; CEUTERICKDEGROOTE C; LUBKE
U; MERCKEN M; TABATON M; GAMBETTI PL; VANDERMEEREN M; MULVIHILL P;
SIEDLAK S; VANHEUVERSWIJN H; MARTIN JJ
Corporate Source: UNIV INSTELLING ANTWERP,BORN BUNGE FDN,NEUROBIOL
LAB/B-2610 WILRIJK//BELGIUM/; UNIV INSTELLING ANTWERP,NEUROPATHOL
LABS/B-2610WILRIJK//BELGIUM/; CASE WESTERN RESERVE UNIV,INST PATHOL,DIV
NEUROPATHOL/CLEVELAND//OH/44106; INNOGENET/GHENT//BELGIUM/
Journal: BRAIN RESEARCH, %%%1991%%%, V558, N1, P43-52
Language: ENGLISH Document Type: ARTICLE
Abstract: A %%%monoclonal%%% antibody, termed NFT200, was raised after in
vitro immunization with sonicated neurofibrillary tangle (NFT)-enriched fractions prepared from Alzheimer brain. The antigen to which NFT200 is directed was expressed in the paired helical filaments of NFT in sporadic and familial Alzheimer disease (AD), in the straight filaments of NFT in AD, progressive supranuclear palsy and of Pick bodies, and the NFT in several other conditions such as Parkinson-dementia complex of Guam and subacute sclerosing panencephalitis. Granulovacuolar degeneration of AD was also labeled with NFT200. Hirano bodies and amyloid deposits in AD, as well as Lewy bodies of idiopathic Parkinson disease lacked in the antigen. The NFT200-antigen was also expressed as a phosphatase-insensitive antigen in normal neurofilaments found in spinal cord and peripheral nerve axons but was absent from the perikaryal accumulation of neurofilaments induced by aluminum intoxication. Nevertheless, immunoblot studies failed to detect the NFT200 in isolated preparations of the neurofilament proteins, MAP-2, %%%tau%%%, ubiquitin or A4-amyloid peptide. The results indicate that the NFT200 %%%monoclonal%%% antibody is directed against a phosphatase-insensitive epitope of an axonal protein associated with neurofilaments but is labile to isolation and expressed as a stable epitope of a 200 kDa component of NFT.

4/7/67 (Item 18 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01199639 Genuine Article#: GD742 Number of References: 34
Title: EFFECTS OF ALUMINUM ON %%%TAU%%%-PROTEINS IN HUMAN
NEUROBLASTOMA-CELLS
Author(s): MESCO ER; KACHEN C; TIMIRAS PS
Corporate Source: NIA,FRANCIS SCOTT KEY MED CTR,GERONTOL RES CTR,4940
EASTERN AVE/BALTIMORE//MD/21224; UNIV CALIF BERKELEY,DEPT MOLEC &
CELLULAR BIOL/BERKELEY//CA/94720
Journal: MOLECULAR AND CHEMICAL NEUROPATHOLOGY, %%%1991%%%, V14, N3, P
199-212
Language: ENGLISH Document Type: ARTICLE
Abstract: The presence of the trivalent metallic cations, aluminum and boron, in the culture medium of differentiated human LAN-5 neuroblastoma cells results in increased amounts of specific isomers of microtubule-associated %%%tau%%% proteins. The cells were differentiated to a neuronal phenotype by the addition of retinoic acid. Six-day exposures of the differentiated cells to a 1-mM dose of aluminum or boron yielded increases in %%%tau%%% protein immunoreactivity to the %%%monoclonal%%% antibodies %%%Tau%%%-1 and
Alz-50. Significant increases in immunoreactivity were seen at

treatment levels of aluminium down to 100-mu-M. The increases in %%%tau%%% proteins were independent from increases in levels of total cell protein. Control cultures treated with the divalent cations zinc and iron showed no increases in levels of %%%tau%%% proteins.

4/7/68 (Item 19 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01117971 Genuine Article#: FX450 Number of References: 22
Title: INCREASED CYTOSOLIC FREE CALCIUM IN LYMPHOCYTES OF ALZHEIMER
PATIENTS
Author(s): ADUNSKY A; BARAM D; HERSHKOWITZ M; MEKORI YA
Corporate Source: MEIR HOSP,ALLERGY IMMUNOL UNIT/IL-44281 KEFAR
SAVA//ISRAEL/; MEIR HOSP,ALLERGY IMMUNOL UNIT/IL-44281 KEFAR
SAVA//ISRAEL/; CHAIM SHEBA MED CTR,DEPT GERIATR MED/TEL AVIV//ISRAEL/;
CHAIM SHEBA MED CTR,DEMENTIA CLIN/TEL AVIV//ISRAEL/; TEL AVIV
UNIV,SACKLER SCH MED/TEL AVIV//ISRAEL/
Journal: JOURNAL OF NEUROIMMUNOLOGY, %%%1991%%%, V33, N2, P167-172
Language: ENGLISH Document Type: ARTICLE
Abstract: Free cytosolic calcium content [Ca2+]i was determined in peripheral blood mononuclear cells (PBMC) from healthy volunteers, Alzheimer's disease and multi-infarct dementia patients. Measurement of [Ca2+]i by the fluorescent dye quin-2, before and at several time intervals during incubation with phytohemagglutinin (PHA), showed a higher resting [Ca2+]i in PBMC of Alzheimer's disease patients as compared to controls and multi-infarct dementia patients. However, the addition of supra-optimal PHA doses (100-mu-g/ml) induced strikingly higher [Ca2+]i levels in Alzheimer's disease patients (1647 +/- 200 nM versus 398 +/- 27 nM in controls, and 346 +/- 40 nM in multi-infarct dementia patients). The increased [Ca2+]i concentration was also found after a specific stimulation with a %%%monoclonal%%% anti-CD3 antibody.
The results may have important implications in understanding the pathophysiology of Alzheimer's disease and suggest that [Ca2+]i may prove diagnostically valuable.

4/7/69 (Item 20 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01106841 Genuine Article#: FW806 Number of References: 50
Title: A PROGRESSIVE DEPOSITION OF PAIRED HELICAL FILAMENTS (PHF) IN THE
BRAIN CHARACTERIZES THE EVOLUTION OF DEMENTIA IN ALZHEIMERS-DISEASE -
AN IMMUNOCYTOCHEMICAL STUDY WITH A %%%MONOCLONAL%%%-ANTIBODY AGAINST
THE PHF CORE
Author(s): MENA R; WISCHIK CM; NOVAK M; MILSTEIN C; CUELLO AC
Corporate Source: MCGILL UNIV,DEPT PHARMACOL & THERAPEUT,MCINTYREMED SCI
BLDG,3655 DRUMMOND ST/MONTREAL H3G 1Y6/QUEBEC/CANADA/; MCGILL UNIV,DEPT
PHARMACOL & THERAPEUT,MCINTYREMED SCI BLDG,3655 DRUMMOND ST/MONTREAL
H3G 1Y6/QUEBEC/CANADA/; UNIV CAMBRIDGE,ADDENBROOKES HOSP,DEPT
PSYCHIAT/CAMBRIDGE CB2 2QQ//ENGLAND/; SLOVAK ACAD SCI/CS-80936
BRATISLAVA//CZECHOSLOVAKIA/; MRC,MOLEC BIOL LAB/CAMBRIDGE//ENGLAND/
Journal: JOURNAL OF NEUROPATHOLOGY AND EXPERIMENTAL NEUROLOGY, %%%1991%%%
, V50, N4, P474-490
Language: ENGLISH Document Type: ARTICLE
Abstract: Using the %%%monoclonal%%% antibody (%%%mAb%%%) 6.423 which recognizes epitopes of the pronase-resistant core of paired helical filaments (PHF), we studied postmortem frontal cortex from Alzheimer's disease (AD) patients with short (Group II) and long (Group III) histories of clinical dementia. Four cases with clinically unconfirmed dementia and a postmortem diagnosis of AD (Group I) were also studied.
In Group I, the 6.423 %%%mAb%%% was negative whereas in Group II, the
antibody recognized primarily neurofibrillary tangles (NFT). In contrast, brains in Group III contained a dense network of 6.423-immunoreactive (IR) thread-like structures ("ghost" neurites) and plaque-like structures with granular appearance, in addition to NFT. The number of 6.423-IR structures appeared to be related to the duration of clinical dementia and the age of onset. Furthermore, "ghost" neurites were more abundant in young AD cases. The possible significance of the 6.423-IR pattern in the pathogenesis of AD is discussed.

4/7/70 (Item 21 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

01092219 Genuine Article#: FV816 Number of References: 52
Title: EPITOPE MAP OF NEUROFILAMENT PROTEIN DOMAINS IN CORTICAL AND
PERIPHERAL NERVOUS-SYSTEM LEWY BODIES
Author(s): SCHMIDT ML; MURRAY J; LEE VMY; HILL WD; WERTKIN A; TROJANOWSKI
JQ
Corporate Source: HOSP UNIV PENN,DIV ANAT PATHOL,MALONEY BLDG BASEMENT,ROOM
A009,3400 SPRUCE ST/PHILADELPHIA//PA/19104; UNIV PENN,SCH MED,DEPT
PATHOL & LAB MED,DIV ANAT PATHOL/PHILADELPHIA//PA/19104; UNIV PENN,SCH
MED,DEPT ANAT/PHILADELPHIA//PA/19104
Journal: AMERICAN JOURNAL OF PATHOLOGY, %%%1991%%%, V139, N1, P53-65
Language: ENGLISH Document Type: ARTICLE
Abstract: A subset of demented elderly patients exhibit large numbers of cortical intraneuronal inclusions similar to the neurofilament (NF)-rich Lewy bodies (LB) found in pigmented subcortical neurons of patients with Parkinson's disease (PD). Because these cortical inclusions may contribute to the emergence of cognitive impairments in afflicted individuals, the authors mapped the distribution of NF epitopes in these so-called cortical LBs. This was done using ethanol-fixed tissues and a large library of %%%monoclonal%%% antibodies (MAbs) with well-characterized binding specificities to various regions of each NF triplet protein. Cortical LBs were examined by light, confocal, and electron microscopy, and they were compared with the subcortical LBs of PD and LBs in the peripheral nervous system (PNS). %%%Monoclonal%%% antibodies specific for the rod regions of each of the three NF subunits, or for phosphate-dependent and independent antigenic sites in the tail region of the high-(NF-H) and middle- (NF-M) molecular weight (M(r)) NF subunits as well as other MAbs to the extreme COOH terminus of NF-L and NF-M or the head region
of NF-M labeled a variable number of cortical LBs. Remarkably one of these anti-NF MAbs, RMO32, which recognized a %%%phosphorylated%%%
epitope in the tail region of NF-M, immunolabeled nearly all cortical LBs, whereas each of the other anti-NF MAbs never labeled more than 10%
of ubiquitin- or RMO32-positive cortical LBs. Further LBs in the PNS resembled those in the central nervous system (CNS) in their immunologic properties, and LBs in both sites were dominated by filamentous aggregates at the ultrastructural level. These findings suggest that NF proteins are profoundly altered during their incorporation into cortical and PNS LBs. Further the authors here identified immunologic and ultrastructural properties common to cortical LBs, PNS LBs, and classic substantia nigra LBs in PD. The accumulation of filamentous, perikaryal inclusions rich in NF proteins at diverse sites in the CNS and PNS of patients with a variety of neurodegenerative disorders suggests a widespread disruption of NF metabolism or transport.

4/7/71 (Item 22 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01079585 Genuine Article#: FU901 Number of References: 44
Title: DIFFERENCE BETWEEN THE %%%TAU%%%-PROTEIN OF ALZHEIMER PAIRED HELICAL
FILAMENT CORE AND NORMAL %%%TAU%%% REVEALED BY EPITOPE ANALYSIS OF
%%%MONOCLONAL%%% ANTIBODIES-423 AND ANTIBODIES-7.51
Author(s): NOVAK M; JAKES R; EDWARDS PC; MILSTEIN C; WISCHIK CM
Corporate Source: MRC,MOLEC BIOL LAB,HILLS RD/CAMBRIDGE CB2 2QH//ENGLAND/;
UNIV CAMBRIDGE,DEPT PSYCHIAT,CTR MRC,CAMBRIDGE BRAIN BANK LAB/CAMBRIDGE
CB2 2QH//ENGLAND/
Journal: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED
STATES OF AMERICA, %%%1991%%%, V88, N13, P5837-5841
Language: ENGLISH Document Type: ARTICLE
Abstract: The microtubule-associated protein %%%tau%%% that is incorporated
into paired helical filaments (PHFs) undergoes some form of aberrant posttranslational processing in Alzheimer disease. Difficulties in deciding which changes are critical for PHF formation stem in part from the lack of immunochemical markers specific for PHF %%%tau%%%. The only
%%%monoclonal%%% antibody (%%%mAb%%%) that is known to react with PHF
%%%tau%%% but not with the predominant normal adult %%%tau%%% species
is %%%mAb%%% 423. Another %%%mAb%%% (7.51, described in this paper)
recognizes a segment of %%%tau%%% that is included in the minimal recognition unit required by %%%mAb%%% 423. Unlike 423, which is PHF
%%%tau%%%-specific, %%%mAb%%% 7.51 recognizes all PHF core-derived
%%%tau%%% as well as native soluble %%%tau%%% and recombinant %%%tau%%%
expressed in bacteria and so serves as a generic %%%tau%%% marker. Both
epitopes are in the 12-kDa fragment released from the Pronase-resistant core of the PHF (which encompasses the tandem repeat region). The
%%%mAb%%% 7.51 epitope requires segments located in the last two repeats, which are common to all %%%tau%%% isoforms. The %%%mAb%%% 423
epitope requires sequences located near both the N and the C terminus of the 12-kDa fragment common to three- and four-repeat %%%tau%%% isoforms. Fragments denatured by concentrated formic acid and SDS regain 423 reactivity when denaturing agents are removed. Since the primary amino acid sequences of PHF %%%tau%%% and normal %%%tau%%% are
identical in the repeat region, we conclude that 423 reactivity also requires a modification(s) occurring within an almost-equal-to 90-residue segment that are not present in %%%tau%%% proteins so far described in the human brain.

4/7/72 (Item 23 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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00855645 Genuine Article#: FB769 Number of References: 43
Title: ALUMINUM MALTOL-INDUCED NEUROCYTOSKELETAL CHANGES IN FETAL RABBIT
MIDBRAIN IN MATRIX CULTURE
Author(s): HEWITT CD; HERMAN MM; LOPES MBS; SAVORY J; WILLS MR
Corporate Source: UNIV VIRGINIA,HLTH SCI CTR,DEPT PATHOL/CHARLOTTESVILLE//VA/22908; UNIV VIRGINIA,HLTH SCI CTR,DEPT PATHOL/CHARLOTTESVILLE//VA/22908; UNIV VIRGINIA,HLTH SCI CTR,DEPT INTERNAL MED/CHARLOTTESVILLE//VA/22908; UNIV VIRGINIA,HLTH SCI CTR,DEPT BIOCHEM/CHARLOTTESVILLE//VA/22908
Journal: NEUROPATHOLOGY AND APPLIED NEUROBIOLOGY, %%%1991%%%, V17, N1, P
47-60
Language: ENGLISH Document Type: ARTICLE
Abstract: We have developed a neuronal culture system to evaluate the neurotoxic effects of aluminium maltol on fetal rabbit midbrain sections containing the oculomotor nucleus. Cultures were treated with 5, 7, 9, 11, 13 and 15-mu-mol/l aluminium maltol or 39 and 45-mu-mol/l maltol (molal equivalents to 13 and 15-mu-mol/l aluminium maltol). Control cultures were maintained in nutrient medium alone. Silver-positive neuritic swellings and occasional perikaryal neurofibrillary tangles were observed in cultures treated with 11, 13 and 15-mu-mol/l aluminium maltol. The number of tangles (involved neurons) produced in aluminium maltol treated cultures were counted and compared to (untreated) controls. We observed a total of 3, 7 and 7% of involved neurons following treatment with 11, 13 and 15-mu-mol/l aluminium maltol respectively, and none in the control group. By immunohistochemistry, neurofibrillary tangles were immunoreactive with MAbs to %%%phosphorylated%%% (SMI-31), non-%%%phosphorylated%%%, %%%phosphorylation%%% dependent (SMI-32) and %%%phosphorylation%%% independent (SMI-33) epitopes of the high (-H) and middle (-M) molecular weight neurofilament subunits (NF-H/M). By contrast these lesions were nonreactive with MAbs recognizing %%%tau%%%, MAP2 or different beta-tubulin isotypes. The perikaryal tangles consisted of focal accumulations of 10 nm straight filaments by electron microscopy.

These findings are in agreement with previous data from rabbit in vivo studies after the administration of aluminium maltol intravenously (Bertholf et al., 1989) or intraventricularly (Katsetos et al., 1990). Using this in vitro system, aluminium-induced neurofibrillary tangles can be consistently produced, and changes in the distribution of neurofilament proteins evaluated. These studies may aid in the assessment of the possible role of aluminium in the aetiology of human neurodegenerative disorders.

4/7/73 (Item 24 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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00755432 Genuine Article#: EU300 Number of References: 38
Title: ABNORMAL %%%PHOSPHORYLATION%%% OF %%%TAU%%%-PRECEDES UBIQUITINATION
IN NEUROFIBRILLARY PATHOLOGY OF ALZHEIMER-DISEASE
Author(s): BANCHER C; GRUNDKEIQBAL I; IQBAL K; FRIED VA; SMITH HT;
WISNIEWSKI HM
Corporate Source: NEW YORK STATE INST BASIC RES DEV DISABILITIES,1050 FOREST HILL RD/STATEN ISL//NY/10314; NEW YORK STATE INST BASIC RES DEV DISABILITIES,1050 FOREST HILL RD/STATEN ISL//NY/10314; ST JUDE CHILDRENS HOSP,DEPT BIOCHEM/MEMPHIS//TN/38101
Journal: BRAIN RESEARCH, %%%1991%%%, V539, N1, P11-18
Language: ENGLISH Document Type: ARTICLE

4/7/74 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE
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05246208 EMBASE No: 1993014293
The antineoplasic agent estramustine and the derivative estramustine-phosphate inhibit secretion of interleukin-3 in leukemic cells. Possible roles of MAPs
Martinez J.; Santibanez J.F.; Vial C.; Maccioni R.B.
INTA, Universidad de Chile, Casilla 138-11,Santiago Chile
Molecular and Cellular Biochemistry (MOL. CELL. BIOCHEM.) (United States) 1992, 117/2 (165-173)
CODEN: MCBIB ISSN: 0300-8177
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The antineoplasic drug estramustine is an adduct of estradiol and nor-nitrogen mustard. It has been shown that this drug interferes with microtubule assembly, an effect mediated by estramustine interaction with microtubule-associated proteins (MAPs). In the present report we demonstrate that estramustine and the %%%phosphorylated%%% derivative of
the drug, estramustine-phosphate, inhibit the secretion of interleukin-3 by WEHI-3B cells. These studies also show that the estramustine derivative specifically interacts with a MAPs component found in these cells, which exhibited characteristics resembling those of %%%tau%%% protein isoforms.
Western blots using a unique %%%monoclonal%%% antibody MTB6.22 that recognizes microtubule-binding domains on MAPs, indicated that this WEHI protein factor contained the antigenic determinant that are functionally significant for microtubule assembly. ELISA assays using this antibody, also showed a decrease in the levels of the immunoreactive protein in WEHI cells after treatment with EMP. Interestingly, it has been recently described that the action of estramustine-phosphate is mediated by a direct
interaction with MAP-binding sites on the microtubule surface, which are recognized by the site-specific %%%monoclonal%%% antibody. These findings
together with immuno-precipitation experiments using anti-interleukin-3 antibodies and the inhibitory effect of the estramustine derivative on WEHI
secretion process suggest that this anti- mitotic agent may block IL-3 secretion by a mechanism involving its interaction with a '%%%tau%%%-like' MAPs component present in these cells.

4/7/75 (Item 2 from file: 73)
DIALOG(R)File 73:EMBASE
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05205388 EMBASE No: 1992345622
A serine <rt arrow> proline change in the Alzheimer's disease-associated epitope %%%Tau%%% 2 results in altered secondary structure, but %%%phosphorylation%%% overcomes the conformational gap
Lang E.; Otvos Jr. L.
Wistar Institute of Anatomy/Biology, 3601 Spruce Street,Philadelphia, PA 19104 United States
Biochemical and Biophysical Research Communications (BIOCHEM. BIOPHYS.
RES. COMMUN.) (United States) 1992, 188/1 (162-169)
CODEN: BBRCA ISSN: 0006-291X
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

%%%Monoclonal%%% antibody %%%Tau%%% 2 was raised against bovine %%%tau%%%
protein, was reported to recognize a conformational epitope, and stained %%%tau%%% was found in neurofibrillary tangles of Alzheimer's disease, but
not normal human %%%tau%%%. We synthesized tetradeka peptides corresponding
to the original bovine sequence, its serine <rt arrow> proline substituted analog, the genuine human sequence of this region, and the bovine epitope %%%phosphorylated%%% on the crucial serine. The secondary structure of the
peptides was determined by circular dichroism. It was found that only the original bovine epitope showed a tendency to form the beta-pleated sheets characteristic of the neurofibrillary tangles. The spectra of the human peptide, its analog, and the %%%phosphorylated%%% bovine sequence were very
similar, featuring a weak, helical beta-turn character. Eventual %%%phosphorylation%%% of epitopes of this otherwise heavily %%%phosphorylated%%% protein may overcome inter-species conformational
gaps.

4/7/76 (Item 3 from file: 73)
DIALOG(R)File 73:EMBASE
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04979949 EMBASE No: 1992120165
Fragmentation of the Golgi apparatus of motor neurons in amyotrophic lateral sclerosis
Gonatas N.K.; Stieber A.; Mourelatos Z.; Chen Y.; Gonatas J.O.; Appel S.H.; Hays A.P.; Hickey W.F.; Hauw J.-J.
Department of Pathology, University of Pennsylvania, School of Medicine, 418 Johnson Pavilion,Philadelphia, PA 19104-6079 United States
American Journal of Pathology (AM. J. PATHOL.) (United States) 1992, 140/3 (731-737)
CODEN: AJPAA ISSN: 0002-9440
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The Golgi apparatus (complex) is at the center stage of important functions of processing and transport of plasma membrane, lysosomal, and secreted proteins. The involvement of the Golgi apparatus in the pathogenesis of chronic degenerative diseases of neurons is virtually unknown. In the present study, fragmentation and atrophy of the Golgi apparatus of motor neurons in amyotrophic lateral sclerosis (ALS), has been detected with organelle specific antibodies. Approximately 30% of motor neurons in five ALS patients showed a fragmented Golgi apparatus whereas only about 1% of motor neurons from seven controls with neurologic or systemic disease showed a similar change. Morphometric studies are consistent with the hypothesis that the alteration of the Golgi apparatus is an early event in the pathogenesis of the neuronal degeneration in ALS. Immunocytochemical studies with antibodies against alpha tubulin, %%%tau%%%
, and %%%phosphorylated%%% subunits of neurofilament polypeptides did not
disclose differences in the staining of neurons with fragmented or normal Golgi apparatus, suggesting that the alteration of the organelle is not secondary to a gross lesion of the cytoskeleton. However, these observations do not rule out the hypothesis that the fragmentation of the Golgi apparatus is secondary to subtle changes of the polypeptides involved in the attachment of membranes of the organelle to the cytoskeleton.

4/7/77 (Item 4 from file: 73)
DIALOG(R)File 73:EMBASE
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04919752 EMBASE No: 1992059968
%%%Tau%%% proteins of Alzheimer paired helical filaments: Abnormal %%%phosphorylation%%% of all six brain isoforms
Goedert M.; Spillantini M.G.; Cairns N.J.; Crowther R.A.
Laboratory of Molecular Biology, Medical Research Council, Hills Road, Cambridge CB2 2QH United Kingdom
Neuron (NEURON) (United States) 1992, 8/1 (159-168)
CODEN: NERNE ISSN: 0896-6273
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Preparations of dispersed paired helical filaments (PHFs) from the brains of Alzheimer's disease and Down's syndrome patients display on gels three principal bands corresponding to abnormally modified forms of the microtubule-associated protein %%%tau%%%. Interpretation of the pattern is
difficult because there are six %%%tau%%% isoforms in normal brain and %%%phosphorylation%%% changes their mobility. By enzymatic dephosphorylation at high temperature, we have shifted the three abnormal bands obtained from dispersed PHFs to align with the six nonphosphorylated %%%tau%%% isoforms. By using antibodies specific for some of the inserts that distinguish the various isoforms and label PHFs, we have established a correspondence between PHFs, abnormal bands, and isoforms. This identification of isoforms is a necessary step in unravelling the molecular pathogenesis of PHFs.

4/7/78 (Item 5 from file: 73)
DIALOG(R)File 73:EMBASE
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04919418 EMBASE No: 1992059634
Effects of elevated intracellular calcium levels on the cytoskeleton and %%%tau%%% in cultured human cortical neurons
Mattson M.P.; Engle M.G.; Rychlik B.
Sanders-Brown Research Center on Aging, and Department of Anatomy and

Neurobiology, University of Kentucky Medical Center, Lexington, KY 40536-0230 United States
Molecular and Chemical Neuropathology (MOL. CHEM. NEUROPATHOL.) (United States) 1991, 15/2 (117-142)
CODEN: MCHNE ISSN: 1044-7393
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Considerable evidence suggests that altered neuronal calcium homeostasis plays a role in the neuronal degeneration that occurs in an array of neurological disorders. A reduction in microtubules, the accumulation of 8-15 nm straight filaments, and altered antigenicity toward antibodies to the microtubule-associated protein %%%tau%%% and ubiquitin, as well as granulovacuolar degeneration, are observed in many human neurodegenerative disorders. Progress toward understanding how and why human neurons degenerate has been hindered by the inability to examine living human neurons under controlled conditions. We used cultured human fetal cerebral cortical neurons to examine ultrastructural and antigenic changes resulting from elevations in intracellular calcium levels. Elevation of intracellular calcium by exposure to a calcium ionophore or a reduced level of extracellular Nasup + for periods of hours to days caused a loss of microtubules, an increase in 8-15 nm straight filaments, and increased immunostaining with Alz-50 and 5E2 (%%%tau%%% antibodies) and ubiquitin antibodies. Granulovacuolar degeneration was also observed. Antigenic changes in %%%tau%%% were sensitive to phosphatases, and the electrophoretic mobility of %%%tau%%% was altered in cells exposed to calcium ionophore, indicating that %%%tau%%% was excessively %%%phosphorylated%%% as the result of elevated intracellular calcium levels. Colchicine also caused an accumulation of straight filaments and altered %%%tau%%% immunoreactivity, suggesting that a disruption of microtubules secondary to altered calcium homeostasis may be a key event leading to altered %%%tau%%% disposition and neuronal degeneration. These data demonstrate that aberrant rises in intraneuronal calcium levels can result in changes in the neuronal cytoskeleton similar to those seen in neurodegenerative disorders, and suggest that this experimental system will be useful in furthering our understanding of the cellular and molecular mechanisms of human neurological disorders.

4/7/79 (Item 6 from file: 73)
DIALOG(R)File 73:EMBASE

04837910 EMBASE No: 1991332646
A68 proteins in Alzheimer's disease are composed of several %%%tau%%% isoforms in a %%%phosphorylated%%% state which affects their electrophoretic mobilities
Brion J.-P.; Hanger D.P.; Couck A.-M.; Anderton B.H.
Laboratory of Pathology, Universite Libre de Bruxelles, 808, route de Lennik, Bldg C-10, 1070-Brussels Belgium
Biochemical Journal (BIOCHEM. J.) (United Kingdom) 1991, 279/3 (831-836)
CODEN: BIJOA ISSN: 0264-6021
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The %%%tau%%%-immunoreactive A68 polypeptides found in brains from patients with Alzheimer's disease have been studied by Western blotting using (1) antibodies to synthetic peptides corresponding to sequences that span the complete human %%%tau%%% molecule, and (2) antibodies specific for inserts 1 and 2 found towards the N-terminus of some %%%tau%%% isoforms. The three major A68 polypeptides were labelled by all of the antibodies to sequences common to all %%%tau%%% isoforms, but the faster-migrating A68 polypeptide was not labelled by either of the two antibodies specific for inserts 1 and 2. Treatment with alkaline phosphatase of non-solubilized A68 did not change its electrophoretic mobility on SDS/PAGE under the conditions described here. However, A68 that was solubilized before treating it with alkaline phosphatase was found to move faster on SDS/PAGE than untreated A68, to a position similar to that of normal %%%tau%%%. We also confirmed that A68 preparations contain numerous paired helical filaments (PHF) . These PHF were labelled by all anti-%%%tau%%% antibodies, including insert-specific antibodies. Our results further support the notion that PHF contain abnormally %%%phosphorylated%%% %%%tau%%% in an aggregated state, and indicate that these abnormally %%%phosphorylated%%% %%%tau%%% forms are composed of several %%%tau%%% isoforms and that the full length of the %%%tau%%% molecule is present in these polypeptides.

4/7/80 (Item 7 from file: 73)
DIALOG(R)File 73:EMBASE

03970271 EMBASE No: 1989139267
Selective expression of epitopes in multiphosphorylation repeats of the high and middle molecular weight neurofilament proteins in Alzheimer neurofibrillary tangles
Trojanowski J.Q.; Schmidt M.L.; Otvos Jr. L.; Gur R.C.; Gur R.E.; Hurtig H.; Lee V.M.Y.
Department of Pathology and Laboratory Medicine, University of Pennsylvania School of Medicine, Hospital of University of Pennsylvania, Philadelphia, PA 19104-4283 United States
Annals of Medicine (ANN. MED.) (Finland) 1989, 21/2 (113-116)
CODEN: ANMDE ISSN: 0785-3890
DOCUMENT TYPE: Journal
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Here we review our recent 'epitope analyses' of a few of the fibrous intraneuronal inclusions that are distinctive hallmarks of human neurodenerative conditions using a large library of %%%monoclonal%%% antibodies (MAbs) raised to normal neuronal cytoskeletal proteins. Analyses of the low (NF-L), middle (NF-M), and high (NF-H) molecular weight neurofilament (NF) proteins with > 500 MAbs enumerated epitopes shared by NF proteins and the intraneuronal neurofibrillary tangles (NFTs) that occur in the hippocampus and brainstem of Alzheimer's disease (AD) subjects. We identified the NF-H multi-%%%phosphorylation%%% repeat domain, i.e. repeats of Lys-Ser-Pro-X (where X is a small uncharged amino acid and Ser acts as a phosphate acceptor), as the determinant recognized by 15/16 MAbs that detected NFTs in sections of AD hippocampus, and 11 of the same 16 MAbs recognised NF-M multi-%%%phosphorylation%%% repeats. Further, the antigen binding regions of these MAbs were shown to comprise 13 separate classes based on their differential binding to 12 synthetic peptides derived from the NF-H and NF-M multi-%%%phosphorylation%%% sites, NF subunits of 10 diverse mammalian and sub-mammalian species, and normal human %%%tau%%% (%%%tau%%%). None of these anti-NF MAbs recognized NFTs in the brainstem of subjects with progressive supranuclear palsy (PSP), but NFTs in AD brainstem sections were reactive with five of these MAbs. Both PSP and AD brainstem NFTs were recognized by MAbs specific for %%%tau%%% and paired helical filament antigens. Hirano bodies (HBs), another intraneuronal inclusion in the hippocampus of AD and non-AD subjects, were immunostained by 4 anti-NF MAbs, but none of these MAbs were specific for the NF-H and NF-M multi-%%%phosphorylation%%% repeats. These studies indicate that NF-H and NF-M multi-%%%phosphorylation%%% repeats are the most likely sequences in NF-H and NF-M present in NFTs, while %%%tau%%%-like determinants are more substantially represented in both AD and PSP NFTs. In contrast, HBs are immunologically distinct from NFTs. Thus, different pathological events are likely to account for the formation of each of these distinct lesions.

4/7/81 (Item 8 from file: 73)

DIALOG(R)File 73:EMBASE

03944470 EMBASE No: 1989113463
Aluminum-induced neurofibrillary degeneration affecfts a subset of neurons in rabbit cerebral cortex, basal forebrain and upper brainstem
Kowall N.W.; Pendlebury W.W.; Kessler J.B.; Perl D.P.; Beal M.F.
Department of Neurology, Massachusetts General Hospital, Boston, MA 02114
United States
Neuroscience (NEUROSCIENCE) (United Kingdom) 1989, 29/2 (329-337)
CODEN: NRSCD ISSN: 0306-4522
DOCUMENT TYPE: Journal
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Neurofibrillary tangles in Alzheimer's disease show a predilection for cortical pyramidal and subcortical projection neurons. The antigenic composition, neuronal specificity and distribution of aluminum-induced neurofibrillary degeneration were examined in regions of rabbit brain analogous to those that develop neurofibrillary tangles in Alzheimer's disease. Neurofibrillary degeneration was induced by intraventricular instillation of aluminum chloride. In aluminum-treated rabbits, intensely immunoreactive filamentous aggregates were seen in affected neuronal perikarya after staining with an anti-%%%phosphorylated%%% neurofilament
antibody (SMI 31), while in controls immunoreactivity was confined to axon-like elements. %%%Monoclonal%%% antibodies against Microtubule-associated protein 2 and %%%tau%%%, which stain human neurofibrillary tangles, did not stain aluminum-induced neurofibrillary degeneration. Pyramidal neurons exhibiting neurofibrillary degeneration formed a discrete linear pattern in layers III and V of cortex. Cortical somatostatin and nicotinamide adenine dinucleotide phosphate diaphorase-reactive neurons identified in double-stained sections were unaffected. Large perikarya in the vicinity of the globus pallidus, some of which contained acetylcholinesterase, were frequently SMI 31-immunoreactive. Among the cell groups affected in the upper brainstem were the nucleus raphe dorsalis and locus coeruleus. These findings show that aluminum-induced neurofibrillary degeneration differs antigenically from neurofibrillary tangles in Alzheimer's disease. Nevertheless, many neuronal subsets that are particularly suceptible to Alzheimer's disease, including cortical pyramidal neurons, basal forebrain cholinergic neurons and upper brainstem catecholaminergic neurons, are also affected by aluminum-induced neurofibrillary degeneration.

4/7/82 (Item 9 from file: 73)
DIALOG(R)File 73:EMBASE

03882293 EMBASE No: 1989051249
Immunocytochemical characterization of neurofibrillary tangles in amyotrophic lateral sclerosis and parkinsonism-dementia of Guam
Shankar S.K.; Yanagihara R.; Garruto R.M.; Grundke-Iqbal I.; Kosik K.S.; Gajdusek D.C.
Laboratory of Central Nervous System Studies, National Institute of Neurological and Communicative Disorders and Stroke, National Institutes of Health, Bethesda, MD United States
Annals of Neurology (ANN. NEUROL.) (United States) 1989, 25/2 (146-151)
CODEN: ANNED ISSN: 0364-5134
DOCUMENT TYPE: Journal
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Cryostat-cut sections of formalin-fixed and unfixed hippocampus from 23 Guamanian Chamorros with clinically and neuropathologically verified amyotrophic lateral sclerosis (ALS) (8 cases) and parkinsonism-dementia (PD) (15 cases) and from 12 neurologically normal Guamanians (5 with and 7 without neurofibrillary degeneration) were evaluated by the immunoperoxidase technique, using %%%monoclonal%%% antibodies against %%%phosphorylated%%% neurofilament, human fetal microtubule-associated
protein %%%tau%%%, and paired helical filaments. On immuostaining, all three antibodies showed intracellular tangles in the hippocampal neurons of patients with ALS, patients with PD, and in neurologically normal Guamanians with neurofibrillary pathology, but the correlation of immunostaining between these antibodies was not absolute. Extracellular or ghost tangles were immunostained only with the antibody against paired helical filaments. Our immunocytochemical data indicate that the antigenic composition of neurofibrillary tangles in Guamanian ALS and PD is similar to that Alzheimer's disease, suggesting a common pathogenic pathway for neurofibrillary tangle formation in these neurodegenerative disorders.

4/7/83 (Item 10 from file: 73)
DIALOG(R)File 73:EMBASE

03131993 EMBASE No: 1986199570
Abnormal %%%phosphorylation%%% of the microtubule-associated protein %%%tau%%% (%%%tau%%%) in Alzheimer cytoskeletal pathology
Grundke-Iqbal I.; Iqbal K.; Tung Y.-C.; et al.
New York State Institute for Basic Research in Developmental Disabilities, Staten Island, NY 10314 United States
Proceedings of the National Academy of Sciences of the United States of America (PROC. NATL. ACAD. SCI. U. S. A.) (United States) 1986, 83/13 (44913-4917)
CODEN: PNASA
DOCUMENT TYPE: Journal
LANGUAGE: ENGLISH

A %%%monoclonal%%% antibody to the microtubule-associated protein %%%tau%%% (%%%tau%%%) labeled some neurofibrillary tangles and plaque
neurites, the two major locations of paired-helical filaments (PHF), in Alzheimer disease brain. The antibody also labeled isolated PHF that had been repeatedly washed with NaDodSOinf 4. Dephosphorylation of the tissue
sections with alkaline phosphatase prior to immunolabeling dramatically increased the number of tangles and plaques recognized by the antibody. The
plaque core amyloid was not stained in either dephosphorylated or nondephosphorylated tissue sections. On immunoblots PHF polypeptides were labeled readily only when dephosphorylated. In contrast, a commercially available %%%monoclonal%%% antibody to a %%%phosphorylated%%% epitope of
neurofilaments that labeled the tangles and the plaque neurites in tissue did not label any PHF polypeptides on immunoblots. The PHF polypeptides, labeled with the %%%monoclonal%%% antibody to %%%tau%%%, electrophoresed
with those polypeptides recognized by antibodies to isolated PHF. The antibody to %%%tau%%%-labeled microtubules from normal human brains assembled in vitro but identically treated Alzheimer brain preparations had to be dephosphorylated to be completely recognized by this antibody. These findings suggest that %%%tau%%% in Alzheimer brain is an abnormally %%%phosphorylated%%% protein component of PHF.

4/7/84 (Item 1 from file: 76)
DIALOG(R)File 76:Life Sciences Collection

01843449 3633759
%%%Phosphorylation%%%-dependent epitopes of neurofilament antibodies on
%%%tau%%% protein and relationship with Alzheimer %%%tau%%%
Lichtenberg Kraag, B.; Mandelkow, E. M.; Biernat, J.; Steiner, B.; Schroeter, C.; Gustke, N.; Meyer, H.E.; Mandelkow, E.
Max-Planck-Unit for Struct. Mol. Biol., c/o DESY, Notkestr. 85, D-2000 Hamburg 52, FRG
PROC. NATL. ACAD. SCI. USA vol. 89, no. 12, pp. 5384-5388 (%%%1992%%%)
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Immunology Abstracts; CSA Neurosciences Abstracts

We have studied the %%%phosphorylation%%% of %%%tau%%% protein from
Alzheimer paired helical filaments, of %%%tau%%% from normal human brain,
and of recombinant %%%tau%%% isoforms. As a tool we used %%%monoclonal%%%
antibodies against neurofilament protein that crossreact with %%%tau%%% in

a %%%phosphorylation%%%-dependent manner. This allowed us to deduce the
state of %%%phosphorylation%%% in normal and pathological %%%tau%%%, as
well as antibody epitopes. The results suggest a role for the
%%%phosphorylation%%% sites in Alzheimer disease, as well as the
involvement of a Ser-Pro-directed protein kinase.

4/7/85 (Item 2 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
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01819917 3600945
A serine arrow right proline change in the Alzheimer's disease-associated epitope %%%Tau%%% 2 results in altered secondary structure, but %%%phosphorylation%%% overcomes the conformational gap
Lang, E.; Otvos, L.,Jr.
Wistar Inst. Anat. and Biol., 3601 Spruce St., Philadelphia, PA 19104, USA
BIOCHEM. BIOPHYS. RES. COMMUN. vol. 188, no. 1, pp. 162-169 (%%%1992%%%)
ISSN: 0006-291X
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: CSA Neurosciences Abstracts

%%%Monoclonal%%% antibody %%%Tau%%% 2 was raised against bovine %%%tau%%% protein, was reported to recognize a conformational epitope, and
stained %%%tau%%% was found in neurofibrillary tangles of Alzheimer's disease, but not normal human %%%tau%%% . We synthesized tetradeka peptides corresponding to the original bovine sequence, its serine arrow right proline substituted analog, the genuine human sequence of this region, and the bovine epitope %%%phosphorylated%%% on the crucial serine.
The secondary structure of the peptides was determined by circular dichroism. It was found that only the original bovine epitope showed a tendency to form the beta -pleated sheets characteristic of the neurofibrillary tangles. The spectra of the human peptide, its analog, and the %%%phosphorylated%%% bovine sequence were very similar, featuring a weak, helical beta -turn character.

4/7/86 (Item 1 from file: 94)
DIALOG(R)File 94:JICST-EPlus
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01734301 JICST ACCESSION NUMBER: 92A0755126 FILE SEGMENT: JICST-E
Anti-PHF %%%monoclonal%%% antibody M4 and C5 recognize fetal type %%%phosphorylation%%% of the %%%tau%%%.
WATANABE ATSUSHI (1); HASEGAWA SHIGETO (1); IHARA YASUO (1); ARAI TAKAO (2)
; TAKIO HIROSHI (3); SUZUKI MASAMI (4); CHITANI KOICHI (4)
(1) Univ. of Tokyo; (2) Science Univ. of Tokyo; (3) Inst. of Physical and Chemical Res.; (4)Fujitahoken'eiseidai
Shinkei Kagaku(Bulletin of the Japanese Society for Neurochemistry), %%%1992%%%, VOL.31,NO.1, PAGE.206-207, FIG.1, REF.6
JOURNAL NUMBER: Y0225AAP ISSN NO: 0037-3796
UNIVERSAL DECIMAL CLASSIFICATION: 616.8 591.18.05+591.481 576.311/.316
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Conference Proceeding
ARTICLE TYPE: Short Communication
MEDIA TYPE: Printed Publication

4/7/87 (Item 2 from file: 94)
DIALOG(R)File 94:JICST-EPlus
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01626289 JICST ACCESSION NUMBER: 92A0522921 FILE SEGMENT: JICST-E
Confocal microscopic immunocytochemistry of neuropil threads and neurofibrillary tangles in aged and Alzheimer's disease brains.
IWATSUBO TAKESHI (1)
(1) Univ. of Tokyo, Faculty of Medicine, Inst. of Brain Res.
Shinkei Kenkyu no Shinpo(Advances in Neurological Sciences), %%%1992%%%,
VOL.36,NO.3, PAGE.511-523, FIG.5, TBL.2, REF.42
JOURNAL NUMBER: Z0693AAP ISSN NO: 0001-8724
UNIVERSAL DECIMAL CLASSIFICATION: 616.83/.89
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Journal
ARTICLE TYPE: Original paper
MEDIA TYPE: Printed Publication
ABSTRACT: I studied immunocytochemically the neuropil threads and neurofibrillary tangles in aged and Alzheimer's disease brains using a confocal laser scanning fluorescence microscope. Some of the neuropil threads visualized by %%%tau%%% antibodies were shown to occur in small
dendrites, although the majority of the threads were not continuous with dendritic branches. This may suggest that normal neuronal cytoskeletons are liable to disappear in thread-bearing neurites. Double-labelling with %%%tau%%%/ubiquitin antibodies revealed that ubiquitin-immunoreactivities were lacking at one, or more often, both ends of the %%%tau%%%-positive threads. It is reasonable to speculate that the thread ends were newly formed portions, and thus the threads grow bidirectionally in dendritic branches. A PHF %%%monoclonal%%% antibody C5, which recognizes a %%%phosphorylated%%% epitope in the carboxyl third of %%%tau%%%, stained both intra- and extracellular NFTs, while antibodies to N-terminus of %%%tau%%% stained only the intracellular ones. N-terminus of %%%tau%%% appears to be removed, once
PHFs are exposed to extracellular environment. (author abst.)

4/7/88 (Item 3 from file: 94)
DIALOG(R)File 94:JICST-EPlus
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01541804 JICST ACCESSION NUMBER: 92A0298363 FILE SEGMENT: JICST-E
Molecular Biology in the Investigation of Dementia. PHF: From the Viewpoint of A68 (Abnormally %%%Phosphorylated%%% %%%Tau%%%).
ENDO RIUKO (1); MORI HIROSHI (1)
(1) Univ. of Tokyo, Faculty of Medicine, Inst. of Brain Res.
Saishin Igaku, %%%1992%%%, VOL.47,NO.4, PAGE.593-601, FIG.5, TBL.2, REF.26
JOURNAL NUMBER: Z0358AAR ISSN NO: 0370-8241 CODEN: SAIGA
UNIVERSAL DECIMAL CLASSIFICATION: 616.831/.832+.85
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Journal
ARTICLE TYPE: Commentary
MEDIA TYPE: Printed Publication
ABSTRACT: Alzheimer's disease is the most common cause of dementia in elderly people. Severity of dementia correlates with brain content of two filamentous lesions: neurofibrillary tangles and senile plaques. Neurofibrillary tangles are made up of abnormal filaments, paired helical filaments composed of %%%tau%%% containing several isoforms (Mr
40,000 to Mr 60,000) that are associated with axonal microtubules. %%%Tau%%% forms in PHF are abnormally %%%phosphorylated%%% and show
characteristic retarded mobility on SDS polyacrylamide gel electrophoresis. Because of its apparent molecular weight, %%%tau%%% in
PHF is referred to as A68; it has been identified as an antigen for Alz-50, a %%%monoclonal%%% antibody. A68 merits attention because it reveals the morphology of PHF on electron microscopy. Detailed examination for A68 may elucidate the mechanism of the pathogenesis of neurofibrillary tangles ; further, prevention of abnormal %%%phosphorylation%%% of %%%tau%%% may suggest new therapeutic approaches. (author abst.)

4/7/89 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal
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10511919 PASCAL No.: 93-0021170
A serine rightarrow proline change in the Alzheimer's disease-associated epitope %%%Tau%%% 2 results in altered secondary structure, but

%%%phosphorylation%%% overcomes the conformational gap
LANG E; OTVOS L JR
Wistar inst. anatomy biology, Philadelphia PA 19104, USA
Journal: Biochemical and biophysical research communications, %%%1992%%%
, 188 (1) 162-169
ISSN: 0006-291X CODEN: BBRCA9 Availability: INIST-8252; 354000032123140240
No. of Refs.: 40 ref.
Document Type: P (Serial) ; A (Analytic)
Country of Publication: USA
Language: English
%%%Monoclonal%%% antibody %%%Tau%%% 2 was raised against bovine
%%%tau%%% protein, was reported to recognize a conformational epitope, and
stained %%%tau%%% was found in neurofibrillary tangles of Alzheimer's disease, but not normal human %%%tau%%% . We synthesized tetradeka
peptides corresponding to the original bovine sequence, its serine rightarrow proline substituted analog, the genuine human sequence of this region, and the bovine epitope %%%phosphorylated%%% on the crucial serine.
The secondary structure of the peptides was determined by circular dichroism

4/7/90 (Item 2 from file: 144)
DIALOG(R)File 144:Pascal
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10447395 PASCAL No.: 92-0650878
Immunological and conformational characterization of a %%%phosphorylated%%% immunodominant epitope on the paired helical filaments
found in Alzheimers's disease
LANG E; SZENDREI G I; LEE V M Y; OTVOS L JR
Wistar inst. anatomy biology, Philadelphia PA 19104, USA
Journal: Biochemical and biophysical research communications, %%%1992%%%
, 187 (2) 783-790
ISSN: 0006-291X CODEN: BBRCA9 Availability: INIST-8252; 354000031587310340
No. of Refs.: 28 ref.
Document Type: P (Serial) ; A (Analytic)
Country of Publication: USA
Language: English
The immunological recognition pattern of one of the most commonly used %%%monoclonal%%% antibodies, PHF-1, which detects the paired helical
filaments of Alzheimer's disease, exhibits a high degree of similanty with the recognition of a polyclonal antibody, anti-T3P, raised against a synthetic phosphopeptide, GAEIVYKS(Phospho)PVVSGD, corresponding to amino
acids 389-402 of the microtubule-associated protein %%%tau%%% . A panel of
16 synthetic non-%%%phosphorylated%%% and %%%phosphorylated%%% peptides,
excised from different regions of %%%tau%%% and eptide analogs thereof,
were used to show that PHF-1 is indeed directed against the T3 fragment

4/7/91 (Item 3 from file: 144)
DIALOG(R)File 144:Pascal
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09353966 PASCAL No.: 91-0144344
Cyclic AMP agonists induce the %%%phosphorylation%%% of phospholipase C-
%%%tau%%% and of a 76kDa protein co-precipitated by anti-(phsopholipase C-
%%%tau%%%) %%%monoclonal%%% antibodies in BABL/c-3T3 cells : relationship
to inositol phosphate formation
OLASHAW N E; RHEE S G; PLEDGER W J
Vanderbilt univ. school medicine, dep. cell biology, Nashville TN 37232, USA
Journal: Biochemical journal : (London. 1984), %%%1990%%%, 272 (2) 297-303
ISSN: 0264-6021 Availability: INIST-5003; 354000018336160020/NUM; INSERM-032
No. of Refs.: 38 ref.
Document Type: P (Serial) ; A (Analytic)
Country of Publication: United Kingdom
Language: English
Previous studies have demonstrated enhanced %%%phosphorylation%%% of
phospholipase C- %%%tau%%% (PLC- %%%tau%%%), a key regulatory enzyme in
phosphoinositide metabolism, in cells treated with platelet-derived growth factor (PDGF) and epidermal growth factor, both a which act via specific receptor tyrosine kinases. Our studies on BALB/c-3T3 cells show that agents
that promote cellular cyclic AMP accumulation also increase the %%%phosphorylation%%%, specifically the serine %%%phosphorylation%%%, of
this enzyme. Increased %%%phosphorylation%%% of PLC- %%%tau%%% (2-3-fold)
was evident within 5-10 min of addition of isobutylmethylxanthine (IBMX) and either cholera toxin or forskolin to cells, and persisted for at least
3 h. Treatment of cells with cyclic AMP agonists also enhanced, with similar kinetics, the %%%phosphorylation%%% of a 76 kDa protein co-precipitated by anti-PLC- %%%tau%%% %%%monoclonal%%% antibodies. Brief
exposure of cells to cholera toxin/IBMX or forskolin/IBMX decreased inositol phosphate formation induced by the GTP-binding protein (G-protein) activator aluminium fluoride by approx. 50 %, but was without effect on PDGF-stimulated inositol phosphate formation. These findings suggest that PLC- %%%tau%%% , and perhaps the 76 kDa co-precipitated protein, are
substrates of cyclic AMP-dependent protein kinase in BALB/c-3T3 cells; however, the lack of effect of cyclic AMP elevation on PDGF-stimulated inositol phosphate formation indicates that the intrinsic activity of PLC-%%%tau%%% is unaltered by cyclic AMP-mediated %%%phosphorylatio%%%

4/7/92 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07582712 93111483 PMID: 1471723
Cytoskeletal immunohistochemistry of central neurocytomas.
Hessler R B; Lopes M B; Frankfurter A; Reidy J; VandenBerg S R
Department of Pathology, University of Virginia, Charlottesville.
American journal of surgical pathology (UNITED STATES) Nov %%%1992%%%,
16 (11) p1031-8, ISSN 0147-5185 Journal Code: 7707904
Contract/Grant No.: T32 NS 7236; NS; NINDS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Central neurocytomas are rare intraventricular tumors. Patients with such tumors have a favorable prognosis after surgical removal. These tumors may be misdiagnosed as neuroblastomas or gliomas, risking the complications of adjuvant therapy. Diagnosis of central neurocytoma requires that the tumor shows the ultrastructural features of mature neuronal differentiation, including the presence of synapses and dense-core and clear vesicles in addition to profiles of neuritic processes with microtubules. The cytoskeletal phenotype of central neurocytomas has not been previously characterized, but it may facilitate their definitive recognition when ultrastructural examination is not possible. Ten central neurocytomas were examined by immunohistochemistry for %%%phosphorylation%%% -dependent/independent neurofilament epitopes, neuron-associated class III
beta-tubulin, microtubule-associated proteins (MAP2, %%%tau%%%), and glial
fibrillary acidic protein (GFAP). The neuronal nature of all neoplasms was documented by immunoreactivity for synaptophysin in nine tumors and for %%%phosphorylation%%% -independent neurofilament-H/M in the remaining

case.
Electron microscopy in four cases showed synapses and dense core vesicles. All tumors were immunoreactive for class III beta-tubulin and MAP2, which
were seen in cytoskeletal structures by immunoelectron microscopy. Two thirds of the cases were immunohistochemically positive for neurofilament epitopes. None of the tumor cells displayed GFAP immunoreactivity, although reactive astrocytes were present. These data suggest that central neurocytomas may be recognized by synaptophysin immunoreactivity and that
the expression of cytoskeletal epitopes indicates that these tumors are well-differentiated neuronal neoplasms.
Record Date Created: 19930126

4/7/93 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07574924 93101309 PMID: 1465214
%%%Tau%%% pathology in a case of familial Alzheimer's disease with a valine to glycine mutation at position 717 in the amyloid precursor protein.
Hanger D P; Mann D M; Neary D; Anderton B H
Department of Neuroscience, Institute of Psychiatry, London, UK.
Neuroscience letters (NETHERLANDS) Oct 12 %%%1992%%%, 145 (2)
p178-80, ISSN 0304-3940 Journal Code: 7600130
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The brain tissue from a case of familial Alzheimer's disease (FAD) caused by a missense (valine to glycine) mutation at codon 717 of the amyloid precursor protein (APP) gene has been examined for the presence of abnormally %%%phosphorylated%%% paired helical filament %%%tau%%% (PHF-
%%%tau%%%). There was abundant PHF-%%%tau%%% present, which on Western
blots, was indistinguishable from the PHF-%%%tau%%% typical of cases of
sporadic Alzheimer's disease and that of another FAD mutation (valine to isoleucine), previously (Neurosci. Lett., 137 (1992) 221-224). This result implies that the cytoskeletal pathology in Alzheimer's disease is biochemically linked to abnormal APP processing and amyloid deposition.
Record Date Created: 19930119

4/7/94 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07513573 93038653 PMID: 1384476
A serine-->proline change in the Alzheimer's disease-associated epitope %%%Tau%%% 2 results in altered secondary structure, but %%%phosphorylation%%% overcomes the conformational gap.
Lang E; Otvos L
Wistar Institute of Anatomy and Biology, Philadelphia, PA 19104.
Biochemical and biophysical research communications (UNITED STATES) Oct
15 %%%1992%%%, 188 (1) p162-9, ISSN 0006-291X Journal Code: 0372516
Contract/Grant No.: AG 10670; AG; NIA
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
%%%Monoclonal%%% antibody %%%Tau%%% 2 was raised against bovine %%%tau%%%
protein, was reported to recognize a conformational epitope, and stained %%%tau%%% was found in neurofibrillary tangles of Alzheimer's disease, but
not normal human %%%tau%%%. We synthesized tetradeka peptides corresponding
to the original bovine sequence, its serine-->proline substituted analog, the genuine human sequence of this region, and the bovine epitope %%%phosphorylated%%% on the crucial serine. The secondary structure of the
peptides was determined by circular dichroism. It was found that only the original bovine epitope showed a tendency to form the beta-pleated sheets characteristic of the neurofibrillary tangles. The spectra of the human peptide, its analog, and the %%%phosphorylated%%% bovine sequence were very
similar, featuring a weak, helical beta-turn character. Eventual %%%phosphorylation%%% of epitopes of this otherwise heavily %%%phosphorylated%%% protein may overcome inter-species conformational
gaps.
Record Date Created: 19921119

4/7/95 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07281845 92212933 PMID: 1557394
A protein kinase associated with paired helical filaments in Alzheimer disease.
Vincent I J; Davies P
Department of Pathology, Albert Einstein College of Medicine, Bronx, NY 10461.
Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Apr 1 %%%1992%%%, 89 (7) p2878-82, ISSN
0027-8424 Journal Code: 7505876
Contract/Grant No.: AG06803; AG; NIA; MH38623; MH; NIMH
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
We have identified a protein kinase in immunoaffinity-purified preparations of paired helical filaments from brain tissue of individuals with Alzheimer disease. The kinase %%%phosphorylates%%% the filament
proteins in vitro in a manner independent of second messenger regulation or of modulation by heparin and polyamines. Physiological concentrations of hemin, an oxidized heme porphyrin, inhibit the kinase and abolish Alz-50 immunoreactivity of the proteins. Since paired helical filaments are composed of hyperphosphorylated proteins, association of a protein kinase with the filaments provides a mechanism for abnormal processing of the proteins in disease.
Record Date Created: 19920506

4/7/96 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07237565 92177459 PMID: 1795405
Regional variation in the abundance of axonal cytoskeletal proteins.
Watson D
Department of Neurology, Wayne State University School of Medicine, Detroit, Michigan 48201.
Journal of neuroscience research (UNITED STATES) Sep %%%1991%%%, 30
(1) p226-31, ISSN 0360-4012 Journal Code: 7600111
Contract/Grant No.: NS00983; NS; NINDS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The relative abundance of several axonal cytoskeletal proteins was determined by immunoassay at various sites in the peripheral and central nervous systems of adult rats. Within the peripheral nervous system, the ratio of tubulin to neurofilaments was greatest for nerves composed of unmyelinated axons and least for nerves with large myelinated axons. MAP1 protein was more prominent in unmyelinated fibers; conversely %%%tau%%%
proteins were relatively more abundant in large myelinated axons. An immunochemical index of neurofilament %%%phosphorylation%%% was less for
unmyelinated fibers than for myelinated ones. In the fimbria-fornix, pyramidal tract, and superior cerebellar peduncle, similar trends were observed: small axons had more MAP1, less %%%tau%%%, and a greater ratio of
tubulin to neurofilament proteins. The %%%phosphorylation%%% index

test for the superior cerebellar peduncle, the tract with the largest
The immunochemical index of neurofilament
osphorylation%%% was
for the optic nerve than for axonal tracts in the brain proper.
results suggest that development of large myelinated axons is
ated with greater neurofilament content, neurofilament
phosphorylation%%%, and with greater abundance of %%%tau%%%
roteins in
the CNS and the PNS; however, quantitative aspects of these relationships differ in the PNS and the CNS.
Record Date Created: 19920408

4/7/97 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06829233 91126483 PMID: 1899488
A68: a major subunit of paired helical filaments and derivatized forms of normal %%%Tau%%%.
Lee V M; Balin B J; Otvos L; Trojanowski J Q
Department of Pathology and Laboratory Medicine, University of Pennsylvania School of Medicine, Philadelphia 19104.
Science (UNITED STATES) Feb 8 %%%1991%%%, 251 (4994) p675-8, ISSN
0036-8075 Journal Code: 0404511
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Putative Alzheimer disease (AD)-specific proteins (A68) were purified to homogeneity and shown to be major subunits of one form of paired helical filaments (PHFs). The amino acid sequence and immunological data indicate that the backbone of A68 is indistinguishable from that of the protein %%%tau%%% (%%%tau%%%), but A68 could be distinguished from normal human
%%%tau%%% by the degree to which A68 was %%%phosphorylated%%% and by the
specific residues in A68 that served as phosphate acceptors. The larger apparent relative molecular mass (Mr) of A68, compared to normal human %%%tau%%%, was attributed to abnormal %%%phosphorylation%%% of A68 because
enzymatic dephosphorylation of A68 reduced its Mr to close to that of normal %%%tau%%%. Moreover, the LysSerProVal motif in normal human
%%%tau%%% appeared to be an abnormal %%%phosphorylation%%% site in A68
because the Ser in this motif was a phosphate acceptor site in A68, but not in normal human %%%tau%%%. Thus, the major subunits of a class of PHFs are
A68 proteins and the excessive or inappropriate %%%phosphorylation%%% of
normal %%%tau%%% may change its apparent Mr, thus transforming %%%tau%%%
into A68.
Record Date Created: 19910313

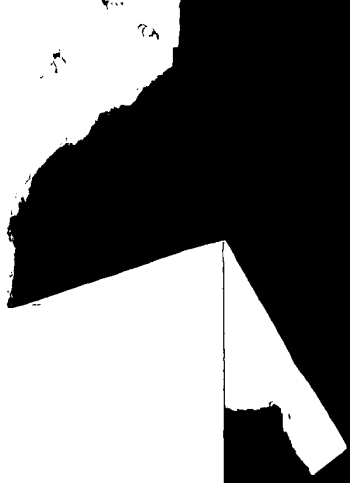
4/7/98 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06460368 90164679 PMID: 1689542
The neuroendocrine and neural profiles of neuroblastomas, ganglioneuroblastomas, and ganglioneuromas.
Molenaar W M; Baker D L; Pleasure D; Lee V M; Trojanowski J Q
Department of Pathology and Laboratory Medicine, University of Pennsylvania, Philadelphia 19104.
American journal of pathology (UNITED STATES) Feb %%%1990%%%, 136 (2)
p375-82, ISSN 0002-9440 Journal Code: 0370502
Contract/Grant No.: CA-36245; CA; NCI; CA-47983; CA; NCI; NS-08075; NS; NINDS; +
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
To establish the neuroendocrine and neural features of peripheral neuroblastic tumors, a prospectively collected group of 12 neuroblastomas (NB), 2 ganglioneuroblastomas (GNB), and 4 ganglioneuromas (GN) was probed
with a panel of %%%monoclonal%%% antibodies (MAbs) to neuroendocrine and
neural antigens. All tumors expressed the pan-neuroendocrine markers synaptophysin and chromogranin A. They also showed extensive expression of
neuronal antigens, ie, of each of the neurofilament (NF) triplet proteins and of the microtubule-associated proteins (MAPs) MAP2 and %%%tau%%%
-protein. However, only in the GNBs and GNs was the pattern of NF phosphoisoforms relatively mature. In the latter tumors glial fibrillary acidic protein (GFAP) and myelin basic protein (MBP) could be demonstrated as well, suggesting the presence of nonmyelinating and myelinating Schwann cells, respectively. The glial markers did not colocalize with the neural markers. On the basis of these data, it was concluded that all peripheral neuroblastic tumors manifest molecular characteristics of neuroendocrine cells and of neurons. The latter were most developed in GNBs and GNs, in which they were accompanied by Schwann cell differentiation in a separate population of cells. The above-outlined neuronal profile of peripheral neuroblastic tumors, including NBs, distinguishes this group of tumors from the much-less neuronally differentiated primitive neuroectodermal tumors of
the central nervous system.
Record Date Created: 19900326

4/7/99 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06428736 90132789 PMID: 1688924
Modified Bielschowsky and immunocytochemical studies on cerebellar plaques in Alzheimer's disease.
Suenaga T; Hirano A; Llena J F; Ksiezak-Reding H; Yen S H; Dickson D W
Department of Pathology, Montefiore Medical Center, Bronx, NY 10467.
Journal of neuropathology and experimental neurology (UNITED STATES) Jan %%%1990%%%, 49 (1) p31-40, ISSN 0022-3069 Journal Code: 2985192R
Contract/Grant No.: AG06803; AG; NIA; AG4145; AG; NIA
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Senile plaques (SP) in the cerebellum of 23 cases of Alzheimer's disease (AD), three with widespread amyloid angiopathy, were studied with a modified Bielschowsky stain and immunocytochemical methods using antibodies
to a beta-amyloid synthetic peptide (beta ASP), %%%phosphorylated%%%
neurofilament proteins, ubiquitin, %%%tau%%% protein, and glial fibrillary acidic protein (GFAP). The four subtypes of SP (diffuse plaques, compact plaques, perivascular plaques, and subpial fibrillar deposits) that were observed with the modified Bielschowsky stain were also stained with antibodies to beta ASP. Many cerebellar SP contained ubiquitin-positive granular elements resembling dystrophic neurites. In contrast to neuritic elements in cerebral SP in AD, ubiquitin-positive elements in cerebellar SP were not labeled with antibodies to %%%phosphorylated%%% neurofilament or
%%%tau%%% proteins. Various degrees of glial reaction were observed in all
subtypes of SP except diffuse plaques. The absence of %%%phosphorylated%%%
neurofilament and %%%tau%%% epitopes in neuritic elements in cerebellar SP
is not surprising since paired helical filaments have not been seen in the cerebellum. Nevertheless, our results suggest that cerebellar SP are frequently associated with dystrophic neurites.
Record Date Created: 19900226

4/7/100 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)



0640945I 90099531 PMID: 2557644
%%%Tau%%% and ubiquitin immunoreactivity at different stages of formation
of Alzheimer neurofibrillary tangles.
Bancher C; Brunner C; Lassmann H; Budka H; Jellinger K; Seitelberger F; Grundke-Iqbal I; Iqbal K; Wisniewski H M
Neurological Institute, University of Vienna, Austria.
Progress in clinical and biological research (UNITED STATES) %%%1989%%%
, 317 p837-48, ISSN 0361-7742 Journal Code: 7605701
Contract/Grant No.: AG 04220; AG; NIA; AG 05892; AG; NIA; NS 18105; NS;
NINDS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
In his original 1911 publication Alois Alzheimer classified neurofibrillary tangles (ANT) into three morphologically defined subgroups according to their stage of maturation. The present study shows that changes in the morphological appearance of ANT during their maturation process are accompanied by changes in their antigenic profile. As shown by several immunocytochemical studies these abnormal
%%%phosphorylated%%%
microtubule-associated protein %%%tau%%% and of ubiquitin. In this study,
immunoreactivity for the altered %%%tau%%% is not only seen in a subset of
tangles but also in the cytoplasm of some nerve cells lacking ANT, which we believe to be at a stage of neuronal alteration preceding the formation of compact tangles (Stage 0 tangles). Similar numbers of Stage 0 tangles are present in the brains of age-matched non-demented individuals as in Alzheimer cases, but are absent in young controls lacking ANT. In extracellular "ghost tangles", the ultimate stage of neurofibrillary degeneration, immunoreactivity for %%%tau%%% is accessible to antibodies
only when tissue sections are pretreated with formic acid to uncover the binding sites. In contrast to %%%tau%%% , presence/accessibility of an epitope residing on residues 50-65 of ubiquitin recognized by a %%%monoclonal%%% antibody raised to paired helical filaments (3-39) increases during the maturation of ANT and is most pronounced in "ghost tangles". Appearance/uncovering of the 3-39 epitope and masking of %%%tau%%% reactivity during tangle maturation may reflect degradation or
conformational changes in the pathological filaments due to their aging and the final loss of their parent nerve cells.
Record Date Created: 19900131

4/7/101 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06272525 89351937 PMID: 2475148
The reinterpretation of the immunochemical study of Alzheimer neurofibrillary tangles.
Nukina N
Center for Neurologic Diseases, Harvard Medical School Brigham and Women's Hospital, Boston, Massachusetts.
Annals of medicine (FINLAND) %%%1989%%%, 21 (2) p117-9, ISSN
0785-3890 Journal Code: 8906388
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Many studies have been done on neurofibrillary tangles occurring in Alzheimer's disease using antibodies, but without agreement on the interpretation of the results. Immunochemical studies using antibodies to neurofilament and %%%tau%%% and the antibody, Alz50, were carried out to
estaslish a common view. The results suggest that: 1) antibodies to neurofilament recognizing tangles react with the
%%%phosphorylated%%%
epitope of %%%tau%%% in paired helical filaments; 2) Alz50 reacts with abnormal %%%tau%%%, which has slower electrophoretic mobility than normal
%%%tau%%%; and 3) a certain part of %%%tau%%% has the protease-resistant
property in brains affected by the disease. (19 Refs.)
Record Date Created: 19891005

4/7/102 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05909622 88310474 PMID: 3136867
Alzheimer's disease: study of the distribution of %%%tau%%% proteins constituting helical filament pairs in human central nervous tissue]
Maladie d'Alzheimer: Etude de la distribution des proteines %%%tau%%%
constitutives des paires de filaments en helice dans le tissu nerveux central humain.
Parent M; Delacourte A; Defossez A; Hemon B; Han K K; Petit H
Laboratoire de Neurosciences, I.N.S.E.R.M. U n. 16, A.D.E.R.M., Faculte de Medecine de Lille.
Comptes rendus de l'Academie des sciences. Serie III, Sciences de la vie (FRANCE) %%%1988%%%, 306 (13) p391-7, ISSN 0764-4469 Journal Code:
8503078
Document type: Journal Article ; English Abstract
Languages: FRENCH
Main Citation Owner: NLM
Record type: Completed
%%%Tau%%% proteins are the major components of Paired Helical Filaments
(PHF) of Alzheimer's disease. Using the immunoblot technique and an antiserum against PHF, we have studied the distribution of %%%Tau%%%
proteins in the different areas of normal human brains and Alzheimer brains. %%%Tau%%% proteins were clearly present in cortical grey matter but
were difficult to detect in the white matter. In Alzheimer brains, we observed two differences: first, there is an important background due to the partial dissociation of the lesions containing %%%Tau%%% aggregates. Second, the profile of %%%Tau%%% proteins is modified, due to abnormal
%%%phosphorylation%%%. Thus, %%%Tau%%% proteins are found in large amounts
in the grey matter of the cortical areas and are not exclusively distributed in the axonal domain. The normal cortical distribution of %%%Tau%%% in the human brain correlates well with the distribution of histological lesions that contain PHF (neurofibrillary tangles and neuritic plaques) in the Alzheimer cortex.
Record Date Created: 19880930

4/7/103 (Item 12 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05219651 86267071 PMID: 3089107
%%%Tau%%% microheterogeneity: an immunological approach with %%%monoclonal%%% antibodies.
Fellous A; Ohayon R; Mazie J C; Rosa F; Luduena R F; Prasad V
Annals of the New York Academy of Sciences (UNITED STATES) %%%1986%%%,
466 p240-56, ISSN 0077-8923 Journal Code: 7506858
Contract/Grant No.: CA 26276; CA; NCI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The family of %%%tau%%% polypeptides purified from mammalian brain
exhibit both extensive heterogeneity and large similarities in their chemical, physical, and functional properties. All the %%%tau%%% isoforms
generated at a transcriptional or posttranscriptional level share the property of interacting with tubulin dimers in a specific manner. They strengthen longitudinal interactions between tubulin dimers and thus may stabilize microtubules once they are formed. Mild proteolysis or %%%phosphorylation%%% does not remove but only modulates the %%%tau%%%

speci,ic function that is probably related to the conserved sequences of the molecules. %%%Monoclonal%%% antibodies raised against %%%tau%%% were
found to recognize epitopes conserved not only between species but also in different tissues. Using indirect immunofluorescence, a specific staining pattern was observed on rat neuronal cells and also on human skin fibroblasts. The same antibodies did not recognize glial cells, suggesting that these cells either do not contain detectable levels of %%%tau%%% or contain %%%tau%%% molecules different from the neuronal ones. These data
suggest that %%%tau%%% protein is widely distributed, highly conserved, and
may be preferentially associated with special subclasses of microtubules.
Record Date Created: 19860814

4/7/104 (Item 13 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05026439 86105177 PMID: 2867809
Cultured neurons contain a variety of microtubule-associated proteins.
Peng I; Binder L I; Black M M
Brain research (NETHERLANDS) Dec 30 %%%1985%%%, 361 (1-2) p200-11,
ISSN 0006-8993 Journal Code: 0045503
Contract/Grant No.: NS17681; NS; NINDS; S 07 RR-0547; RR; NCRR
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The non-tubulin proteins associated with microtubules (MAPs) in cultures of pure sympathetic neurons have been identified using a variety of biochemical and immunochemical methods. MAPs of cultured sympathetic
neurons include proteins corresponding to brain MAP-1 (consisting of MAP-1a and MAP-1b species), MAP-2, MAP-3, %%%tau%%%, 4 proteins that range in
molecular weight from 60,000 to 76,000, and proteins with molecular weights
of 210,000, 130,000 and 32,000. Many of the MAPs are %%%phosphorylated%%%
in situ. MAP-2 and %%%tau%%% of cultured sympathetic neurons differ from
their counterparts of brain in electrophoretic mobility. The observed variety of MAPs in sympathetic neurons together with the differences in MAPs of brain and sympathetic neurons are discussed in terms of microtubule
heterogeneity in the nervous system.
Record Date Created: 19860324

4/7/105 (Item 1 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
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09735631 Genuine Article#: AT454 Number of References: 37
Title: %%%TAU%%%-PROTEIN BECOMES LONG AND STIFF UPON %%%PHOSPHORYLATION%%%
- CORRELATION BETWEEN PARACRYSTALLINE STRUCTURE AND DEGREE OF
%%%PHOSPHORYLATION%%%
Author(s): HAGESTEDT T; LICHTENBERG B; WILLE H; MANDELKOW EM; MANDELKOW E
Corporate Source: MAX PLANCK UNIT STRUCT MOLEC BIOL/D-2000 HAMBURG 52//FED
REP GER/
Journal: JOURNAL OF CELL BIOLOGY, %%%1989%%%, V109, N4, P1643-1651
Language: ENGLISH Document Type: ARTICLE

4/7/106 (Item 2 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
(c) 1998 Inst for Sci Info. All rts. reserv.

09539517 Genuine Article#: T0136 Number of References: 13
Title: DIRECT BIOCHEMICAL-EVIDENCE FOR AN ABNORMAL %%%PHOSPHORYLATION%%% OF
%%%TAU%%% PROTEINS DURING ALZHEIMERS-DISEASE
Author(s): FLAMENT S; DELACOURTE A; HEMON B; DEFOSSEZ A
Corporate Source: FAC MED LILLE,ADERMA,NEUROSCI LAB,INSERM,UNITE 16/F-59045
LILLE//FRANCE/
Journal: COMPTES RENDUS DE L ACADEMIE DES SCIENCES SERIE III-SCIENCES DE LA
VIE, %%%1989%%%, V308, N3, P77-82
Language: FRENCH Document Type: ARTICLE

4/7/107 (Item 3 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
(c) 1998 Inst for Sci Info. All rts. reserv.

08836546 Genuine Article#: N7766 Number of References: 41
Title: ALZ-50, A %%%MONOCLONAL%%%-ANTIBODY TO ALZHEIMERS-DISEASE ANTIGEN,
CROSS-REACTS WITH %%%TAU%%%-PROTEINS FROM BOVINE AND NORMAL HUMAN-BRAIN
Author(s): KSIEZAKREDING H; DAVIES P; YEN SH
Corporate Source: YESHIVA UNIV ALBERT EINSTEIN COLL MED,DEPT PATHOL/BRONX//NY/10461
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, %%%1988%%%, V263, N17, P7943-7947
Language: ENGLISH Document Type: ARTICLE

4/7/108 (Item 4 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
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08738468 Genuine Article#: N0443 Number of References: 20
Title: THE %%%MONOCLONAL%%%-ANTIBODY, ALZ 50, RECOGNIZES %%%TAU%%%-PROTEINS
IN ALZHEIMERS-DISEASE BRAIN
Author(s): NUKINA N; KOSIK KS; SELKOE DJ
Corporate Source: BRIGHAM & WOMENS HOSP,CTR NEUROL DIS,DEPT MED NEUROL,75
FRANCIS ST/BOSTON//MA/02115; HARVARD UNIV,SCH MED,DEPT NEUROL
NEUROSCI/BOSTON//MA/02115
Journal: NEUROSCIENCE LETTERS, %%%1988%%%, V87, N3, P240-246
Language: ENGLISH Document Type: ARTICLE

4/7/109 (Item 5 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
(c) 1998 Inst for Sci Info. All rts. reserv.

06516517 Genuine Article#: AKC67 Number of References: 54
Title: DEPHOSPHORYLATION OF MICROTUBULE-ASSOCIATED PROTEIN-2, %%%TAU%%%
-FACTOR, AND TUBULIN BY CALCINEURIN
Author(s): GOTO S; YAMAMOTO H; FUKUNAGA K; IWASA T; MATSUKADO Y; MIYAMOTO E
Corporate Source: KUMAMOTO UNIV,SCH MED,DEPT PHARMACOL/KUMAMOTO 860//JAPAN/
; KUMAMOTO UNIV,SCH MED,DEPT NEUROSURG/KUMAMOTO 860//JAPAN/
Journal: JOURNAL OF NEUROCHEMISTRY, %%%1985%%%, V45, N1, P276-283
Language: ENGLISH Document Type: ARTICLE

4/7/110 (Item 6 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
(c) 1998 Inst for Sci Info. All rts. reserv.

06295666 Genuine Article#: ACC69 Number of References: 45
Title: CA-2', CALMODULIN-DEPENDENT REGULATION OF MICROTUBULE FORMATION VIA
%%%PHOSPHORYLATION%%% OF MICROTUBULE-ASSOCIATED PROTEIN-2, %%%TAU%%%

-FACTOR, AND TUBULIN, AND COMPARISON WITH THE CYCLIC AMP-DEPENDENT
%%%PHOSPHORYLATION%%%
Author(s): YAMAMOTO H; FUKUNAGA K; GOTO S; TANAKA E; MIYAMOTO E
Corporate Source: KUMAMOTO UNIV,SCH MED,DEPT PHARMACOL/KUMAMOTO 860//JAPAN/
Journal: JOURNAL OF NEUROCHEMISTRY, %%%1985%%%, V44, N3, P759-768
Language: ENGLISH Document Type: ARTICLE

4/7/111 (Item 7 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
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05749895 Genuine Article#: SP385 Number of References: 34
Title: %%%PHOSPHORYLATION%%% AFFECTS THE ABILITY OF %%%TAU%%%-PROTEIN TO
PROMOTE MICROTUBULE ASSEMBLY
Author(s): LINDWALL G; COLE RD
Corporate Source: UNIV CALIF BERKELEY,DEPT BIOCHEM/BERKELEY//CA/94720
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, %%%1984%%%, V259, N8, P5301-5305
Language: ENGLISH Document Type: ARTICLE
? ds

Set	Items	Description
S1	1305	TAU AND PHOSPHORYL? AND (MONOCLONAL OR MAB)
S2	599	RD S1 (unique items)
S3	304	S2 AND PY<1996
S4	111	S3 AND PY<1993

? e au=mercken m

Ref	Items	Index-term
E1	2	AU=MERCKEN LOY
E2	15	AU=MERCKEN LUC
E3	137	*AU=MERCKEN M
E4	60	AU=MERCKEN M.
E5	2	AU=MERCKEN M.M.
E6	31	AU=MERCKEN MARC
E7	1	AU=MERCKEN MARC M
E8	2	AU=MERCKEN MARK
E9	1	AU=MERCKEN MM
E10	1	AU=MERCKEN, ARC
E11	1	AU=MERCKEN, H. P. F.
E12	40	AU=MERCKEN, L.

Enter P or PAGE for more

? s e3-e9

	137	AU=MERCKEN M
	60	AU=MERCKEN M.
	2	AU=MERCKEN M.M.
	31	AU=MERCKEN MARC
	1	AU=MERCKEN MARC M
	2	AU=MERCKEN MARK
	1	AU=MERCKEN MM
S5	234	E3-E9

? e au=mandeldow e m

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E6	1	AU=MANDELENAKI-LAMBROU K
E7	1	AU=MANDELERT
E8	1	AU=MANDELERT N
E9	1	AU=MANDELERT, N.
E10	30	AU=MANDELES S
E11	2	AU=MANDELES S.
E12	1	AU=MANDELES, M. D.

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? e au=mandelkow e m

Ref	Items	Index-term
E1	1	AU=MANDELKOW E -M
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E4	4	AU=MANDELKOW E.- M.
E5	113	AU=MANDELKOW E.-M.
E6	13	AU=MANDELKOW E.M.
E7	185	AU=MANDELKOW E-M
E8	59	AU=MANDELKOW ECKHARD
E9	192	AU=MANDELKOW EM
E10	49	AU=MANDELKOW EVA-MARIA
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E12	42	AU=MANDELKOW H

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? s e1-e11

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	151	AU=MANDELKOW E.
	4	AU=MANDELKOW E.- M.
	113	AU=MANDELKOW E.-M.
	13	AU=MANDELKOW E.M.
	185	AU=MANDELKOW E-M
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	2	AU=MANDELKOW EVA-MARIE
S6	805	E1-E11

? e au=vandermeeren m

Ref	Items	Index-term
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E5	3	AU=VANDERMEEREN M M
E6	6	AU=VANDERMEEREN M M P P
E7	26	AU=VANDERMEEREN M.
E8	1	AU=VANDERMEEREN M.A.
E9	4	AU=VANDERMEEREN M.M.P.P.
E10	3	AU=VANDERMEEREN MA
E11	17	AU=VANDERMEEREN MARC
E12	3	AU=VANDERMEEREN MMPP

Enter P or PAGE for more

? s e3-e11

	83	AU=VANDERMEEREN M
	5	AU=VANDERMEEREN M A
	3	AU=VANDERMEEREN M M
	6	AU=VANDERMEEREN M M P P
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	3	AU=VANDERMEEREN MA
	17	AU=VANDERMEEREN MARC
S7	148	E3-E11

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Set	Items	Description
S1	1305	TAU AND PHOSPHORYL? AND (MONOCLONAL OR MAB)
S2	599	RD S1 (unique items)
S3	304	S2 AND PY<1996
S4	111	S3 AND PY<1993
S5	234	E3-E9
S6	805	E1-E11
S7	148	E3-E11

? s s5 or s6 or s7

	234	S5
	805	S6
	148	S7
S8	1128	S5 OR S6 OR S7

? s s8 and tau and (monoclonal or mab)

1128	S8
127081	TAU

959154 MONOCLONAL
131828 MAB
S9 77 S8 AND TAU AND (MONOCLONAL OR MAB)
? rd s9
...examined 50 records (50)
...completed examining records
S10 33 RD S9 (unique items)
? t s10/7/all
>>>Format 7 is not valid in file 143

10/7/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

13327015 BIOSIS NO.: 200100534164
%%%Monoclonal%%% antibodies directed against the microtubule-associated
protein %%%tau%%%.
AUTHOR: %%%Mercken Marc%%%; %%%Mandelkow Eva-Maria%%%(a); %%%Vandermeeren%%%
%%% Marc%%%; Vanmechelen Eugeen; Van De Voorde Andre
AUTHOR ADDRESS: (a)Hamburg**Germany
JOURNAL: Official Gazette of the United States Patent and Trademark Office
Patents 1246 (5):pNo Pagination May 29, 2001
MEDIUM: e-file
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A %%%monoclonal%%% antibody which forms an immunological complex
with a phosphorylated epitope of an antigen belonging to human abnormally phosphorylated %%%tau%%% protein. The %%%tau%%% protein ca be obtained
from a brain homogenate, itself isolated from the cerebral cortex of a patient having Alzheimer's disease.

10/7/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

13301244 BIOSIS NO.: 200100508393
Isolated human %%%tau%%% peptide epitope which specifically binds %%%monoclonal%%% antibody AT120.
AUTHOR: %%%Vandermeeren Marc%%%(a); Vanmechelen Eugeen; %%%Mercken Marc%%%;
Van de Voorde Andre
AUTHOR ADDRESS: (a)Geel**Belgium
JOURNAL: Official Gazette of the United States Patent and Trademark Office
Patents 1246 (3):pNo Pagination May 15, 2001
MEDIUM: e-file
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: An isolated human %%%tau%%% peptide epitope which specifically
binds %%%monoclonal%%% antibody AT120 consisting of the amino acid sequence selected from the group consisting of SEQ ID Nos. 2, 3, 4, 15, 16, 17, 18, 19 and 20.

10/7/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

12551157 BIOSIS NO.: 200000304659
Isolated human %%%tau%%% peptide.
AUTHOR: %%%Vandermeeren Marc%%%(a); %%%Mercken Marc%%%; Vanmechelen Eugeen;
Van De Voorde Andre
AUTHOR ADDRESS: (a)Geel**Belgium
JOURNAL: Official Gazette of the United States Patent and Trademark Office
Patents 1230 (1):pNo pagination Jan. 4, 2000
MEDIUM: e-file
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The invention deals with isolated human %%%tau%%% peptide epitopes of SEQ ID Nos: 1 to 4, 7 and 15 to 20 which have the capability of binding AT120 %%%monoclonal%%% antibody.

10/7/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

12545308 BIOSIS NO.: 200000298810
%%%Monoclonal%%% antibodies specific for PHF-%%%tau%%%, hybridomas secreting them, antigen recognition by these antibodies and their applications.
AUTHOR: %%%Vandermeeren Marc%%%(a); Vanmechelen Eugeen; Van De Voorde Andre
AUTHOR ADDRESS: (a)Geel**Belgium
JOURNAL: Official Gazette of the United States Patent and Trademark Office
Patents 1229 (4):pNo pagination Dec. 28, 1999
MEDIUM: e-file
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Monoclonal%%% antibody AT180 secreted by the hybridoma
deposited at ECACC on Dec. 22, 1992 under No. 92122204, and %%%monoclonal%%% antibody AT270 secreted by the hybridoma deposited at
ECACC on Jul. 7, 1993 under 93070774, each of which forms an immunological complex with a phosphorylated epitope of an antigen belonging to abnormally phosphorylated %%%tau%%% protein (PHF-%%%tau%%%)
residing in the region spanning positions 143-254 with the following amino acid sequence: 143 150 NH2 - Lys Gly Ala Asp Gly Lys Thr Lys Ile - 160 Ala Thr Pro Arg Gly Ala Ala Pro Pro Gly - 170 Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile - 180 Pro Ala Lys Thr Pro Pro Ala Pro Lys Thr - 190 Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser - 200 Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly - 210 Ser Pro Gly Thr Pro Gly Ser Arg Ser Arg - 220 Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg - 230 Glu Pro Lys Lys Val Ala Val Val Arg Thr - 240 Pro Pro Lys Ser Pro Ser Ser Ala Lys Ser - 250 Arg Leu Gln Thr Ala Pro Val Pro Met Pro - Asp Leu Lys COOH with each %%%monoclonal%%% antibody specifically detecting abnormally phosphorylated %%%tau%%% protein (PHF-%%%tau%%%) in cerebrospinal fluid (CSF).

10/7/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

11850901 BIOSIS NO.: 199900097010
%%%Monoclonal%%% antibodies directed against the microtubule-associated
protein %%%tau%%%, hybridomas secreting these antibodies, antigen recognition by these %%%monoclonal%%% antibodies and their applications.
AUTHOR: %%%Vandermeeren M%%%; %%%Mercken M%%%; Vanmechelen E; Van De Voorde
A
AUTHOR ADDRESS: Geel**Belgium
JOURNAL: Official Gazette of the United States Patent and Trademark Office
Patents 1218 (3):p2174 Jan. 19, 1999

ISSN: 0098-1133
RECORD TYPE: Citation
LANGUAGE: English

10/7/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11825253 BIOSIS NO.: 199900071362
%%%Monoclonal%%% antibodies directed against the microtubule-associated
protein %%%Tau%%%, and hybridomas secreting these antibodies.
AUTHOR: %%%Vandermeeren M%%%; %%%Mercken M%%%; Vanmechelen E; De Voorde A
AUTHOR ADDRESS: Geel**Belgium
JOURNAL: Official Gazette of the United States Patent and Trademark Office
Patents 1217 (1):p493 Dec. 1, 1998
ISSN: 0098-1133
RECORD TYPE: Citation
LANGUAGE: English

10/7/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11824334 BIOSIS NO.: 199900070443
Sequential phosphorylation of %%%Tau%%%-protein by GSK-3beta and PKA at
THR212 and SER214 generates the Alzheimer-specific epitope of antibody AT100 and requires a paired helical filament-like conformation.
AUTHOR: Zheng-Fischhoefer Q; Biernat J; %%%Mandelkow E-M%%%; Illenberger S;
Godemann R; Mandelkow E
AUTHOR ADDRESS: Max-Planck-Unit Structural Mol. Biol., Notkestr. 85, D-22607 Hamburg**Germany
JOURNAL: Society for Neuroscience Abstracts 24 (1-2):p1267 1998
CONFERENCE/MEETING: 28th Annual Meeting of the Society for Neuroscience,
Part 2 Los Angeles, California, USA November 7-12, 1998
ISSN: 0190-5295
RECORD TYPE: Citation
LANGUAGE: English

10/7/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11394110 BIOSIS NO.: 199800175442
Sequential phosphorylation of %%%Tau%%% by glycogen synthase kinase-3beta
and protein kinase A at Thr212 and Ser214 generates the Alzheimer-specific epitope of antibody AT100 and requires a paired-helical-filament-like conformation.
AUTHOR: Zheng-Fischhoefer Qingyi; Biernat Jacek; Mandelkov Eva-Maria; Illenberger Susanne; Godemann Robert; %%%Mandelkow Eckhard%%%(a
AUTHOR ADDRESS: (a)Max-Planck-Unit Structural Mol. Biol., Notkestr. 85, D-22607 Hamburg**Germany
JOURNAL: European Journal of Biochemistry 252 (3):p542-552 March, 1998
ISSN: 0014-2956
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: AT100, is a %%%monoclonal%%% antibody highly specific for phosphorylated %%%Tau%%% in Alzheimer paired helical filaments. Here we
show that the epitope is generated by a complex sequence of sequential phosphorylation, first of Ser199, Ser202 and Thr205 (around the epitope of antibody AT8), next of Thr212 by glycogen synthase kinase (GSK)-3beta (a proline-directed kinase), then of Ser214 by protein kinase A (PKA). Conversely, if Ser214 is phosphorylated first it protects Thr212 and the Ser-Pro motifs around the AT8 site against phosphorylation, and the AT100
epitope is not formed. The generation of the AT100 epitope requires a conformation of %%%tau%%% induced by polyanions such as heparin, RNA or
poly(Glu), conditions which also favor the formation of paired helical filaments. The Alzheimer-like phosphorylation can be induced by brain extracts. In the extract, the kinases responsible for generating the AT100 epitope are GSK-3beta and PKA, which can be inhibited by their specific inhibitors LiCl and RII, respectively. A cellular model displaying the reaction with AT100 is presented by Sf9 insect cells transfected with %%%Tau%%%. Knowledge of the events and kinases generating the AT100 epitope in cells might allow us to study the degeneration of the cytoskeleton in Alzheimer's disease.

10/7/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10182315 BIOSIS NO.: 199698637233
Three distinct axonal transport rates for %%%tau%%%, tubulin, and other microtubule-associated proteins: Evidence for dynamic interactions of %%%tau%%% with microtubules in vivo.
AUTHOR: %%%Mercken M%%%; Fischer I; Kosik K S; Nixon R A(a
AUTHOR ADDRESS: (a)Lab. Moelcular Neuroscience, Mailman Res. Cent., McLean
Hosp., 115 Mill Street, Belmont, MA 0217**USA
JOURNAL: Journal of Neuroscience 15 (12):p8259-8267 1995
ISSN: 0270-6474
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Microtubule-associated proteins (MAPs), such as %%%tau%%%, modulate neuronal shape and process outgrowth by influencing the stability and organization of microtubules. The dynamic nature of MAP-microtubule interactions in vivo, however, is poorly understood. Here, we have assessed the stability of these interactions by investigating the synthesis and axoplasmic transport of %%%tau%%% in relation to that of tubulin and other MAPs within retinal ganglion cells of normal adult mice in vivo. Using immunoprecipitation and Western blot analysis with anti-%%%tau%%% %%%monoclonal%%% and polyclonal antibodies,
we unequivocally identified in optic axons a family of 50-60 kDa %%%tau%%% isoforms and a second 90-95 kDa %%%tau%%% family, the members
of which were shown to contain the domain of %%%tau%%% encoded by exon
4A. To measure the rates of translocation of %%%tau%%% proteins in vivo, we injected mice with 35S-methionine intravitreously and, after 6-30 d, quantitated the radiolabeled %%%tau%%% isoforms immunoprecipitated from
eight consecutive 1.1 mm segments of the nerve and optic tract and separated by electrophoresis. Linear regression analysis of protein transport along optic axons showed that the %%%tau%%% isoforms advanced
at a rate of 0.2-0.4 mm/d, and other radiolabeled MAPs, identified by their association with taxol-stabilized microtubules, moved three- to fivefold more rapidly. By contrast, tubulins advanced at 0.1-0.2 mm/d, significantly more slowly than %%%tau%%% or other MAPs. These studies establish that %%%tau%%% is not cotransported with tubulin or microtubules, indicating that associations of %%%tau%%% with microtubules
within axons are not as stable as previously believed. Our findings also reveal differences among various MAPs in their interactions with microtubules and provide evidence that assembly and reorganization of the microtubule network is an active process even after axons establish connections and fully mature.

10/7/10 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09413384 BIOSIS NO.: 199497421754

Epitope mapping of %%%monoclonal%%% antibodies to the paired helical filaments of Alzheimer's disease: Identification of phosphorylation sites in %%%tau%%% protein.
AUTHOR: Goedert Michel(a); Jakes Ross; Crowther R Anthony; Cohen Philip; Vanmechelen Eugeen; %%%Vandermeeren Marc%%%; Cras Patrick
AUTHOR ADDRESS: (a)MRC Lab. Mol. Biol., Cambridge CB2 2QH**UK
JOURNAL: Biochemical Journal 301 (3):p871-877 1994
ISSN: 0264-6021
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Tau%%% is a neuronal phosphoprotein the expression of which is developmentally regulated. A single %%%tau%%% isoform is expressed in fetal human brain but six isoforms are expressed in adult human brain, with the fetal isoform corresponding to the shortest adult isoform. Phosphorylation is also developmentally regulated, as fetal %%%tau%%% is phosphorylated at more sites than adult %%%tau%%%. In Alzheimer's disease, the six adult %%%tau%%% isoforms become hyperphosphorylated and form the paired helical filament (PHF), the major fibrous component of the neurofibrillary lesions. One way to identify phosphorylated sites in %%%tau%%% is to use antibodies that recognize phosphorylated residues within a specific amino acid sequence. We here characterize the two novel phosphorylationdependent anti-%%%tau%%% antibodies AT270 and AT180 and identify their epitopes as containing phosphorylated Thr-181 and Thr-231 respectively. With these antibodies we show that these two threonine residues are partially phosphorylated in fetal and adult %%%tau%%% and almost fully phosphorylated in PHF %%%tau%%%. This result contrasts with previous studies of Ser-202 and Ser-396 which are partially phosphorylated in fetal %%%tau%%%, unphosphorylated in adult %%%tau%%% but almost fully phosphorylated in PHF %%%tau%%%.

10/7/11 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09002362 BIOSIS NO.: 199497010732
Detection of %%%tau%%% proteins in normal and Alzheimer's disease cerebrospinal fluid with a sensitive sandwich enzyme-linked immunosorbent assay.
AUTHOR: %%%Vandermeeren Marc%%%; %%%Mercken Marc%%%; Vanmechelen Eugeen; Six Jan; Van De Voorde Andre; Martin Jean-Jacques; Cras Patrick(a
AUTHOR ADDRESS: (a)Lab. Neurobiol., Born-Bunge Foundation, Univ. Antwerp, UIA Build. T., Universiteitplein 1, B-261**Belgium
JOURNAL: Journal of Neurochemistry 61 (5):p1828-1834 1993
ISSN: 0022-3042
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Alzheimer's disease is a progressive degenerative dementia characterized by the abundant presence of neurofibrillary tangles in neurons. This study was designed to test whether the microtubule-associated protein %%%tau%%% a major component of neurofibrillary tangles, could be detected in CSF. Additionally, we investigated whether CSF %%%tau%%% levels were abnormal in Alzheimer's disease as compared with a large group of control patients. We developed a sensitive sandwich enzyme-linked immunosorbent assay using AT120, a %%%monoclonal%%% antibody directed to human %%%tau%%%, as a capturing antibody. With this technique, the detection limit for 7 was less than 5 pg/ml of CSF. Using AT8, which recognizes abnormally phosphorylated serines 199-202 in %%%tau%%%, the detection limit was below 20 pg/ml of CSF. However, with AT8, we found no immunoreactivity in CSF, suggesting that only a small fraction of CSF %%%tau%%% contains the abnormally phosphorylated AT8 epitope. Our results indicate that CSF %%%tau%%% levels are significantly increased in Alzheimer's disease. Also, CSF %%%tau%%% levels in a large group of patients with a diversity of neurological diseases showed overlap with CSF T levels in Alzheimer's disease.

10/7/12 (Item 12 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08855919 BIOSIS NO.: 199396007420
The phosphatase inhibitor okadaic acid induces a phosphorylated paired helical filament %%%tau%%% epitope in human LA-N-5 neuroblastoma cells.
AUTHOR: %%%Vandermeeren Marc%%%; Lubke Ursula; Six Jan; Cras Patrick(a
AUTHOR ADDRESS: (a)Lab. Neurobiology, Born-Bunge Foundation, Univ. Antwerp, Univ. 1, B-2610 Wilrijk**Belgium
JOURNAL: Neuroscience Letters 153 (1):p57-60 1993
ISSN: 0304-3940
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Recently, a mitogen activated protein kinase has been implicated in the generation of a phosphorylated paired helical filament (PHF) epitope recognized by the %%%monoclonal%%% antibody AT8. This epitope consists of phosphorylated serines 199 and/or 202 of the human microtubule associated protein %%%tau%%%. Theoretically, aside from abnormal kinase activity, inhibition of phosphatase activity could also be involved in the abnormal phosphorylation status of the microtubule associated protein %%%tau%%%. To investigate this, we incubated LA-N-5 neuroblastoma cells with okadaic acid, a specific inhibitor of phosphatase 2A. We found that incubating neuroblastoma cells with okadaic acid induces the abnormally phosphorylated AT8 epitope. The effect of okadaic acid is time and dose dependent and is reversible. Our findings suggest that phosphatase activity is important in the regulation of the phosphorylation state of %%%tau%%%. Phosphatases may act directly on %%%tau%%% or may influence the activity of mitogen activated protein kinase. Incubation of LA-N-5 neuroblastoma cells with okadaic acid provides a cellular model in which the generation of a well-defined PHF-%%%tau%%% epitope can be investigated.

10/7/13 (Item 13 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

08427296 BIOSIS NO.: 000094134500
%%%MONOCLONAL%%% ANTIBODIES WITH SELECTIVE SPECIFICITY FOR ALZHEIMER %%%TAU%%% ARE DIRECTED AGAINST PHOSPHATASE-SENSITIVE EPITOPES
AUTHOR: %%%MERCKEN M%%%; %%%VANDERMEEREN M%%%; LUEBKE U; SIX J; BOONS J; VAN DE VOORDE A; MARTIN J-J; GHEUENS J
AUTHOR ADDRESS: LABORATORY MOLECULAR NEUROSCIENCE AGING RESEARCH, MAILMAN RESEARCH CENTER, MCLEAN HOSPITAL, BELMONT, MASS. 02178, USA.
JOURNAL: ACTA NEUROPATHOL 84 (3). 1992. 265-272. 1992
FULL JOURNAL NAME: Acta Neuropathologica
CODEN: ANPTA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A modified form of the microtubule-associated protein %%%Tau%%% is the major component of the paired helical filaments (PHF) found in Alzheimer's disease. The characterization of these posttranslational %%%Tau%%% modifications is hindered by the lack of sufficient PHF-%%%Tau%%%-specific markers. Here we describe several %%%monoclonal%%%

antibodies, prepared by immunization with PHF, two of which showed a selective specificity for PHF-%%%Tau%%% without cross-reactivity with normal %%%Tau%%%. Epitope recognition by these two monoclonals was sensitive to alkaline phosphatase treatment. In Western blotting these %%%monoclonal%%% antibodies reacted specifically with the abnormally phosphorylated epitopes on Alzheimer's disease-associated PHF-%%%Tau%%%.

One of the new antibodies can be used for the construction of a sandwich enzyme-linked immunosorbent assay for the specific detection of PHF-%%%Tau%%% without cross-reactivity to normal %%%Tau%%% proteins.

10/7/14 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08293779 BIOSIS NO.: 000094065077
PHOSPHORYLATION-DEPENDENT EPITOPES OF NEUROFILAMENT ANTIBODIES ON %%%TAU%%%
PROTEIN AND RELATIONSHIP WITH ALZHEIMER %%%TAU%%%
AUTHOR: LICHTENBERG-KRAAG B; %%%MANDELKOW E-M%%%; BIERNAT J; STEINER B; SCHROETER C; GUSTKE N; MEYER H E; MANDELKOW E
AUTHOR ADDRESS: MAX-PLANK-UNIT FOR STRUCTURAL MOLECULAR BIOL., C/O DESY, NOTKESTRASSE 85, D-2000 HAMBURG 52, WEST GERMANY.
JOURNAL: PROC NATL ACAD SCI U S A 89 (12). 1992. 5384-5388. 1992
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have studied the phosphorylation of %%%tau%%% protein from Alzheimer paired helical filaments, of %%%tau%%% from normal human brain, and of recombinant %%%tau%%% isoforms. As a tool we used %%%monoclonal%%% antibodies against neurofilament protein that crossreact with %%%tau%%% in a phosphorylation-dependent manner. This allowed us to deduce the state of phosphorylation in normal and pathological %%%tau%%%, as well as antibody epitopes. The epitope of antibody SMI33 is at the first Lys-Ser-Pro sequence motif (residues 234-236) and requires an unphosphorylated Ser-235. Antibody SMI31 binds between Ser-396 (in the second Lys-Ser-Pro motif) and Ser-404, both of which must be phosphorylated. SMI34 has a conformational epitope that depends on the interaction between regions on either side of the microtubule-binding region; it also requires phosphorylation. The phosphorylatable serines detected by the SMI antibodies are part of Ser-Pro motifs and can be phosphorylated by a protein kinase activity that can be used to induce a paired helical filament-like state in human brain %%%tau%%% in vitro. The phosphates are incorporated in several stages that can be identified by antibody reactivity and gel shift. This sguggests a role for the phosphorylation sites in Alzheimer disease, as well as the involvement of a Ser-Pro-directed protein kinase.

10/7/15 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08224951 BIOSIS NO.: 000094025915
THE JUVENILE MICROTUBULE-ASSOCIATED PROTEIN MAP2C IS A ROD-LIKE MOLECULE
THAT FORMS ANTIPARALLEL DIMERS
AUTHOR: WILLE H; %%%MANDELKOW E-M%%%; MANDELKOW E
AUTHOR ADDRESS: MAX-PLANCK-UNIT STRUCTURAL MOLECULAR BIOLOGY, DEUTSCHES ELEKTRONEN SYNCHROTRON, NOTKESTRASSE 85, D-2000 HAMBURG 52, GER.
JOURNAL: J BIOL CHEM 267 (15). 1992. 10737-10742. 1992
FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have developed a procedure to isolate the microtubule-associated protein 2c (MAP2c), a juvenile form of MAP2 occurring in mammalian brain. The shape, size, self-association, and antibody interactions of MAP2c were studied. Monomeric MAP2c is an elongated molecule with a length approximately 48 nm, considerably shorter than the higher molecular weight forms MAP2a or b of adult brain. Two %%%monoclonal%%% antibodies whose epitopes are near the N or C terminus, respectively, are located close to the opposite ends of the MAP2c rods. This places constraints on the types of internal folding of the molecule. MAP2c self-associates into dimers and fibrous aggregates. The dimers are predominantly antiparallel and nearly in register, as judged by antibody labeling.

10/7/16 (Item 16 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08183925 BIOSIS NO.: 000094007698
THE SWITCH OF %%%TAU%%% PROTEIN TO AN ALZHEIMER-LIKE STATE INCLUDES THE
PHOSPHORYLATION OF TWO SERINE PROLINE MOTIFS UPSTREAM OF THE MICROTUBULE
BINDING REGION
AUTHOR: BIERNAT J; %%%MANDELKOW E-M%%%; SCHROETER C; LICHTENBERG-KRAAG B; STEINER B; BERLING B; MEYER H; %%%MERCKEN M%%%; VANDERMEEREN A; GOEDERT M ; MANDELKOW E
AUTHOR ADDRESS: MAX-PLANCK-UNIT STRUCTURAL MOL. BIOL., C/O DESY, NOTKESTRASSE 85, D-2000 HAMBURG 52, GER.
JOURNAL: EMBO (EUR MOL BIOL ORGAN) J 11 (4). 1992. 1593-1597. 1992
FULL JOURNAL NAME: EMBO (European Molecular Biology Organization) Journal
CODEN: EMJOD
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The paired helical filaments (PHFs) of Alzheimer's disease consist mainly of the microtubule-associated protein %%%tau%%%. PHF %%%tau%%% differs from normal human brain %%%tau%%% in that it has a higher Mr and a special state of phosphorylation. However, the protein kinase(s) involved, the phosphorylation sites on %%%tau%%% and the resulting conformational changes are only poorly understood. Here we show that a new %%%monoclonal%%% antibody, AT8, records the PHF-like state of %%%tau%%% in vitro, and we describe a kinase activity that turns normal %%%tau%%% into a PHF-like state. The epitope of AT8 is around residue 200, outside the region of internal repeats and requires the phosphorylation of serines 199 and/or 202. Both of these are followed by a proline, suggesting that the kinase activity belongs to the family of proline-directed kinases. The epitope of AT8 is nearly coincident with that of another phosphorylation-dependent antibody, TAU1 [Binder, L.I., Frankfurter, A. and Rebhun, L. (1985) J. Cell Biol., 101, 1371-1378], but the two are complementary since TAU1 requires a dephosphorylated epitope.

10/7/17 (Item 17 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08046168 BIOSIS NO.: 000093079516
AFFINITY PURIFICATION OF HUMAN %%%TAU%%% PROTEINS AND THE CONSTRUCTION OF A
SENSITIVE SANDWICH ENZYME-LINKED IMMUNOSORBENT ASSAY FOR HUMAN %%%TAU%%%
DETECTION

AUTHOR: %%%MERCKEN M%%%; %%%VANDERMEEREN M%%%; LUBKE U; SIX J; BOONS J;
VANMECHELEN E; VAN DE VOORDE A; GHEUENS J
AUTHOR ADDRESS: LABORATORY NEUROBIOLOGY, BORN BUNGE FOUNDATION, UNIVERSITY
ANTWERP, UIA, UNIVERSITEITSPLEIN 1, B-2610 WILRIJK, BELGIUM.
JOURNAL: J NEUROCHEM 58 (2). 1992. 548-553. 1992
FULL JOURNAL NAME: Journal of Neurochemistry
CODEN: JONRA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Immunoaffinity chromatography with a %%%monoclonal%%% antibody produced against bovine .%%%tau%%%. protein was used to purify .%%%tau%%% . proteins from human brain. Fifty grams of brain tissue yielded .apprx. 2 mg of pure .%%%tau%%%. proteins. The affinity-purified human .%%%tau%%% . was used to produce a high-titered rabbit anti-human .%%%tau%%%. serum. The %%%monoclonal%%% anti-.%%%tau%%%. antibody and the polyclonal rabbit anti-.%%%tau%%%. serum were then used to construct a sandwich enzyme-linked immunosorbent assay for detection of human .%%%tau%%%. proteins, with sensitivity of 1 ng/ml.

10/7/18 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07844834 BIOSIS NO.: 000092115000
DEMONSTRATION OF A NOVEL NEUROFILAMENT ASSOCIATED ANTIGEN WITH THE
NEUROFIBRILLARY PATHOLOGY OF ALZHEIMER AND RELATED DISEASES
AUTHOR: GHEUENS J; CRAS P; PERRY G; BOONS J; CEUTERICK-DE GROOTE C; LUBKE U
; %%%MERCKEN M%%%; TABATON M; GAMBETTI P L; ET AL
AUTHOR ADDRESS: DIV. NEUROPATHOL., CASE WESTERN RESERVE UNIVERSITY, 2085
ADELBERT RD., CLEVELAND, OHIO 44106-4901.
JOURNAL: BRAIN RES 558 (1). 1991. 43-52. 1991
FULL JOURNAL NAME: Brain Research
CODEN: BRREA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A %%%monoclonal%%% antibody, termed NFT200, was raised after in vitro immunization with sonicated neurofibrillary tangle (NFT)-enriched fractions prepared from Alzheimer brain. The antigen to which NFT200 is directed was expressed in the paired helical filaments of NFT in sporadic and familial Alzheimer disease (AD), in the straight filaments of NFT in AD, progressive supranuclear palsy and of Pick bodies, and the NFT in several other conditions such as Parkinson-dementia complex of Guam and subacute sclerosing panencephalitis. Granulovacuolar degeneration of AD was also labeled with NFT200. Hirano bodies and amyloid deposits in AD, as well as Lewy bodies of idiopathic Parkinson disease lacked in the antigen. The NFT200-antigen was also expressed as a phosphatase-insensitive antigen in normal neurofilaments found in spinal cord and peripheral nerve axons but was absent from the perikaryal accumulation of neurofilaments induced by aluminum intoxication. Nevertheless, immunoblot studies failed to detect the NFT200 in isolated preparations of the neurofilament proteins, MAP-2, .%%%tau%%%., ubiquitin or A4-amyloid peptide. The results indicate that the NFT200 %%%monoclonal%%% antibody is directed against a phosphatase-insensitive epitope of an axonal protein associated with neurofilaments but is labile to isolation and expressed as a stable epitope of a 200 kDa component of NFT.

10/7/19 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

10285496 Genuine Article#: 510AY Number of References: 59
Title: Specific %%%tau%%% phosphorylation sites correlate with severity of neuronal cytopathology in Alzheimer's disease
Author(s): Augustinack JC; Schneider A; %%%Mandelkow EM%%%; Hyman BT
(REPRINT)
Corporate Source: Harvard Univ,Sch Med, Massachusetts Gen Hosp, Alzheimers Res Unit,114 16th St,Rm 2009/Charlestown//MA/02129 (REPRINT); Harvard Univ,Sch Med, Massachusetts Gen Hosp, Dept Neurol,Alzheimers Unit,Charlestown//MA/02129; Max Planck Unit Struct Mol Biol,D-22607 Hamburg//Germany/
Journal: ACTA NEUROPATHOLOGICA, 2002, V103, N1 (JAN), P26-35
ISSN: 0001-6322 Publication date: 20020100
Publisher: SPRINGER-VERLAG, 175 FIFTH AVE, NEW YORK, NY 10010 USA
Language: English Document Type: ARTICLE
Abstract: Microtubule associated protein %%%tau%%% is abnormally phosphorylated in Alzheimer's disease (AD) and aggregates as paired helical filaments (PHFs) in neurofibrillary tangles (NFTs). We show here that the pattern of %%%tau%%% phosphorylation correlates with the loss of neuronal integrity. Studies using 11 phosphorylation dependent %%%tau%%% antibodies and a panel of AD cases of varying severity were evaluated in terms of three stages of neurofibrillary tangle development: (1) pre-neurofibrillary tangle, (2) intra-, and (3) extra-neuronal neurofibrillary tangles. The pretangle state, in which neurons display nonfibrillar, punctate regions in the cytoplasm, sound dendrites, somas, and nuclei, was observed especially with phosphotau antibodies TG3 (pT231), pS262, and pT153. Intraneuronal neurofibrillary tangles are homogenously stained with fibrillar %%%tau%%% structures, which were most prominently stained with pT175/181, 12E8 (pS262/pS356), pS422, pS46, pS214 antibodies. Extracellular NFTs, which contain substantial filamentous %%%tau%%%, are most prominently stained with AT8 (pS199/pS202/pT205), AT100 (pT212/pS214), and PHF-1 (pS396/pS404) antibodies, which also stain intracellular NFT. The sequence of early %%%tau%%% phosphorylation suggests that there are events prior to filament formation that are specific to particular phosphorylated %%%tau%%% epitopes, leading to conformational changes and cytopathological alterations.

10/7/20 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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09278691 Genuine Article#: 387GJ Number of References: 81
Title: Glycogen synthase kinase-3 beta phosphorylates protein %%%tau%%% and rescues the axonopathy in the central nervous system of human four-repeat %%%tau%%% transgenic mice
Author(s): Spittaels K; Van den Haute C; Van Dorpe J; Geerts H; %%%Mercken%%%
%%% M%%%; Bruynseels K; Lasrado R; Vandezande K; Laenen I; Boon T; Van Lint J; Vandenheede J; Moechars D; Loos R; Van Leuven F (REPRINT)
Corporate Source: Katholieke Univ Leuven,Ctr Human Genet, Flemish Inst Biotechnol, Expt Genet Grp,Campus Gasthuisberg O&N 06/B-3000 Leuven//Belgium/ (REPRINT); Katholieke Univ Leuven,Ctr Human Genet, Flemish Inst Biotechnol, Expt Genet Grp,B-3000 Leuven//Belgium/; Janssen Res Fdn,B-2340 Beerse//Belgium/; Katholieke Univ Leuven,Fac Med, Dept Biochem,B-3000 Leuven//Belgium/; Katholieke Univ Leuven,Dept Genet Epidemiol,B-3000 Leuven//Belgium/
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 2000, V275, N52 (DEC 29), P 41340-41349
ISSN: 0021-9258 Publication date: 20001229
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650

ROCKVILLE
PIKE, BETHESDA, MD 20814 USA
Language: English Document Type: ARTICLE
Abstract: Protein %%%tau%%% filaments in brain of patients suffering from
Alzheimer's disease, frontotemporal dementia, and other tauopathies consist of protein %%%tau%%% that is hyperphosphorylated.,The responsible kinases operating in vivo in neurons still need to be identified. Here we demonstrate that glycogen synthase kinase-3 beta (GSK-3 beta) is an effective kinase for protein %%%tau%%% in cerebral neurons in vivo in adult GSK-3 beta and GSK-3 beta x human tau40 transgenic mice; Phosphorylated protein %%%tau%%% migrates slower during electrophoretic separation and is revealed by phosphorylation-dependent anti-%%%tau%%% antibodies in Western blot analysis. In addition, its capacity to bind to re-assembled paclitaxel (Taxol(R))-stabilized microtubules is reduced, compared with protein %%%tau%%% isolated from mice not overexpressing GSK-3 beta. Co-expression of GSK-3 beta reduces the number of axonal dilations and alleviates the motoric impairment that was typical for single htau40 transgenic animals (Spittaels, K., Van den Haute, C., Van Dorpe, J., Bruynseels, K., Vandezande, K., Laenen, I., Geerts, H., Mercken, M., Sciot, R., Van Lommel, A., Loos, R., and Van Leuven, F. (1999) Am. J. Pathol. 155, 2153-2165). Although more hyperphosphorylated protein %%%tau%%% is available, neither an increase in insoluble protein %%%tau%%% aggregates nor the presence of paired helical filaments or tangles was observed. These findings could have therapeutic implications in the field of neurodegeneration, as discussed.

10/7/21 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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08251686 Genuine Article#: 262XD Number of References: 68
Title: Prominent axonopathy in the brain and spinal cord of transgenic mice overexpressing four-repeat human %%%tau%%% protein
Author(s): Spittaels K; VandenHaute C; VanDorpe J; Bruynseels K; Vandezande
K; Laenen I; Geerts H; %%%Mercken M%%%; Sciot R; VanLommel A; Loos R;
VanLeuven F (REPRINT)
Corporate Source: KATHOLIEKE UNIV LEUVEN,CTR HUMAN GENET, VLAAMS INST
BIOTECHNOL, EXPT GENET GRP/B-3000 LOUVAIN//BELGIUM/ (REPRINT);
KATHOLIEKE UNIV LEUVEN,CTR HUMAN GENET, VLAAMS INST BIOTECHNOL, EXPT
GENET GRP/B-3000 LOUVAIN//BELGIUM/; JANSSEN RES FDN,/B-2340
BEERSE//BELGIUM/; KATHOLIEKE UNIV LEUVEN HOSP,DEPT
PATHOL/LOUVAIN//BELGIUM/; KATHOLIEKE UNIV LEUVEN,DEPT GENET
EPIDEMIOL/LOUVAIN//BELGIUM/
Journal: AMERICAN JOURNAL OF PATHOLOGY, 1999, V155, N6 (DEC), P2153-2165
ISSN: 0002-9440 Publication date: 19991200
Publisher: AMER SOC INVESTIGATIVE PATHOLOGY, INC, 428 EAST PRESTON ST,
BALTIMORE, MD 21202-3993
Language: English Document Type: ARTICLE
Abstract: Mutations in the human %%%tau%%% gene cause frontotemporal dementia and parkinsonism linked to chromosome 17, Some mutations, including mutations in intron 10, induce increased levels of the functionally normal four-repeat %%%tau%%% protein isoform, leading to neurodegeneration, We generated transgenic mice that overexpress the four-repeat human %%%tau%%% protein isoform specifically in neurons. The transgenic mice developed axonal degeneration in brain and spinal cord. In the model, axonal dilations with accumulation of neurofilaments, mitochondria, and vesicles were documented. The axonopathy and the accompanying dysfunctional sensorimotor capacities were transgene-dosage related. These findings proved that merely increasing the concentration of the four-repeat %%%tau%%% protein isoform is sufficient to injure neurons in the central nervous system, without formation of intraneuronal neurofibrillary tangles. Evidence for astrogliosis and ubiquitination of accumulated proteins in the dilated part of the axon supported this conclusion. This transgenic model, overexpressing the longest isoform of human %%%tau%%% protein,
recapitulates features of known neurodegenerative diseases, including Alzheimer's disease and other tauopathies. The model makes it possible to study the interaction with additional factors, to be incorporated genetically, or with other biological triggers that are implicated in neurodegeneration.

10/7/22 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06936898 Genuine Article#: 105MY Number of References: 82
Title: Mitotic phosphorylation of %%%tau%%% protein in neuronal cell lines resembles phosphorylation in Alzheimer's disease
Author(s): Preuss U (REPRINT) ; %%%Mandelkow EM%%%
Corporate Source: UNIV BONN,INST GENET, MOL GENET SECT, ROMERSTR
164/D-53117 BONN//GERMANY/ (REPRINT); DESY,MAX PLANCK UNIT STRUCT MOL
BIOL/D-2000 HAMBURG//GERMANY/
Journal: EUROPEAN JOURNAL OF CELL BIOLOGY, 1998, V76, N3 (JUL), P176-184
ISSN: 0171-9335 Publication date: 19980700
Publisher: GUSTAV FISCHER VERLAG, VILLENGANG 2, D-07745 JENA, GERMANY
Language: English Document Type: ARTICLE
Abstract: %%%Tau%%% protein, a neuronal microtubule-associated protein is
phosphorylated on several sites when extracted from brain tissue and is a substrate for many protein kinases in vitro. In Alzheimer's disease it becomes hyperphosphorylated, notably at Ser-Pro or Thr-Pro motifs, and forms the paired helical filaments (PHFs). The increased phosphorylation ran be detected by several antibodies raised against Alzheimer %%%tau%%%. We show here that a similar type of phosphorylation can be observed in cells of neuronal origin during mitosis. Murine neuroblastoma cells (N2a) were stably transfected with htau40, the largest of the six human %%%tau%%% isoforms in the brain. We used several antibodies reporting on the state of phosphorylation of %%%tau%%% (%%%Tau%%%-1, AT8, AT180, PHF-1, and T46) and the antibody
MPM-2 that recognizes phosphorylated mitotic proteins. The results show that %%%tau%%% is in a state of low phosphorylation in interphase cells, whereas during mitosis it becomes highly phosphorylated. This behavior was also found for endogenous tan protein in human neuroblastoma cells (LAN-5). The similarity between %%%tau%%% phosphorylation in dividing neuronal cells and Alzheimer degenerating neurons may indicate that aging neurons exposed to inappropriate signals respond by an attempt to activate their machinery for regeneration.

10/7/23 (Item 5 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06805166 Genuine Article#: ZT687 Number of References: 102
Title: The endogenous and cell cycle-dependent phosphorylation of %%%tau%%%
protein in living cells: Implications for Alzheimer's disease
Author(s): Illenberger S; ZhengFischhofer QY; Preuss U; Stamer K; Baumann K
; Trinczek B; Biernat J; Godemann R; %%%Mandelkow EM%%%; Mandelkow E
(REPRINT)
Corporate Source: MAX PLANCK UNIT STRUCT MOL BIOL,/D-22603 HAMBURG//GERMANY/ (REPRINT); MAX PLANCK UNIT STRUCT MOL BIOL,/D-22603
HAMBURG//GERMANY/
Journal: MOLECULAR BIOLOGY OF THE CELL, 1998, V9, N6 (JUN), P1495-1512
ISSN: 1059-1524 Publication date: 19980600
Publisher: AMER SOC CELL BIOLOGY, PUBL OFFICE, 9650 ROCKVILLE PIKE,
BETHESDA, MD 20814

Language: English Document Type: REVIEW
Abstract: In Alzheimer's disease the neuronal microtubule-associated protein %%%tau%%% becomes highly phosphorylated, loses its binding properties, and aggregates into paired helical filaments. There is increasing evidence that the events leading to this hyperphosphorylation are related to mitotic mechanisms. Hence, we have analyzed the physiological phosphorylation of endogenous %%%tau%%% protein in metabolically labeled human neuroblastoma cells and in Chinese hamster ovary cells stably transfected with %%%tau%%%. In nonsynchronized cultures the phosphorylation pattern was remarkably similar in both cell lines, suggesting a similar balance of kinases and phosphatases with respect to %%%tau%%%. Using phosphopeptide mapping
and sequencing we identified 17 phosphorylation sites comprising 80-90% of the total phosphate incorporated. Most of these are in SP or TP motifs, except S214 and S262. Since phosphorylation of microtubule-associated proteins increases during mitosis, concomitant with increased microtubule dynamics, we analyzed cells mitotically arrested with nocodazole. This revealed that S214 is a prominent phosphorylation site in metaphase, but not in interphase. Phosphorylation of this residue strongly decreases the %%%tau%%% -microtubule interaction in vitro, suppresses microtubule assembly, and may be a key factor in the observed detachment of %%%tau%%% from microtubules during mitosis. Since S214 is also phosphorylated in Alzheimer's disease %%%tau%%%, our results support the view that reactivation of the cell cycle machinery is involved in %%%tau%%% hyperphosphorylation.

10/7/24 (Item 6 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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04163215 Genuine Article#: RJ792 Number of References: 41
Title: DIFFERENTIAL SENSITIVITY PROTEOLYSIS BY BRAIN CALPAIN OF ADULT
HUMAN-%%%TAU%%%, FETAL HUMAN-%%%TAU%%% AND PHF-%%%TAU%%%
Author(s): %%%MERCKEN M%%%; GRYNSPAN F; NIXON RA
Corporate Source: MCLEAN HOSP,MAILMAN RES CTR,MOLEC NEUROSCI LABS,115 MILL
ST/BELMONT//MA/02178; HARVARD UNIV,SCH MED,DEPT PSYCHIAT/BELMONT//MA/02178; HARVARD UNIV,SCH MED,PROGRAM
NEUROSCI/BELMONT//MA/02178
Journal: FEBS LETTERS, 1995, V368, N1 (JUL 10), P10-14
ISSN: 0014-5793
Language: ENGLISH Document Type: ARTICLE
Abstract: Reduced turn-over of %%%tau%%% by calpains is a possible mechanism to facilitate the incorporation into paired helical filaments (PHFs) in Alzheimer's disease. The present study shows that the differently phosphorylated fetal tan isoforms are all rapidly proteolysed to an equal extent by human brain m-calpain. This result argues against the hypothesis that this type of fetal phosphorylation is involved in reducing %%%tau%%% turn-over by calpain in Alzheimer's disease. Adult and fetal %%%tau%%% fragments in vitro generated by m-calpain, but not trypsin, cathepsin D or chymotrypsin resemble the post-mortem in situ degradation patterns, suggesting a possible role for calpains in %%%tau%%% metabolism in vivo. Tan incorporated into PHFs was considerably more resistant to proteolysis by calpain which can help to explain the persistence of these structures in Alzheimer's disease.

10/7/25 (Item 7 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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03321197 Genuine Article#: NV430 Number of References: 66
Title: PHOSPHORYLATION OF MICROTUBULE-ASSOCIATED PROTEINS MAP2A,B AND MAP2C
AT SER136 BY PROLINE-DIRECTED KINASES IN-VIVO AND IN-VITRO
Author(s): BERLING B; WILLE H; ROLL B; %%%MANDELKOW EM%%%; GARNER C;
MANDELKOW E
Corporate Source: DESY,MAX PLANCK GESELL,STRUCT MOLEC BIOL RES UNIT,NOTKESTR 85/D-22603 HAMBURG//GERMANY/; DESY,MAX PLANCK
GESELL,STRUCT MOLEC BIOL RES UNIT/D-22603 HAMBURG//GERMANY/; UNIV
HAMBURG,CTR MOLEC NEUROBIOL/W-2000 HAMBURG//GERMANY/
Journal: EUROPEAN JOURNAL OF CELL BIOLOGY, 1994, V64, N1 (JUN), P120-130
ISSN: 0171-9335
Language: ENGLISH Document Type: ARTICLE
Abstract: The microtubule-associated protein 2 (MAP2) and its juvenile splicing variant MAP2c contain a phosphorylation site at Ser136 which is part of a Ser-Pro motif. This site lies within the N-terminal region common to MAP2b and MAP2c. It has been mapped by site-directed mutagenesis of recombinant MAP2c and by a %%%monoclonal%%% antibody
AP18 whose epitope contains the phosphorylated Ser136. In vitro this site is phosphorylated by proline-directed kinases such as MAP kinase, GSK-3, or members of the cdk family, but not by other kinases such as PKA, PKC, or CaMK-II. MAP2a,b or MAP2c isolated hom brain is found to be endogenously phosphorylated at Ser136. After microinjection into several cell lines dephosphorylated MAP2 isoforms or recombinant MAP2c become also phosphorylated at Ser136 in vivo. Injection of MAP2a,b or MAP2c into living cells causes reorganization of microtubules, including bundle formation. This effect is independent of the phosphorylation at Ser136. The specificity of the phosphorylation reaction provides a tool for analyzing the role and posttranslational processing of MAP2 in nerve cell development.

10/7/26 (Item 8 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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03314124 Genuine Article#: NV861 Number of References: 71
Title: MICROTUBULE-ASSOCIATED PROTEIN-%%%TAU%%% EPITOPES ARE PRESENT IN
FIBER LESIONS IN DIVERSE MUSCLE DISORDERS
Author(s): LUBKE U; SIX J; VILLANOVA M; BOONS J; %%%VANDERMEEREN M%%%;
CEUTERICK C; CRAS P; MARTIN JJ
Corporate Source: UNIV INSTELLING ANTWERP,BORN BUNGE FDN,NEUROBIOL LAB,UNIV
PL 1/B-2610 WILRIJK//BELGIUM/; UNIV INSTELLING ANTWERP,BORN BUNGE
FDN,NEUROBIOL LAB/B-2610 WILRIJK//BELGIUM/; UNIV INSTELLING
ANTWERP,BORN BUNGE FDN,NEUROPATHOL LAB/B-2610 WILRIJK//BELGIUM/;
INNOGENET/GHENT//BELGIUM/; UNIV SIENA,NEUROPATHOL LAB/I-53100
SIENA//ITALY/
Journal: AMERICAN JOURNAL OF PATHOLOGY, 1994, V145, N1 (JUL), P175-188
ISSN: 0002-9440
Language: ENGLISH Document Type: ARTICLE
Abstract: The microtubule-associated protein %%%tau%%% is a major cytoskeletal protein involved in the neurofibrillary tangles of Alzheimer's disease. Although %%%tau%%% is predominantly a neuronal protein, it has been demonstrated in glia and other nonneuronal cells. We describe the presence of microtubule-associated protein %%%tau%%%
epitopes in various muscle fiber lesions in oculopharyngeal and Becker muscular dystrophy, dermatomyositis, central core disease, neurogenic atrophy, and in the recovery phase of an attack of malignant hyperthermia. Western blot demonstrated a 100- to 110-kd %%%tau%%% -immunoreactive protein probably corresponding to 'big %%%tau%%%' as described in peripheral nerves. %%%Tau%%% immunoreactivity in muscle fiber lesions usually co-localized with tubulin, although electron microscopy failed to show an increase in microtubules. %%%Tau%%% and tubulin reactivity also correlated with the presence of desmin and vimentin epitopes. Possible explanations for the presence of %%%tau%%% are briefly discussed.

10/7/27 (Item 9 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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03225554 Genuine Article#: NN763 Number of References: 63
Title: A SEQUENCE OF CYTOSKELETON CHANGES RELATED TO THE FORMATION OF
NEUROFIBRILLARY TANGLES AND NEUROPIL THREADS
Author(s): BRAAK E; BRAAK H; %%%MANDELKOW EM%%%
Corporate Source: UNIV FRANKFURT,ZENTRUM MORPHOL,THEODAR STERN KAI
7/D-60590 FRANKFURT//GERMANY/; DESY,MAX PLANCK GESELL,ARBEITSGRP
STRUKTURELLE MOLEK BIOL/D-22607 HAMBURG//GERMANY/
Journal: ACTA NEUROPATHOLOGICA, 1994, V87, N6 (JUN), P554-567
ISSN: 0001-6322
Language: ENGLISH Document Type: ARTICLE
Abstract: Frontal sections of the temporal lobe including the transentorhinal/entorhinal region, amygdala, and/or hippocampus from human adult brains are studied for cytoskeleton changes using immunostaining with the antibodies AT8 and Alz-50 and selective silver impregnation methods for neurofibrillary changes of the Alzheimer type. For the purpose of correlation, the two methods are carried out one after the other on the same section. Layer pre-alpha in the transentorhinal/entorhinal region harbours nerve cells which are among the first nerve cells in the entire brain to show the development of neurofibrillary changes. This presents the opportunity for study of both early events in the destruction of the cytoskeleton in individual neurons, and to relate changes which occur in the neuronal processes in the absence of alterations in their immediate surroundings to those happening in the soma. Immunoreactions with the AT8 antibody in particular reveal a clear sequence of changes in the neuronal cytoskeleton. Group 1 neurons present initial cytoskeleton changes in that the soma, dendrites, and axon are completely marked by granular AT8 immunoreactive material. These neurons appear quite normal and turn out to be devoid of argyrophilic material when observed in silver-stained sections. Group 2 neurons show changes in the cellular processes. The terminal tuft of the apical dendrite is replaced by tortuous varicose fibres and coarse granules. The distal protions of the dendrites are curved and show appendages and thickened portions. Intensely homogeneously immunostained rod-like inclusions are encountered in these thickened portions and in the soma. A number of these rod-like inclusions are visible after silver staining, as well. Group 3 neurons display even more pronounced alterations of their distal - most dendritic portions. The intermediate dendritic parts lose immunoreactivity, but the soma is homogeneously immunostained. Silver staining reveals in most of the distal dendritic parts neuropil threads, and in the soma a classic neurofibrillary tangle. Group 4 structures are marked by accumulations of coarse AT8-immunoreactive granules. Silver staining provides evidence that the fibrillary material has become an extraneuronal, ''early'' ghost tangle. Finally, group 5 structures present ''late'' ghost tangles in silver-stained sections but fail to demonstrate AT8 immunoreactivity. It is suggested that the altered %%%tau%%% protein shown by the antibody AT8 represents an early cytoskeleton change which eventually leads to the formation of argyrophilic neurofibrillary tangles and neuropil threads.

10/7/28 (Item 10 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01462227 Genuine Article#: HA732 Number of References: 52
Title: SPECIFIC %%%MONOCLONAL%%%-ANTIBODIES AGAINST NORMAL
MICROTUBULE-ASSOCIATED PROTEIN-2 (MAP2) EPITOPES PRESENT IN ALZHEIMER
PATHOLOGICAL STRUCTURES DO NOT RECOGNIZE PAIRED HELICAL FILAMENTS
Author(s): SIX J; LUBKE U; %%%MERCKEN M%%%; %%%VANDERMEEREN M%%%; CEUTERICK
C; VANDEVOORDE A; BOONS J; GHEUENS J
Corporate Source: UNIV INSTELLING ANTWERP,BORN BUNGE FDN,NEUROBIOL
LAB,UNIVERSITEITSPLEIN 1/B-2610 WILRIJK//BELGIUM/; UNIV INSTELLING ANTWERP,NEUROPATHOL LABS/B-2610WILRIJK//BELGIUM/; INNOGENETICS/GHENT//BELGIUM/
Journal: ACTA NEUROPATHOLOGICA, 1992, V83, N2 (JAN), P179-189
Language: ENGLISH Document Type: ARTICLE
Abstract: We have developed %%%monoclonal%%% antibodies that detect normal microtubule-associated protein-2 (MAP2) epitopes in routinely fixed, paraffin-embedded tissue. The somatodendritic distribution of MAP2 in bovine and human nervous tissue was confirmed with several of these antibodies. Furthermore, some of these antibodies immunohistochemically labeled certain pathological structures in Alzheimer brain, especially neurites in senile plaques. Electron microscopic observations, however, indicate that these MAP2 epitopes are not located in the Alzheimer paired helical filaments themselves, but in amorphous granular structures coexistent with them. While the pathological nature of these structures is undetermined, they may represent artefactual modifications of normal cytoskeletal components.

10/7/29 (Item 1 from file: 73)
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07742031 EMBASE No: 1999224250
Phosphorylation of %%%tau%%% protein by recombinant GSK-3beta: Pronounced phosphorylation at select Ser/Thr-Pro motifs but no phosphorylation at Ser262 in the repeat domain
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FEBS Letters (FEBS LETT.) (Netherlands) 1999, 454/1-2 (157-164)
CODEN: FEBLA ISSN: 0014-5793
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NUMBER OF REFERENCES: 60

Glycogen synthase kinase-3beta (GSK-3beta) has been described as a proline-directed kinase which phosphorylates %%%tau%%% protein at several sites that are elevated in Alzheimer paired helical filaments. However, it has been claimed that GSK-3beta can also phosphorylate the non-proline-directed KXGS motifs in the presence of heparin, including Ser262 in the repeat domain of %%%tau%%%, which could induce the detachment of %%%tau%%% from microtubules. We have analyzed the activity of recombinant GSK-3beta and of GSK-3beta preparations purified from tissue, using two-dimensional phosphopeptide mapping, immunoblotting with phosphorylation-sensitive antibodies, and phosphopeptide sequencing. The most prominent phosphorylation sites on %%%tau%%% are Ser396 and Ser404 (PHF-1 epitope), Ser46 and Thr50 in the first insert, followed by a less efficient phosphorylation of other Alzheimer phosphoepitopes (antibodies AT-8, AT-270, etc). We also show that the non-proline-directed activity at KXGS motifs is not due to GSK-3beta itself, but to kinase contaminations in common GSK-3beta preparations from tissues which are activated upon addition of heparin. Copyright (C) 1999 Federation of European Biochemical Societies.

10/7/30 (Item 2 from file: 73)
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06229171 EMBASE No: 1995265576
Alteration in %%%tau%%% antigenicity and electrophoretic migration by PKCalpha under cell-free conditions
Cressman C.M.; %%%Mercken M.M.%%%; Shea T.B.
Cen Cell Neurobiol Neurodegen Res, Department of Biological Sciences, University of Massachusetts,Lowell, MA 01854 United States
Neuroscience Research Communications (NEUROSCI. RES. COMMUN.) (United

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CODEN: NRCOE ISSN: 0893-6609
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LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

Previous studies have demonstrated that PKC is capable of phosphorylating %%%tau%%% under cell-free conditions. However, PKC did not induce the 'AD-like' alterations in %%%tau%%% antigenicity and electrophoretic migration that have been reported for several other kinases. In the present study, we observed that short-term (30 min) incubation of purified human brain %%%tau%%% with PKCalpha indeed did not induce significant alterations
in %%%tau%%% antigenicity or electrophoretic migration. By contrast, extended (20 hr) incubation with PKCalpha altered %%%tau%%% migration to
produce a form that migrated at 68 kDa on SDS-gels, significantly increased its reactivity with ALZ-50, and induced the de novo appearance of the PHF-1 epitope. These findings, taken together with previous studies, underscore the potential involvement of PKC in modulation of %%%tau%%% function, especially during neuronal development and neurodegeneration.

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DIALOG(R)File 73:EMBASE
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05414892 EMBASE No: 1993182991
The abnormal phosphorylation of %%%tau%%% protein at Ser-202 in Alzheimer
disease recapitulates phosphorylation during development
Goedert M.; Jakes R.; Crowther R.A.; Six J.; Lubke U.; %%%Vandermeeren%%%
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Proceedings of the National Academy of Sciences of the United States of America (PROC. NATL. ACAD. SCI. U. S. A.) (United States) 1993, 90/11 (5066-5070)
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DOCUMENT TYPE: Journal; Conference Paper
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

%%%Tau%%% is a neuronal phosphoprotein whose expression is developmentally regulated. A single %%%tau%%% isoform is expressed in fetal
human brain but six isoforms are expressed in adult brain, with the fetal isoform corresponding to the shortest of the adult isoforms. Phosphorylation of %%%tau%%% is also developmentally regulated, as fetal %%%tau%%% is phosphorylated at more sites than adult %%%tau%%%. In Alzheimer disease, the six adult %%%tau%%% isoforms become abnormally phosphorylated and form the paired helical filament, the major fibrous component of the characteristic neurofibrillary lesions. We show here that Ser-202 (in the numbering of the longest human brain %%%tau%%% isoform) is
a phosphorylation site that distinguishes fetal from adult %%%tau%%% and we
identify it as one of the abnormal phosphorylation sites in Alzheimer disease. The abnormal phosphorylation of %%%tau%%% at Ser-202 in Alzheimer
disease thus recapitulates normal phosphorylation during development.

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12183691 PASCAL No.: 95-0398612
Neuronal kinase stimulation leads to aberrant %%%tau%%% phosphorylation
and neurotoxicity. Commentaries
The cytoskeleton and Alzheimer's disease
NUYDENS R; DE JONG M; NUYENS R; CORNELISSEN F; GEERTS H; AVILA J comment;
%%%MANDELKOW E M%%% comment
Janssen res. foundation, dep. cellular physiology life sci., 2340 Beerse, Belgium
Schmitt symposium (Rochester NY USA) 1994-05-21
Journal: Neurobiology of aging, 1995, 16 (3) 465-477
ISSN: 0197-4580 CODEN: NEAGDO Availability: INIST-20387; 354000051039660210
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Country of Publication: USA
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NUYDENS, R., M. DE JONG, R. NUYENS, F. CORNELISSEN AND H. GEERTS.
Neuronal kinase stimulation leads to aberrant %%%tau%%% phosphorylation and
neurotoxicity. NEUROBIOL AGING 16(3) 465-477, 1995.-
Neurofibrillary
tangles in Alzheimer's disease brain consist mainly of abnormally phosphorylated %%%tau%%% proteins organised in paired helical filaments.
Induction of %%%tau%%% phosphorylation in living neurons by hyperstimulation is monitored by specific %%%monoclonal%%% antibodies, such
as AT-8 and PHF-1. By quantitative immunocytochemistry, we show that aberrant phosphorylation at the Ser199/Ser202 epitope (AT-8) and at the Ser
396 epitope (PHF-I) are moderately induced, proportionally to the degree of kinase stimulation. Whereas AT8 expression is prominent after 48 h, cell death becomes significant at 72 h and is related to the degree of stimulation and the expression level of aberrant %%%tau%%% phosphorylation.
Time-lapse videomicroscopy of individual neuroblastoma cells suggest that hyperstimulation leads to a form of morphological over-differentiation. Immediately before cell death, some cells tend to display some features of mitosis. The data suggest a strong correlation between the expression of specific PHF-epitopes and subsequent cell death. The extended time scale of toxicity in this model may be appropriate to study in more detail the steps leading to aberrant phosphorylation associated neurotoxicity.

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DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
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09735631 Genuine Article#: AT454 Number of References: 37
Title: %%%TAU%%%-PROTEIN BECOMES LONG AND STIFF UPON PHOSPHORYLATION -
CORRELATION BETWEEN PARACRYSTALLINE STRUCTURE AND DEGREE OF
PHOSPHORYLATION
Author(s): HAGESTEDT T; LICHTENBERG B; WILLE H; %%%MANDELKOW EM%%%;
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